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(54) Title: BIALLELIC MARKERS

(57) Abstract

The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.

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BIALLELIC MARKERS

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; WO90/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., WO 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include β -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater

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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a
5 polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays
10 employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for
15 their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to
20 both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

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SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION

DEFINITIONS

- An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.
- Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.
- Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).
- As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 5 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with 15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same 20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site 25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include 30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

II. Analysis of Polymorphisms

A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For
5 example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); *PCR* (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988),
20 transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence
25 amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the
amplification products in a ratio of about 30 or 100 to 1, respectively.

30 B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

3. Allele-Specific Primers

5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in
10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows
15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of
20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of
25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,
30 1988)).

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5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with ~ polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

$p(ID)$ is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote: $p(AA) = x^2$
- Homozygote: $p(BB) = y^2 = (1-x)^2$
- Single Heterozygote: $p(AB) = p(BA) = xy = x(1-x)$
- Both Heterozygotes: $p(AB+BA) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity $p(ID)$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

$$25 \quad p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$$

In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(ID)$ and $p(exc)$.

The cumulative probability of identity ($\text{cum } p(ID)$) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

$$\text{cum } p(ID) = p(ID1)p(ID2)p(ID3) \dots p(IDn)$$

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The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5 If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10 B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15 Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20 If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child
25 attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- 30 The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3})\dots p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of
5 individuals who have been tested for the presence or
absence of a phenotypic trait of interest and for
polymorphic markers sets. To perform such analysis, the
presence or absence of a set of polymorphisms (i.e. a
polymorphic set) is determined for a set of the
10 individuals, some of whom exhibit a particular trait, and
some of which exhibit lack of the trait. The alleles of
each polymorphism of the set are then reviewed to determine
whether the presence or absence of a particular allele is
associated with the trait of interest. Correlation can be
15 performed by standard statistical methods such as a χ^2 -
squared test and statistically significant correlations
between polymorphic form(s) and phenotypic characteristics
are noted. For example, it might be found that the
presence of allele A1 at polymorphism A correlates with
20 heart disease. As a further example, it might be found
that the combined presence of allele A1 at polymorphism A
and allele B1 at polymorphism B correlates with increased
milk production of a farm animal.

Such correlations can be exploited in several ways. In
25 the case of a strong correlation between a set of one or
more polymorphic forms and a disease for which treatment is
available, detection of the polymorphic form set in a human
or animal patient may justify immediate administration of
treatment, or at least the institution of regular
30 monitoring of the patient. Detection of a polymorphic form
correlated with serious disease in a couple contemplating a
family may also be valuable to the couple in their
reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijkpn} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record; μ is an overall mean; YS_i is the effect common to all cows calving in year-season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms; PE_n is permanent environmental effect common to all records of cow n ; a_n is effect of animal n and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and e_p is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-

5 segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the

10 odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction θ , versus the situation in which the two are not linked, and thus segregating independently (Thompson &

15 Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (θ),

20 ranging from $\theta = 0.0$ (coincident loci) to $\theta = 0.50$ (unlinked). Thus, the likelihood at a given value of θ is: probability of data if loci linked at θ to probability of data if loci unlinked. The computed likelihoods are usually expressed as the \log_{10} of this ratio (i.e., a lod

25 score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod

30 scores for differing values of θ (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate
5 of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV. Modified Polypeptides and Gene Sequences

20 The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or
5 other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate
10 promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host
15 sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include
20 fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as
25 *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing
30 includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby, 5 *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is 10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene 15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating 20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292 25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and
5 antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to
10 corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A*
15 *Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of
20 immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

V. Kits

25 The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific
30 oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

15 EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference
25 sequences of the fragments shown in the Table, column 1. The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three

10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and
5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
						TGTGAACTCCACTTGAAGCCAAAGAAAGAACTCACACTTAAACACATGCCAGTTGGGAAGGTCT
						GAAACTCAGTGCATAATAGGAACACTTGAGACTAATGAAAGAGAGAGTTGAGACCAATCTTTATTT
						GTACTGGCCAAATACTGAATAACAGTTGAAGGAAAGACATTGGAAAAAGCTTTTGAGGATAATGT
WI-7070	226	C	T	---	---	TACTAGACTTTATGCCATGGTCTTTC/TJAGTTTAAATGCTGTCTCTGTCTG
						AAGCATTGACGTAACATCTCAGAGGTTATTTGCATGGATTGACTCCTGGGACAAAAGGAC[G/C]AA
						AAACACTCTTCTGTGGATATCTGTGCAGATAGATGACCCAAAGATCAGATGCTACCCAGATGTGTTT
						GATAATACATAAGCCCTAGGATTTAGATACAATCTTGAAGAAACTGAGACAGATAAATCTGAATT
WI-10744	61	G	C	---	---	AAATGAGGTAAAGTTTCAGGCACTCA
						GGGCAAAATACCAGCAAAAAGTCAAAATACCAGCATCAAAAGTCAGGTGCAAGGAGGTAGAACA
						TTACAGTAACATATGTCATCTTTTGTATATTAGTATTATCTGCCCAATGCCCTAGAAAT[C/T]JAGTG
						GGTCCCTAATAGTTATTAGTCTTTTCTCCTCTTCTCACTCTCTGAATTTATTTTATACTTAA
WI-9975	126	C	T	---	---	GGGATTAGTTACCACCAAAATGTATGTATCAATTTGATTTACTGAA
						GCTAGGTTTGTCTGTCTGCTCTCACTAGACTGAGATGACTTGATTACAGTAATCCCTATGT
						GATGTAACATAGTCTAGACCTTCCCTCTCCGCAATCCAGCTCCAGGTTTCAGAAAGTATGCCACAC
						TCAACCTTCTCTCCAGTTCATCTGTATTAAATTTCTCCCATATTAATTCAAAAGGAGTGGACAGGT
WI-8010	247	G	T	---	---	CCCTGGCTGAAAGAAATAAGAGATCCCAAGGGTGGGG[G/T]CTT
						GCCGGCCTATCTTTAAATTTAACTTGATCTTTGGTGTCTTCCATCTCCTAGGATTCGCCCTATAAT
						CTTTGTCTGTCTGTAG[C/T]JATTACCTGATTTCTAGCTTTTGATACACAAGGCTGATGGCTCACAATGT
						AGTAGTGCCAAATCTTCAGGTCTCTTTGAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA
WI-5222b	85	G	C	---	---	TCTCGACTCTATAACAACCTCCAACAGAA
						GCCGGCCTATCTTTAAATTTAACTTGATCTTTGGTGTCTCCATCCTA[G/C]JGATTCGCCCTAT
						AATCTTTGTCTGTCTGTAGATTACCTGATTTCTACTTTTGATACACAAGGCTGATGGCTCACAATGT
						AGTAGTGCCAAATCTTCAGGTCTCTTTGAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA
WI-5222	52	G	C	---	---	TCTCGACTCTATAACAACCTCCAACAGAA
						TATGCACTTCCACAAAAGCGATATAATTTAAAAGTTTTTTCATTAGAAATAAATGTATAAAAATAA
						ATATGTTATTATAGGCATTTATTACTAACTATAGTCTTCTTGGAAGGAACACCCAAACCAATACTT
						ATAAAGTACATGTAATTTATAGTAACATATTTTACTATATACATATGGAATAATCATATTTCTCACA
WI-8007	242	C	A	---	---	GAAAGCTGAACAGACATTCACAGGATACGACTGTGGAC[C/A]JAGTGTCTG
						TCAGTTGCAAAAATGCTGCCATAAACATGCTTTGCTTATCTCTGTCATATGATGTGTTTTGTAG
						TCTATATTCACACATATGAGTGAAATTT[C/T]JGGGGCATGGGAATACATCTTTATGAGACATTGA
						ACTGCTCACCACACTATCATAGTATCCATTTAAACAGACCAACAATGTATAAGAAATCCCTTTGTTTAC
WI-9823	97	C	T	---	---	ATGCTTTCCAATCTGATTTGTATGACTATTGTATGCACAGTTGGATCACC

WI-9651b	105 A T ---	---	TCCTACATTCATGGACAACCTCCATGCCCTTTCACATGCTGATCCCTCCTCTGGAATTCCTTCCT ACTGTCTCATGTACAAATTTCTGCTGCTCTTCA/ATGGGCGAGCTTGCAAGCCTCCCTTTAGAC ACCTACAGGTACAGCCGACCATGCTACCTACCTCCATGCGAGCTGCCAGGGACCTTATAGGCTCTG TCCTTAAACCTGTATGGTATATTAATCCTTGGTGTGAATGCTCTC
WI-9651	139 T C ---	---	TCCTACATTCATGGACAACCTCCATGCCCTTTCACATGCTGATCCCTCCTCTGGAATTCCTTCCT ACTGTCTCATGTACAAATTTCTGCTGCTCTTCAAGGGCGAGCTTGCAAGCCTCCCTTTAGACACCT CTTACAGGTACAGCCGACCATGCTACCTACCTCCATGCGAGCTGCCAGGGACCTTATAGGCTCTGT CTTAAACCTGTATGGTATATTAATCCTTGGTGTGAATGCTCTC
WI-7676b	309 A C ---	---	GTGACCTTCCTGCAGCGTGAGATGGACATCCTTGTCTGGGAGCTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAAAGGTAGATGGGAGGGTCTGTGTGAAGGG GCCGGCTCTCTGGTGGCTGCTGGTTCAGGGGCGAGGAAGCTGTGGACTGCAGCTTCTGCTGGTGC TCCCCCGTCTCTGGAGGCAGTATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139 C T ---	---	GTGACCTTCCTGCAGCGTGAGATGGACATCCTTGTCTGGGAGCTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAAAGGTAGATGGGAGGGTCTGTGTGAAGGG GC/ATGGCTTCTTGGTGGCTGCTGGTTCAGGGGCGAGGAAGCTGTGGACTGCAGCTTCTGCTG GTGCTCCCCCTCTCTGGAGGCAGTATAGGAGAGAGAGCAAGGATT
WI-10072	105 G A ---	---	CATTATCTGTCTGGTCTGTTCAATTCACCTTCTCTCTCCAAAGAGGATATTTAAGCATCATTT CATCTGGCCCTTTTGGATTTTGAATATTTTGTG/ATGACTCTTATGCACATGATAAATTTGTTA TGTGTCTCTTATCTTATCTTTTGTATAGGAGTTTGGCCATGACCCCTTATGAGGAGAAAAGGGA TCACCCCTTTTGGCTCTACAACTTATAGATATTTAAATATCTTT
WI-9986	42 T C ---	---	TTGGTGTGAATCAGAAATATAGGAAAATAAGACAATTTGAATTA/CJGTACCCCGAGGAAACAAGAG CCCTGCACCTTGACTCCAAAGGAGTTCTATTTCTGGCTGTTCCAGACTTTATTGTATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCTGTATCCAGGGTAGTACTCACAAACAATGTCA ATATCAATAGCATGCATATGGGGTGTGGATTCTTAGAACTTATTGCAATT
WI-7041	174 C A ---	---	GTCTATTGCAGGAGAAACGTCCCTTGGCACTCCCACTCTCATCAGGCAAGTGAGGACTGGCCAGA GGGCTGCACATGCAAACTCCAGTCCCTGCTCAGAGAGCTGAAAAGGGTCCCTCGGTCTTTTATTT CAGGGCTTGCATGCGCTTATTOOCCCTCTGCCCTCTC/ATCCACCTTCTTTGGAGCAAGGAGATGC AGCTGATTGTGTAAACAGCTCATTTGTACAGTGTCTGTATGTAATAA
WI-7224	134 T C ---	---	ATAACCCCTTGTGTATGTATCACCACCTCACTAATTAATCAACTTATGTGCTATCAGATATCCTCTCT ACCCTCACGTTATTTGAAGAAAATCCTAAACATCAAAATCTTTTCCATCCATAAAAATGTCAGCATTT /CJATTAATAAACAAATACTTTTAAAGAAACATAGGACACATTTTCAAAATTAATAAAAATAAAG GCATTTAAGGATGGCTGTGATTATCTTTGGGAAGCAGAGTATTCATGCTAG

WI-10826	132 A C ---	---	TCTATTGCAATTCACAGTAGCCCATGAAGTAGGTATAACAGCCTCTATTTAAACATGAGAAGAT GGAGGCCTTTTCCAAATGGACTAAGTAATGTGCTCAGGTTTCTTAAGCAAGACCTGCAJAG JCCCTGGCTTCTGACTCCAAAGCTTATCCCTTCTCATGCTGTGCTCAGCCAGGACCCCATGCGCA GAAAGCCAGCCTCTCCATCCCCAC
TIGR- A004S25	145 G A ---	---	AGATCTGCCATTAGTATTATTCCTTTGAAGATACCTTTGGAGATTCAITTTCTTGAGTGGCACTGCAT GCTCATTAGTGAAACCTTGTTGGGTATAGAAATGGAATGGAGATTTCAACAGCTTTGCTGAAAC TGACTTTGG[G/G]ACTCCAGACTTCACTGTCTTAGGCAATGAAACCATCACCTGGTTTGCACTTCTC ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24 A T ---	---	AAACACACAGAATCATCAAAAGCAC[A/T]ATCTGTGTTTGAGATAAATGATAGTCTGAGTCACCTATG TAAGAAGTAACCTGTAATAGTAGGATAGTATTATCATTTCTCTGTAAATAGATTACCTCTCAGCAAT TGGTCTGTTTTCATCTATGGAACCTCTCCGTACTGTAAATTTCTATGGAACCTCCCATACTGT AATTGGACAGTTTGGTTCCAC
WI-4687	121 G T ---	---	TAGTATGTCACGTCCCATGGTAAGGACTTTGATCACTAGGAATAAGAACACTTTGAATGGTCTTGTC TTTCAATAAAAGAGTGACATGATTGAACATGTGTTTATAGATAAAGGGCACTT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAGATTAAAGGAAGATCAGGAAGAAAGTAGCAATGGGAATGAAAAATAG GAGCCCTGAGATCCACTGGATAATCTAAAAACCAAGAGAAAGAACTTTGAT
WI-4719b	107 T G ---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTAAGGCTAGTGTGGGTGAGCGGATT ATGCTGACGCCATGGGTTCATAAGTGACTTGAGAGTT[G/G]ACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGATTCATTCAACAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCCTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-4719	70 G A ---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTAAGGCTAGTGTGGGTGAGCGGATT AT[G/A]TCTGACGCCATGGGTTCATAAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGATTCATTCAACAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCCTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-9484b	216 G C ---	---	TCAACACGCTTTTATGCCCACCTTCTGGCTCCCTCGTCCAGCAAGATTCCTACCTCTTACCCCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTCTCCTCTGCACACTGCCAAGT TAAAGAAACCCCTGCTTGTCTGGAGAGGGAGGGCCAGACAGGGAGGAATCAAGGGCATGTATGGCTC AGTCCCACTTCT[G/G]ACTGCAGAGTATAGGGACCGGGTTCCAAACCTT
WI-9484	178 G A ---	---	TCAACACGCTTTTATGCCCACCTTCTGGCTCCCTCGTCCAGCAAGATTCCTACCTCTTACCCCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTCTCCTCTGCACACTGCCAAGT TAAAGAAACCCCTGCTTGTCTGGAGAGGGAGGGCCAGACAGG[G/G]AGGAAATCAAGGGCATGTATG GCTCAGTCCCACTTCTGACTGCAGAGTATAGGGACCGGGTTCCAAACCTT

WI-7330	207	C T ---			AGGATGGAAGGAGACACGGGGCAGGGAGAACTCTCTTCTGCTAAATCGATAGGAGTCAGTTTGTCT TAAATGCTGACTACAGCCACTGACATGGTTGGCTGGAATTTCTCTTTAATGTGGCATATAGGTTT GTGACACAAGAAAGTCATACCTTTGGTGGCTAAGTTTACTAAGGAAAAAATAACTGAAAAAGATTAAAAAG TGAGAGTC/TTGAAAAGAGAAATGATAATGCTTCCAACTGTAGCTGTACAG
WI-9443	211	G A ---			TTAAAAACAGTTCAGGTTGGTGAAGCAGAAAGGGATGTATTACAATTTAAATGAATCAGTCACATT GCACAAATTAATCCTCTTGGCATCATACAACTGGGTTTAAATGGCAAATGATGACATCATAGCATGA CCAACTCATGGAAGGCAGTCTAGAGTCCATCAGCTCACACCTGAGGGGAAAGGCACTGCAOCCA CTGACGAGAC[G/A]CAGAGACCTTGGACTACAGATGACACCAATGCCACATT
WI-7166	59	C T ---			TCCTCAAAAGAGAAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA/C/TTGGAT CATCAACAAGATTTCCTTTGTGCAAAATATTTGACTATTCTGTATCTTTTCATCCTTGACTAAATTCGTG ATTTCAAGCAGCATCTCTGGTTTAAACTTTGCTGTGAACAAATGTGAAAAAGAGTCTTCCAAT TAATGCTTTTATATCTAGGCTACCTGTTGGTTAGATTCAAGGCCCGAG
WI-7259b	189	T C ---			GCCTTCCCAAGGAGGGGTCTTGGCCTGGAACCTTCAGAGAGGAGGGGAGCAATTTTAGCC CCACCTGCTCCCATCTGCCCCCTGCAACAGCTGCAGGGCTGCTTCTCTCTGAGTTCTCTGGCT GGCAGGCTCCCCCTGGGAATAGAGCAAGACGTGAGTCTTAACCTGCCACAGT/C/TTGGGGGAGCAG AGCAGCAGGTGGACAGGTGTTTCAGGGGGCCCAACTTCCCCTGGAGCTC
WI-7259	188	G T ---			GCCTTCCCAAGGAGGGGTCTTGGCCTGGAACCTTCAGAGAGGAGGGGAGCAATTTTAGCC CCACCTGCTCCCATCTGCCCCCTGCAACAGCTGCAGGGCTGCTTCTCTCTGAGTTCTCTGGCT GGCAGGCTCCCCCTGGGAATAGAGCAAGACGTGAGTCTTAACCTGGCCACA[G/C,TTTGGGGGAGCA GAGCCAGCAGGTGGACAGGTGTTTCAGGGGGCCCAACTTCCCCTGGAGC
WI-7322	275	A G ---			GTACTTTAGGCCTGTGGAGGGTGGGCAATTTAGTGGTGACCTTGACCCAGGGTTTCTAACAGATGAC CCTGTGAATCATAATTTAAACCTGCATATATTTATAGCCAGTCACATTTGCCCTCTCACCCCTATATG GCCATAAAGTGCCTAAGCACTCAGGCCTCCCACTCATCAACCCCTTGACCAGAGAAAGCACTC TGGTTCTCTATCCCTTGTACATAGAGAGTTTGTATGGGGCCCTCTGGCTG
WI-7685	46	T C ---			TCAGTTCTAGTCTCTGGGGCCACACAGAACTCTTTTGGGCTC/CTTTTCTCCCTCTGGATCA AAGTAGGCAGGACCATGGGACAGGTCTTGGAGCTGAGCCTCTCACCTGACTCTCCGAAAAATCCT CTTCTCTGAGGCTGGATCCTAGCCTTATCCTCTGATCTCATGGCTTCTCTCCCTCTGCGGACTC CTGGGTGAGCTGTTGCCCTCAGTCCCCCAACAGATGCTTTTCTGTCTC
WI-563	87	G A ---			TGTGACCAATTTGTTATTTTAGAGGGTTTAAACATGGCCTGACTATCACCTGATGGTCGCCAGAAATTC CTGGGGGAGGGCCCTCCCT[G/A]CCCTGATCATGTCTACCTAAGTGCCTACTCTAACAACTACTCTCC TGTGGTATGGGATCCTAAGCCAAAAAGCTGAATGAACATGTTCTAGCACTACAGAAATCCATACT GCCCTCAGTAAAGGCAAAATTTAAATCTCTTTGGATAACCCAGGGCAGAT

WI-931c	191	C A ---	---		GACCAGGGCACCAGAAAGCCACGGAAAGCCACAGCCACTAGCCCTGAACCTTGACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTATTCTGTGTGTCAAAATGATCCTTCT GTTGCTGCAGTGTCACTTACTGTTGTATGGATTATAATTATTGTCCAAAAGCC[C/A]CGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTGAGA
WI-931b	81	A G ---	---		GACCAGGGCACCAGAAAGCCACGGAAAGCCACAGCCACTAGCCCTGAACCTTGACACCCCTGGAGTT TCTCTCCCTCCCTA/GTCCCTCACCACACCTTCCAGTGTATTCTGTGTGTCAAAATGATCCT TCTGTGTGCTGCAGTGTCACTTACTGTTGTATGGATTATAATTATTGTCCAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTGAGA
WI-931	31	A G ---	---		GACCAGGGCACCAGAAAGCCACGGAAAGCCAC/A/GGCCACTAGCCCTGAACCTTGACACCCCTGGA GTTTCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTATTCTGTGTGTCAAAATGATCCT TCTGTTGCTGCAGTGTCACTTACTGTTGTATGGATTATAATTATTGTCCAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTGAGA
WI-10870b	91	C T ---	---		GGATGACTTACCCATAGCAGGGTGGGTACATTTCATGGGTAACAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGG[C/T]ACCTACTTAGAGCAGTGGAGTACCCCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGGACCTGTACTCTGATACAAAATAAGGACATGGGTGAGC CTGAGCCACTCTTAAACCATGAACCATCACCAITTTAAATAACGTTGCCCCCCC
WI-10870	103	G A ---	---		GGATGACTTACCCATAGCAGGGTGGGTACATTTCATGGGTAACAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGCACCTACTTAGA/GA/CAGTGGAGTACCCCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGGACCTGTACTCTGATACAAAATAAGGACATGGGTGAGC CTGAGCCACTCTTAAACCATGAACCATCACCAITTTAAATAACGTTGCCCCCCC
WI-7719b	281	T C ---	---		AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGGCATTGGTCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTTCTGGACATTGCCCATGTATAATCTCACTGATGATTTCAAGCTAAAGCAA
WI-7719	163	A G ---	---		AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGGCATTGGTCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCCA/GTJTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTGCCCATGTATAATCTCACTGATGATTTCAAGCTAAA
WI-10396	72	C A ---	---		GCCTGGAGTATATCTAAACTGTGGCCTCCACTTTCATTTTCTTGAACATTGCTATCAACTGGGAA GAGT[C/A]GTGACTTTTATGCCCAGTTTCCCTCTCAGATTTTATGACGGTGTGTTTTCTTTTGTTA TGCCATTTGAGGGAATTGATGTTTCTTAAACTATGAAGTACTTGGCTGTCTCTCTCCATTGCTGTTTCAGG TTAACAGCCACCATTTGTAAACACTTTGT

WI-10673	94 C G ---	---	TCCCTTTATGCAOCCCAAGAGATATTTATTAAACACCAATTACGTAGCAGGCCATGGCTCATGGGACC CACCCCCGTGGCACTCATGGAGGGGCGJTGACAGTTGGAACATATGCACTGTGCTCGGCCACACA TCCTGCTGGGCCCCCTACCCTGCCCAATTCAATCTGCCAATAAATCCTGTCTTATTGTTTCATCCTG GAGAAITGAAGGGAGGTCAAGTTGTTGTCAATGATTGTGTGAGAGAACCT
WI-7842	57 T C ---	---	CACAGCCATGCCCTTGAGGAGCCGCCACCAGATGCTGAATCCCCTATCCCATTCTGTCJGTATGAG TCCCATTTGCCTTGCAATTAGCAATCTGTCTCCCCCAAAAAGAAATGTGTATGAAGCTTTCTTTCCCT ACACACTCTGAGTCTCTGAATGAAGCTGAAGGTCTTAGTACCAGAGCTAGTTTTCAGTCTCAGAAAT TCATCTGAAGAGAGACTTAAGATGAAAGCAAAATGATTGAGCTCCCTTATA
WI-7721	145 A C ---	---	CTGCTCATCAGCCACTGGAGTCCACACTTGAATTTGGGAGCTACCACGGGTCTGCCATGCTCTGG AGGAGCAAGGGGGCCACATCCOACCCAGCTGTACCCAGCCGGGAGGTGCAGCCCTTCTCTOOC TGCTCTGCAJCTGACTCTCTTTTGAAGTCCCTGTATGTCTACCTCTGACTTCTGTGTCCCTCTG TGCTGCTCTCATCCATTCCTCTTACTGGGGCTGGGGCTCTAGCCCCAA
WI-4767b	173 C A ---	---	TTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGAAATTCATAAAGAGTTCCCT CAGGTCTGGGTAATCCTAGATCTTCCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGGTATGTTT CTTGCCCTTGAGAAATCCTAGAAAGCACAGGGATGACA/CJA/AAATCACTAAGGAATTCACCTAAGA CTOCTCTAACCCAGAGATTTTAACTT
WI-4767	50 A G ---	---	TTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGA/CJA/ATTCATAAAGAGTT CCTCAGGTCTGGTAATCCTAGATCTTCCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGGTATG TTTCTTGCCCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCACTAAGGAATTCACCTAAGAC TCCTCTAACCCAGAGATTTTAACTT
WI-7718f	222 C T ---	---	ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTCTGGGGCCCCGGAGATAGTG ACTTTGCAGATGGAAGAGGTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAA/CJTCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718e	60 T C ---	---	ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGAT/CJGCAA GGATTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTCTGGGGCCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718d	31 G A ---	---	ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAA GGATTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTCTGGGGCCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCCATGCAGGAAGGAAAACTATGTATTAAAT

WI-7718c	91 C G ---			ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGG[C/G]TGAGTGAGTTCAACTACATGTTCTGGGGCCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTTGAAACAGAAAAATAAGTC AAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAT
WI-7718b	248 A G ---			ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCCGGAGATAGTG ACTTTCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATT[AG/G]AT
WI-7718a	42 A T ---	C		ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGC[A/C, T]GTTACTCCCTACACTGATGC AAGGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCCGGAGAT AGATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTTGAAACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTA
WI-7227d	99 G C ---			AGGGAATTGTTGCTCCTGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTTCATCTTTCAGACAAGCTTTA[G/C]AGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGTGTAAATAGGGGATTAGCCCAAGAGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCCAGCGACTAATG
WI-7227c	291 G A ---			AGGGAATTGTTGCTCCTGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTTCATCTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTTT GGTAGTATCTGTGTTCCGGTGGTGTAAATAGGGGATTAGCCCAAGAGGACTGAGCTAAACAGTG TTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCCAGCGACTAATGCAAT
WI-7227b	93 G T ---			AGGGAATTGTTGCTCCTGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTTCATCTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGTGTAAATAGGGGATTAGCCCAAGAGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCCAGCGACTAATG
WI-7227a	24 A G ---			AGGGAATTGTTGCTCCTGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTACCTGGCTGGC TTCCGTGGACCAATTTCATCTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGTGTAAATAGGGGATTAGCCCAAGAGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCCAGCGACTAATG
WI-7310b	234 A C ---			CCACAATGCCTCTCCACGATGTCAGGACTCCTGTCTGTCTGAGGTGGGAGACAAGGAACCTCGG AAGAGGAAGCAAGAAAGCCGCTACTGTCTATGTTGTGATCCTTCATCGAACAACTGATGCGAAAACT TGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAACTGAGCCAAACACACTGTAAAT ATCCACAGACTCCCTCCCTGCCCCCATCCCA[A/C]ATGATCTTGAGATTC

WI-7310a	64 T A ---			CCACAATGCCTCTCCACGATGTCAAGGACTCCTGTGTCTGCTGGAGGTGGGAGACAAAGGAACCTT/A JCCGAAGAGGAAGCAAGAACCCGTACTGTCTATGTGTGATCCTTCATCGAACAACTGATGCGAA AACTTGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAAGTGAAGCCAAACACACTGT AAATATCCACAGACTCCTCCCTGCCCTGCCCATCCCAATGATCTTGAGATTTC
WI-7878b	162 A G ---			CCAGCAACACCTACACCCCTTGTACCTGCCCTGGACTCCTATGATGGCTGCTGGTTGATAATAATCA GATCATGCCCAAGACGGCCCTCCTGATAATCGCTTGGGCATGATTGCAATGGAGGGCAAAATGCGTCC CTGAGGAGAAATCTGGGAGGAGCTGAGGTGATGAAGGTGTATGTTGGGAGGGAGACACAGTGT CTGTGGGAGGCCAAGGAGCTGCTACCAAGATTGTTGGCAGGAAACTA
WI-7878a	51 C G ---			CCAGCAACACCTACACCCCTTGTACCTGCCCTGGACTCCTATGATGGCTGCTGGTTGATAATAA TCAGATCATGCCCAAGACGGCCCTCCTGATAATCGCTTGGGCATGATTGCAATGGAGGGCAAAATGCG GTCCCTGAGGAGAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGTATGTTGGGAGGGAGCACAGTG TCTGTGGGAGGCCAAGGAGCTGCTACCAAGATTGTTGGCAGGAAACTA
WI-7381c	213 C T ---			CTCCACATTCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAAATCCCTTTCTTCTAACC AGCCCTGCAAGTTTCTCATGGACGCTCGCAGGAGCAGGCTGCAGGTTCTCGCTATGGTGAGATC AGATGTGGCCAAAGGAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAGACA AAAGGCTCTGCTGAGCAGATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54 C G ---			CTCCACATTCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAAATCCCTTTCTTCTTCT ACCAGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTTCCCTATGGTGAG ATCAGATGTGGCCAAAGGAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAACGGCTCCTCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53 C G ---			CTCCACATTCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAAATCCCTTTCTTCTTCT ACCAGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTTCCCTATGGTGAG ATCAGATGTGGCCAAAGGAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAACGGCTCCTCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93 G A ---			AAATTGCTCTATTGGACCTCATATTAATAAGAGCAATGAGAGCGAGGGGAAATTTGAACCTCTCTC AGGTACTGACTGTGGACCCAGACAAAG[G/A]GATGTAGATTGTACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTTCTCCCATTTACAAATAAGGAGACAAATAATAGGAGATTAAATAACTCATCAC TGTTTCAAAATAAGGAGTGTGAGGTTTGTCCC
WI-1017a	92 G A ---			AAATTGCTCTATTGGACCTCATATTAATAAGAGCAATGAGAGCGAGGGGAAATTTGAACCTCTCTC AGGTACTGACTGTGGACCCAGACAAAG[G/A]GGATGTAGATTGTACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTTCTCCCATTTACAAATAAGGAGACAAATAATAGGAGATTAAATAACTCATCAC TGTTTCAAAATAAGGAGTGTGAGGTTTGTCCC

WI-1795b	130 T C ---			GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGTCTGGGTTCCTCCAGACTCCTACGATTA AATTGATGCATGTGAACAACCTGATGAGTACTTAGATCTCAGTGCCTTGCAGAAAGAAAAGTTC/C GTCTACCATTTTACCACAAATTCGTAGTACAATTTAAGTATCTCTTGTTATCTCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-1795a	47 T C ---			GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGTCTGGGTTCCTCCAGACTCCTACGGA TTAAATTGATGCATGTGAACAACCTGATGAGTACTTAGATCTCAGTGCCTTGCAGAAAGAAAAGTC GTCTACCATTTTACCACAAATTTCTGTAGTACAATTTAAGTATCTCTTGTTATCTCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-10616d	136 G A ---			CACACAATTTGCAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTCTGGTCTCTCATCACAATTGCCA C/GA/TAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTCAGGGCCCAAGTCCCTCTGAGACTCCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGAATTTAACTCCTTTTTTGT
WI-10616c	136 G A ---			CACACAATTTGCAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTCTGGTCTCTCATCACAATTGCCA C/GA/TAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTCAGGGCCCAAGTCCCTCTGAGACTCCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGAATTTAACTCCTTTTTTGT
WI-10616b	141 C T ---			CACACAATTTGCAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTCTGGTCTCTCATCACAATTGCCA CGTAGC/C/TCTCCCTTCCCTTCCCTACAGGCCCTCTTCAGGGCCCAAGTCCCTCTGAGACTCCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGAATTTAACTCCTTTTTTGT
WI-10616a	116 G C ---			CACACAATTTGCAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTCTGGTCTCTCATCACAATTG CCAGTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTCAGGGCCCAAGTCCCTCTGAGACTCCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGAATTTAACTCCTTTTTTGT
WI-1126c	52 G A ---			CTCTTATTTCTCTGGGCACCTGCTTTCTTTGGGGGCAAACTTCCAGTATCACTG/AJATACTAATAA AAACCCGTGAAGTCTGCTTGCAATTTCAAGATTCAATATATATCCAGATTGTTTCCAGCAAGAA AATTTTATTTCTCAAGATATAAAAAATAAATAATTTAATTCAGTTTCTCAAAGGAATATGAAATTT TGTTAAATGCAAAATCCAGCTGTAACTTTTTTGGACTTGCTCTTTATTTCT
WI-1126b	230 T C ---			CTCTTATTTCTCTGGGCACCTGCTTTCTTTGGGGGCAAACTTCCAGTATCACTGATACTAATAAAAA CCCTGTGAAGTCTGCTTGCAATTTCAAGATTCAATATATATCCAGATTGTTTCCAGCAAGAAATTT TTATTTCTCAAGATATAAAAAATAAATAATTTAATTCAGTTTCTCAAAGGAATATGAAATTTGTT AAAAATGCAAAATCCAGCTGTAACTTTTTTGGACTTGCTCTTTATTTCT

WI-1126a	97 TC ---			CTCTTATTTCTGCGCACTGCTTTCTTTGGGGCAAACTCCAGTATCAGTACATAATAAAAA CCCTGTAAAGTGTGCTTGCATTTTCAAGATT/CJCAATATATATCAGAGTTGTTTCCAGCAAGAAA ATTTTATTTCTCAAGATATAAAAAATAATATTAATTTTCAGTTTCTCAAAAGGAATATGAAATTT GTTAAATGCAATCCAGCTGTAACCTTTTGGGACTTGCTTTTATTTCTT
WI-11183c	124 CT ---			TAGTGCTAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCTTGTC/TAATAACA TTTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGAAGTAGAGTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183b	192 TC ---			TAGTGCTAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCTTGTCACATAACATTT ATGACATACAAATGACCAAAATGATGTTTTATGAAGTGAAGTAGAGTTTAAAT/CJATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183a	118 CT ---			TAGTGCTAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCTTGTCACATAACA TTTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGAAGTAGAGTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-10770b	174 GA ---			GCTTGGTTGCTTTAGTCTTATTGTCAGTCTTGAGTTCTCCCTTTCTGCTGGCCCTTTTGATTTCA CCCATACCTCTATGCTCGTCTCAGACCATTTCTCTATCTGGAGCGCTCTTCTTGACTTTCTCCTG TTCACCAACCTCTTTTATTTCTCAGGACACTCA/GA/TTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCTTTCCC
WI-10770a	49 GT ---			GCTTGGTTGCTTTAGTCTTATTGTCAGTCTTGAGTTCTCCCTTTCTTG/TCCTGGCCCTTTTGATTT TCACCCATACCTCTATGCTCGTCTCAGACCATTTCTCTATCTGGAGCGCTCTTCTTGACTTTCTC CTGTTTACCAACCTTTCTTTTATTTCTCAGGACACTCAGTTTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCTTTCCC
WI-9667b	82 CT ---			GATGACAACTTCTGCTGTGACCCCTTAGTCTGCTCATGACACTTTTCAATCTCTGCCCTTGATCATGG TTATCACTGGACA/C/TAGCCACCTCCCAGCAGGCTTAGAACTCCATGAGTAAGGGACCCCTGTCTA ATGTGCGGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAACTTGCAATCT
WI-9667a	68 GC ---			GATGACAACTTCTGCTGTGACCCCTTAGTCTGCTCATGACACTTTTCAATCTCTGCCCTTGATCATG G/C/TTATCACTGGACACAGCCACCTCCCAGCAGGCTTAGAACTCCATGAGTAAGGGACCCCTGTCTA ATGTGCGGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAACTTGCAATCT

WI-10400d	189 A G ---			ACATTTTATTAGCAAAACAAATCAGCAAAATAATAATAGAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAAAGCACCTTACTAACACAAATATTTTATTCTAATTT TCITTCCTTACCTTTACTCTCCACCCCAAAATAACGTAAGTACCTATGTC[A/G]TGCCATGTAG TTTTTGGTTCATTTACTTGCAAAATATTCAAAGGCGTTAATGCATTATG
WI-10400c	166 A C ---			ACATTTTATTAGCAAAACAAATCAGCAAAATAATAATAGAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAAAGCACCTTACTAACACAAATATTTTATTCTAATTT TCITTCCTTACCTTTACTCTCCACCCCAAAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAAATATTCAAAGGCGTTAATGCATTATG
WI-10400b	165 A G ---			ACATTTTATTAGCAAAACAAATCAGCAAAATAATAATAGAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAAAGCACCTTACTAACACAAATATTTTATTCTAATTT TCITTCCTTACCTTTACTCTCCACCCCAAAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAAATATTCAAAGGCGTTAATGCATTATG
WI-10400a	46 T C ---			ACATTTTATTAGCAAAACAAATCAGCAAAATAATAATAGAAAGTAAT[C/T]GCATTTTCAGACATCT GCTGGTTAACTGTTATAAGATGGTTTAGCACACATGTAAAGCACCTTACTAACACAAATATTTTATTCTA ATTTTCCTTCCCTTACCTTTACTCTCCACCCCAAAATAACGTAAGTACCTATGTCATGCCATGT AGTTTITGGTTCATTTACTTGCAAAATATTCAAAGGCGTTAATGCATTATG
WI-10809b	78 C T ---			AAAGGGCTACAAACTAAGGCCAAACCATGAACGGTATAAGGAGGGTAATGCAAGGGGAGACCC CACCTCTACCA[C/T]TTAGAAAGGGCATTCAAGCACATTCATAGGCTTCATATACTGGTTAG CAACAAATGGAATGTATTAGCCCAAGGCGAGGTATGGACCAAAAGTGCCAGTGATGAGGCCACA GTGAATATCCACCTAACGACCTTCTTGGATGATGACACATGACATAGGCTTAA
WI-10809a	33 C T ---			AAAGGGCTACAAACTAAGGCCAAACCATGAAC[C/T]GGTATAAGGAGGGTAATGCAAGGGGAGA CCCCACCTCTACCACTTAGAAAGGGCATTCAAGCACATTCATAGGCTTCATATACTGGTTAGC AAACAAATGGAATGTATTAGCCCAAGGCGAGGTATGGACCAAAAGTGCCAGTGATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGACACATGACATAGGCTTAA
WI-7038c	266 T C ---			CGAGCTTGGGATAAAGCAAGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATAGTATGAGATGCTGGGCTGTCTCTCCCTTCAGGAATGCTGGGCCCCAGCCTGGCCAGAC AAGAAGACTGTCAGGAAGGTCGGAGTCTGTAAACCAGCATACAGTTGGCTTTTTCACATTGAT CATTTTATATGAAATAAAAGATCCTGCATTTATGGTGTAGTTCTGAGTCC
WI-7038b	140 A C ---			CGAGCTTGGGATAAAGCAAGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATAGTATGAGATGCTGGGCTGTCTCTCCCTTCAGGAATGCTGGGCCCCAGCCTGGCCAGAC AAGA[C/G]GACTGTCAGGAAGGTCGGAGTCTGTAAACCAGCATACAGTTGGCTTTTTCACATT GATCATTTTATGAAATAAAAGATCCTGCATTTATGGTGTAGTTCTGA

WI-7038a	31	G A	---	---	CGAGCTTGGGATAAAGCAAGGGGACCTTGGC[G/A]CTCTCAGCTTTCCCTGCCACATCCAGCTTGTG TCCCAATGAAATACTGAGATGCTGGGCTGTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCA GACAAGAAGACTGTCAGGAAGGTCGGAGTCTGTAACACAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAATAAAAGATCCTGCAATTTATGGTGTAGTTCTGA
WI-3429b	64	G T	---	---	ATAGGCTTCTGTCTGCCACAGTGGAAACAGACCCAGGTGGCCAGGGTCCACACA[G/T] CCCTCAGCCCTTCAGCTTTGCATGTGTCCATCGGTGACTCAGCAGAGATTTTCCAACTCATGTGA CAAAAATACAGATTCAGATCTCCTCTCTCTGGATTGGATCTAGCAAGACAGAGACGGTCTCTAGAA TCCTGACTGTTAACAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-3429a	62	C T	---	---	ATACGCTTCTGTCTGCCACAGTGGAAACAGACCCAGGTGGCCAGGGTCCACAC[CT/TA] CCCTCAGCCCTTCAGCTTTGCATGTGTCCATCGGTGACTCAGCAGAGATTTTCCAACTCATGTGA CAAAAATACAGATTCAGATCTCCTCTCTCTGGATTGGATCTAGCAAGACAGAGACGGTCTCTAGAA TCCTGACTGTTAACAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-6786c	151	G A	---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGTCACT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGGAAAGGATAAAGAGTGAAGTACGGTGACCT GTAGCCCCATCTCT[G/A]TGGGATAAGGTGCCATTTGTTCTTGGAGGGTGAATGCCACATTC TTTTGGCAGGGGACACTCTCTCTGGGTGCTCTATGCTCAGTTTCATCATT
WI-6786b	111	A T	---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGTCACT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGGAAAGGATAAAGAGTGAAGTACGGTGACCT CCTGTAGCCCCATCTCTGTGGGATAAGGTGCCATTTGTTCTTGGAGGGTGAATGCCACATTC TTTTGGCAGGGGACACTCTCTCTGGGTGCTCTATGCTCAGTTTCATCATT
WI-6786a	106	A T	---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGTCACT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGGAAAGGATAAAGAGTGAAGTACGGTGACCT CCTGTAGCCCCATCTCTGTGGGATAAGGTGCCATTTGTTCTTGGAGGGTGAATGCCACATTC TTTTGGCAGGGGACACTCTCTCTGGGTGCTCTATGCTCAGTTTCATCATT
WI-6711b	226	G T	---	---	GGCTATTTGTAAATGCTTGGTATTGACTCCAAAATTGAATAAGTATTGGGGAAGAATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCTAAACCTTCAGTTCCAATCACTGAAAT TTCAATACCTCCATTATAAATTCAATACATCATTCAGAGAGAAAGACAAACGGTGCCAACTGGGTT TGGTTGGTGCCTGCACACCCACA[G/T]TGGCAACTAAGTGAATCTCTAAA
WI-6711a	36	T C	---	---	GGCTATTTGTAAATGCTTGGTATTGACTCCAAAAT/GTGAATAAGTATTGGGGAAGAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCTAAACCTTCAGTTCCAATCACTCT GAATTCATATACCTCCATTATAAATTCAATACATCATTCAGAGAGAAAGACAAACGGTGCCAACTG GGTTGGTGGTGCCTGCACACCCACAGTGGCAACTAAGTGAATCTCTAAA

WI-10613b	172	A C	---	---	---	ATGTATGCCAAAATCATAATACCCCTGCATTCTAGAAACATACAGTGTAAATAGAATTTTGAGCCATA TGGTGAAAAATTTAGAAGTATTATCTCTATATGTATATACTACGTTTAAACATCAATGAATGTGATTT TTTGTCAACTTTTGACAAGGCCAGGCAATTTATTTG/C/GCCCTAGGAGGGTTACTATAATTTAGA AAGGCTCTACCTTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-10613a	44	G A	---	---	---	ATTGTATGCCAAAATCATAATACCCCTGCATTCTAGAAACATACAGTGTAAATAGAATTTTGAGCC ATATGGTGAAAAATTTAGAAGTATTATCTCTATATGTATATACTACGTTTAAACATCAATGAATGTG ATTTTGTCAACTTTTGACAAGGCCAGGCAATTTATTTGAGCCCTAGGAGGGTTACTATAATTTAG AAAGGCTCTACCTTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-7587c	133	A T	---	---	---	GCTCTAGTGGGAAACCTCAGGTAGTCTCCCGAAGATCTGTGCTTCCAAACAAGTGACTACCCCTTGAAGC ACATCCCCTTCTGGATCTGAAAAGAGCCCTTGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA(A TJGGAAATGAACCACTCCCTGCCCATTCCTCTATAAGAAATATCCCAAGACCCAGGCAATTTTGCCCTCT TTCCACATGCCCCCATATGCTGAGCCAAACTGCACCTGGGGGCTGCCCTC
WI-7587b	81	G A	---	---	---	GCTCTAGTGGGAAACCTCAGGTAGTCTCCCGAAGATCTGTGCTTCCAAACAAGTGACTACCCCTTGAAGC ACATCCCCTTCTG/G/ATCTGAAAAGAGCCCTTGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCCATTCCTCTATAAGAAATATCCCAAGACCCAGGCAATTTTGCCCTCTT TCCACATGCCCCCATATGCTGAGCCAAACTGCACCTGGGGGCTGCCCTC
WI-7587a	28	C T	---	---	---	GCTCTAGTGGGAAACCTCAGGTAGTCTC/C/J/GAAGATCTGTGCTTTCCAAACAAGTGACTACCCCTTGA AGCACATCCCTTCTGGATCTGAAAAGAGCCCTTGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCCATTCCTCTATAAGAAATATCCCAAGACCCAGGCAATTTTGCCCTCTT TCCACATGCCCCCATATGCTGAGCCAAACTGCACCTGGGGGCTGCCCTC
WI-10681b	103	T A	---	---	---	ATGACTCAGGTGACAAAAGAACATGTCCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCAAACC ACAGAAAAGCTAAAGACATCCCTTTTAAAAAAGCC(T/A)AAAGACAGCCATTTTAACTCAATTGG TAGTTTATGATTTTCTCAAAATTTCCCCACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTGGAGAAGGAGGAGTGACGCTCTGTTAAAG
WI-10681a	41	A T	---	---	---	ATGACTCAGGTGACAAAAGAACATGTCCTAGACCCCATTTG/A/TCTTACGCAAACTCAATCAGCCAA ACCACAGAAAAGCTAAAGACATCCCTTTTAAAAAAGCC(TA)AAGACAGCCATTTTAACTCAATTGG TAGTTTATGATTTTCTCAAAATTTCCCCACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTGGAGAAGGAGGAGTGACGCTCTGTTAAAG
WI-7222c	126	G T	---	---	---	GCCTCTCCTCAACTGTCCTGGACCCCAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACCCCTGTTCTCAAGTTGGGGATGGG/G/TAATAA AGGAGGGGGAATCCCTTGAACAAGAACTGGGGATAGTTATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGGTGTGATTTTCAAAAGACTCGAATTCATTTT

WI-7222b	255	G A ---	---		GCCTCCTCAACTGCTCTGGAOCCAGGCTAGGAAGGGCTGCTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCGAGTGAGCTCAGGTGTCACCTGTTCTCAAGTTGGGGATGGGAATAAAGG AGGGGGAATCCCTTGAACAAGAAGAACTGGGATAGTTATATTTCCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGTAGGTTGATTTCAAAGACTCGAATTCATTTCTCA
WI-7222a	126	G T ---	---		GCCTCCTCAACTGCTCTGGAOCCAGGCTAGGAAGGGCTGCTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCGAGTGAGCTCAGGTGTCACCTGTTCTCAAGTTGGGGATGGG(G/TAATAA AGGAGGGGGAATCCCTTGAACAAGAAGAACTGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAGGTTGATTTCAAAGACTCGAATTCATTTT
WI-8054d	41	C A ---	---		AAAGATGACACTTAGAACTGGATCACTTGGCCCTTCTCTTTC/AJTATCTCTCCAGTTCAAAATG CTTGATCTTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCA CAATCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTGGCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGGCGTACAGAGAATCCCTTGGCCCTT
WI-8054c	237	G T ---	---		AAAGATGACACTTAGAACTGGATCACTTGGCCCTTCTCTTCTTATCTCTCCAGTTCAAAATGCTT GCATCTTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCACA TCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTGGCCACCATAGCCACTCTGCTTCC TGTATAACGCCGCTTCCCTGGGCGTACAGAGAATCCCTTGGCCCTT
WI-8054b	148	T C ---	---		AAAGATGACACTTAGAACTGGATCACTTGGCCCTTCTCTTCTTATCTCTCCAGTTCAAAATGCTT GCATCTTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCACA TCTCTTTGTAGTTC/TCTTTAGCCTTTTCCGGAAATCGGCTTAGTTGGCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGGCGTACAGAGAATCCCTTGGCCCTT
WI-8054a	131	C G ---	---		AAAGATGACACTTAGAACTGGATCACTTGGCCCTTCTCTTCTTATCTCTCCAGTTCAAAATGCTT GCATCTTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGC/GJA CAATCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTGGCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGGCGTACAGAGAATCCCTTGGCCCTT
WI-10854b	152	G T ---	---		TCCACAAAAACTTCCCTGGGCGGGGTGACTAAGATGAGAAGTGGGAGAAGTGGATAGTTTAATAA ATGTTTATATTTACTTTAAGCGAAGTTGAACACGAAAGACGATAGTTAACGCTGTTAAGTTTAT ACGGTGTGCGAGGCAACA(G/JGGAGAGGTACGGGAATAGTTCTACTTCTGTTTTTATCTTGTG TTTTAGACACAGGGTCTGCTGTGTG
WI-10854a	102	C T ---	---		TCCACAAAAACTTCCCTGGGCGGGGTGACTAAGATGAGAAGTGGGAGAAGTGGATAGTTTAATAA ATGTTTATATTTACTTTAAGCGAAGTTGAACACGAAAGTGAACACGATAGTTAACGCTGTTAAGTT TATACGGTGTGCGAGGCAACAGGGAGAGGTACGGGAATAGTTCTACTTCTGTTTTTATCTTGTG TTTTAGACACAGGGTCTGCTGTGTG

WI-9826b	127	G A ---	---	---	AAATTTATATGTGAAGGGTTAGCAAACTATGGCCACAGGCCCATCTAGCCATGCCTATTTTGTG TGCTGATGGCTGTTGGTGTTTGCACGCAGTTAGCCATTGTGACAGAGGCTGTATG[A]GCCTT CAAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGGAAAGTTTGCTGATTCTAGATATTTAAA GGCAGAGAAGATCAGAAGTGTGAA
WI-9826	125	A T ---	---	---	AAATTTATATGTGAAGGGTTAGCAAACTATGGCCACAGGCCCATCTAGCCATGCCTATTTTGTG TGCTGATGGCTGTTGGTGTTTGCACGCAGTTAGCCATTGTGACAGAGGCTGT[A]TJGGCCTTC AAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGGAAAGTTTGCTGATTCTAGATATTTAAAG GCAGAGAAGATCAGAAGTGTGAA
WI-15986	60	T G GTGGGTTTT	TGACATTATAT AAACGTAAAA GAAAATGT	---	CGGACACGTGTATATACAAATACAGATCGTATGGGTTTGTGTGTGGGTTTTTTTTTJGJTTAC ATTTCTTTTACGTTTTATATAATGTCAGCAITTTCAA
WI-8655	29	A G AG	AACTGCAAAAT AGGAAACCAG	CCACCTGGGGC TCCC	TTCAAGTAACTGCAAAATAGGAAACCAGAG[A]GJGGGAGCCCCAGGTGGGACAAATCATGGCTACCCC TCCCCAACAGAACAGGGGGAGGAGGTGGCCCTACACCTTTAT
WI-8170b	259	G A ---	---	---	GCACCTCTCTCTGAGCAACAGGTACACATTTTTTCTCTAACATTGATCTATAACACACAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTTAAGTACTCTACCAAGATGCTGTGAAGGTTAG CATTTGGTGGAGAGATTACAAGGTTAAGATCATGTGCCATCAAAAGTGCAATCCTATCAATCAGAA ATAAAGTAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACACAAGA
WI-8170a	204	T A ---	---	---	GCACCTCTCTCTGAGCAACAGGTACACATTTTTTCTCTAACATTGATCTATAACACACAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTTAAGTACTCTACCAAGATGCTGTGAAGGTTAG CATTTGGTGGAGAGATTACAAGGTTAAGATCATGTGCCATCAAAAGTGCAATCCTATCAATCAGAA A[T/A]AAAGGTAAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACAC
WI-8172	136	C G GACA	CCTTTATTAAA ATTGTTTTCTT	GAAGAGAAAT GTAATACCTGT AAAGGTAC	CAGGATTCCTTAAGTCATCTTCCAACTACTCCAGGTACATGGTGAAGAGTCACCTGTTAAACACGAA ATCTAACCATTAACAAAGCTTTTAAATCCTTCGGTAACTCCCTTTATTAAAATGTTTTCTTGACAT A[C/G]AGTACCTTTACAGGTATTACATTTCTCTCACCGTTTACA
WI-8183	56	G A TGC	TGAAATAAAA ACAAATTTCTGT	TGTGTTGAAAT CAAACCTGC	AGCAGGGTTTGAAATTGATCCCTTATTTTACATGAAATAAAACAAATTTCTGTTGC[G/A]GCAGGTT TGATTTCAACACAGTTGAATCTGTAAAAACCAAGCTCGTTTCTGATGCAGGACAAATATCCACAAT ATTTAAACTGCAAGCACCATGC
WI-14149	83	C T ---	---	---	GCCTTATGGGATTGCAAGCGTTACAAGGTTAAAGACAAAAACCCCAAGCATGGGATTTTGCCGGAAT ATTAGCGTTAAAGGAG[C/T]TGAGTTGAGTCAAAACACGGG
WI-8712	44	G A G	CACAGGGAAG AGGTAGTGA	CAGGAAGCCTG ACCATCTC	TCAACAATGACACTGTGTAAACAGCACAGGGAAGAGGTAGTGGAG[G/A]GAGATGTCAGGCTTCCTG TTCCCTAACAGCAGAGCCCAACCTAGAAAGCGCCTACCTAGCCTCTTAAT

WI-8827	22	C T	TOCCCTGGGAG T TTAGTGTTCA C	GGGATTAGGAT	GGTGTCCCTGGGAGACTATGG[C]/TAGTGAACACTAAATCCTAATCGCCATGCATTGGAATTATT CCGACTATTACTTCTTCTTAGTCCCTTCTTATCCACCAGTCTTCT
WI-8833	51	A T	TCTTCCATGCC A T ATTCTCTG	CCTCACACATT ATAGGGCA	CTCCGGCCTCTTAAAGCTCTCTGTAGACTGTCTCTTCCATGCCATTCTCTG[A]/TTGCCCTTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACCTGCCTTGTCTATAAAAGGTCAAGCTATGT
WI-8377	63	A G	---	---	ATTTTtagccatgTTGGTAAAGTTCAITTTTcagTACATGGGTAAACCCAGGCCCTTTCC[C]/GJT TATATCCAGGTATGCTACAAGTTCTTTTAACTCTTATCAGAAGTTATATTACTGTCTTCTTAGAGAG GCTACCAGGCTAAATTCACITTAGTTGGTTGTCTAATGTCCTCATATTATCCIGAAGCTCGTG
WI-8850	21	A G	GGGACTTAAC CTTTGGCCT	CAACAGCCA GGCAGG	GAGGGACTTAACCTTTGGCCT[A]/GJCCTGCCCTGGCTGTTGGCTCTGCGCTTGTCTTTTGGTTCTT TCTCTTCTACTGGTCTTCTTTGTCTTTGCCAGCCACTATGCTGCTGT
WI-8853	79	C T	COGGGCATTG AGGATA	AGTCTTCTGA GCTTCCAT	ACTTTCTTGAGCTGAGCAACCTCATCATCTTTAGCTTCTGGTTGATAACGCTGGTTAATCCCCGGG CATTGAGGATA[C]/TATGGAAGGCTCAGGAAGACTTTCATTCTCAA
WI-8865b	52	A G	---	---	AGGGTACTGGGAATCACAGGCACAGACTGAGGAAGACAGTGCATGGTGAACA[A]/GJACAACATGCT TCGGACTTACCAAAGGGAGATCGAGCTTTCCATATAAA
WI-8865a	42	T C	CACAGACTGA GGAAGACAGT CA	GGTAAGTCCGA AGCATGTTG	AGGGTACTGGGAATCACAGGCACAGACTGAGGAAGACAGTCAIT/[C]/GGTCGAACAACAACATGCT TCGGACTTACCAAAGGGAGATCGAGCTTTCCATATAAA
WI-8895	32	A C	---	---	GTGCCACAAACCTGGACACCAACCAACAGAA[A]/CJCTCCCGTCTTTGAAATTTCCATTAAAGAGCA CAATGGGGTAATTATACCAGGGATGCTCCAATCGCTCTTTC
WI-8456	93	G C	---	---	CCTTTAAAGTCACAGTCAACTCGACTGGACTGATATTTGTGAAATATAATAAACTCTTTTCC AAGGCTCCCATGCTTGGATGTCACA[G/C]TTATGTCAAGTTAATAAACAATTTCTAAGTGTCACTC TCAACTTCTGTATTCTTGCCATGGTCCAGTAACAGTTACACGGCAGACCCACAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACCTCCCGTCTGCTCAGTCAACCCAC
WI-8496b	157	A G	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGAAATGGTAATGTTGTATCAGTGCATATTCTATGGAAA ATTCAATCTCAAGTAAGTACAGCTAGCAATCAGAGACAGCACTATGTCAAGCTAGTATACAAGTCA AAGACACAATGCTGCCAATGCA[G/J]TAGTATAGAAATAATACGCAGCTGTTAGAAAAAAGTCT GTGGCCAAAGTGGGATAAAACAGTAGCAGTGCCAC
WI-8496	41	A	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGAAATGGTAATGTTGTATCAGTGCATATTCTATGG AAAAATTCATATCTCAAGTAAGTACAGCTAGCAATCAGAGACAGCACTATGTCAAGCTAGTATACAAG GTCAAAGACACAATGCTGCCAATGCAATTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAAGTC TGTGGCCAAAGTGGGATAAAACAGTAGCAGTGCCAC
WI-14153	28	A G	GTGAGGGAAG GCCAGC	AACGGCAGGA GGGA	CTGCAGGTCTATGTGCAGGAAGGCCAGC/[G/J]TCCCTCTGCGGTTGTACCCACATCCACAGAGCA GCCCTAGTCCAGGTGACGCACTGCCACCCACGGCACACGGGAACAGGACCCATGCTGC

WI-12108	40	C	T	A	T	TGAAAAGGG TTAAACTCAA	TTGACCTGGTA TAATGAAAGT ATTC	TCATGTATTACTTCTGGAAAAGGGTTAAACTCAAATATC[CT]GAAATACTTTTCATTATACCAGGT CAAGAAAAATGCCACAGCCAGAAAAATTTATTTAA
WI-5989	29	G	A	C	A	CCACAAAGGT CACAGGCA	GGGTATAACAG AACCGTATGTA OG	CAGGCAACGTCACAAAGGTACAGGCA[GA]CGTACATACGGTCTGTATACCCCATATATTAC CCCTTCATGTCCTAAAGAAGACATTTCTCTAGAGATTTTCATTTAGTGATCTTTAAAAAAAAT CTTGTTAACTTGCCTCCATCTTTCTTGGGTGAGGACACC
WI-12201	61	C	T	O	C	CCACTGATCA OCTGCATG	CCGACCACATA OCTGGC	ATAGCTTTTAGCCCTTTTCTCGAGTGTTATGTCCCAAGCCCACTGATCACCTGCATG[CT]GCCA GGTATGTGGTCGGGTGTGATGACGTGGGTTTGCAGCCCTCCACTGCTCGATAAAAGGC
WI-12018	31	A	T	T	C	GGCAGCCAGC TCTGACTT	GGAGAGATGAC AGAAACAGAG AG	TTTTATCTGTCAGGCAGCCAGCTCTGACTT[AT]CTCTCTGTTTCTGTCATCTCTCCCCACATACCA ACTTCTCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGAAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57	A	G	C	C	TGGCTCGCTG CCTC	AGGGATCAA GAGAAAGGC	TTTTCGTTTGTAAATGATCCGAATGCTTGAGAAGAAACCCCTGGCCCTCGCTGCCTC[AG]GCCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAGATGAGGTCCCAATGAGAGCTACCAAGATGTAGTCG AGCGG
WI-15407	92	A	G	T	T	CATGCCCTTA AGGATTAAGT	TCCTTTCTCTTT TGGTAGTGTGG	AGCATGTAAGGAGCAGTTTTATTGATTGGTATATTCAGGTTCTAACCCAGCTGAAAAATTCAAATA CATGCCCTTTAAGGATTAAGTTAA[AG]CCACACTACCAAAAAGAGAAAAATTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109	T	C	A	A	GTTGAGTATTT GTTCTGCTCAT	GGGAAGGCTGTG GTACATATTGG	TCTGATGTCATTTATTGGCACAAAAATTATTCTGATACAACATGGTGTCTAGACATGGCTACACTTTA TACTTTGTGCATTTAGTTGAGTATTTGTTCTGCTCATAATTT[C]CCAAATATGTACCAGACCTTCCC
WI-12326	25	G	A	C	A	GACAGACTC AAAGCAATT	AGGTTTGA TATGTATTAA TACTTTGT	CTGACAGACTTCAAAAAGCAATTCAC[GA]CTTCCAGAATACAAAGTACTTTAATACATATTTTCAAAG CTGTTTGCAATTCAAACAAAGTTAGCGTTTGTAAATCAAAATTTGATAACCCGACTAAAAAT
WI-12361	63	C	T	---	---	---	---	TTAAATCCACACTGAAGATCTGGAGTATGGGGGGGATATAGGAATTCAGCATATGTATTAT[C/T] TGAACATAATTTACAAAAGTGAACAGTTGGAAGGTACTTATAGGTAGACCTGAGGGTCTGTACC
WI-11305	87	C	T	A	T	CAGACACAGC ATCACACCA	GACCCTOCCGT GGGC	ATACTGGTTTAATCCATGTCAAATGTAGTTTACAAAGGGAAGGACAAAGTACCTTTGTATAGAATAT ACAGACACAGCATCACACCA[C/T]AGGGCCACACGGGAGGGTGGGGAGACGACACTTTTCCCTGGG AAAGG
WI-11321	67	A	G	T	T	GGGAGGAAAA TCCAATAAT	CATTGGGGAAT AGCTAAACCTT	ATTTTATATGAAGGTTTTCTGGTGAATCTTTTAAGCAGGGGAGAAAAATCCAAATAAATTTTTTAA[A/G]AAGGTTTAGCTATTCCTCCCAATGCTATTTAATACAATTGAGGTAGGACGTTAAGTCTTATCAGA CTGTACTGGAGCCCCG
WI-11324	40	C	G	T	G	GGATAAATCA TGTGCCCCA	ATCAAGCTTTG GGGCTCT	AGCATACTGCATCTCCTTTATGGATAAATCATGTGCCCCA[C/G]AGAGAGCCCCAAAGCTTGATGACAT TCTGTAAAGTTACAAAAATGTATCTGAAGAAGTTATCTGTTCTTGTC

WI-11352a	69	T C G	AGCAGCAG ATAGTGGAAA	GACCTCTCGTA GGACACTTAGC	TGACACATGTTTCTGTTTCCAGAAGGAGAGAGAGTATCATATAAGCACAGCACATAGTGGAA AGTC/GCTAGTGTCTACGAGAGGTACAGATCATATCCATAGAAAACAGCTCTCTTTACTTGCA CACCTA
WI-11371	84	C T G	CAGCTGGAG ATTCTGATTCA	GCCCCGCTGA GCAC	TTAGCCCATGCTGTCATTGCAATCACCTGTGAACCTATGAAACTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTACGTC/GTGTCTAGCGGGCTGACATCCATGTTTGGGAAGAGTTGCGCGGGT GATTCGATCGGTATAT
WI-11385	75	T C G	ACAGAAGACT TTCATATTCCT	GATTCATTCT AGTCATGGTCA	CTTAAAGCATTATAGTTTGGCTGTGGTGACACAGAACACTTTCATATTTCTTTTAAAGTC TCTTCAGTC/GAGGAAAAAGCTACAGATTAAATAATATGACCATGACTAGAAATAGAAATCAGC
WI-11388	88	C A A G T T C	TGTTGAAAT ACACGTAAC	TGCCCTGTATC CAAGTTAAAT	TCATGTGGCCAGTTAGCTCAGTTGGTTAGAGTGTGGAGCTCATAAAAAATTAAGAAATGAATGTTT AAATTACACGTAACTAAGTTC/CATATAATTTAAGTTGGATACAGGCATTGTTATGCTAAT
WI-11392	55	T G A T A A T A C	GGTATGTGT CTTGAACCTTA	GTACATTCAG TGTTTTGTAAA	TTCTATCATTCCTAAATGGGAGTTATGTGTTCTTGAACCTTAAATAATAC/TGCTTTTACA AAACAGTGAATGACTTCTTGTGCAAGGGAACACTGAGTCTCCGCTCTAGATCCATTAACTGT CATACTCTTCCCCAGA
WI-11396	52	A T T	TTTGTGTTTG AAATGGTGT	AGCTTATTTTC ATATTCACCCA	AAAGAATAAGATGGCATTGTTCAGTTAATTTTGTGTTTGAATGGTGT/TAT/GATGGGTGAATA TGAAAAAAGCTTACCTCATCCACTCTAAAGGTAGTTGGTGAITTTGAACCGTTGTCAAT
WI-11441	100	C A C A G C	TCCCCACCAAC TATTTG	TGCCAGGGCCT TATTTG	CTGTGAGCTTTCCCAACTAAACCGTGAGTCCAGTATGTCTGGCAGCAGCTGTCTGTCTTGGTG TATTCCTTACTGTAATCCCAACCAACCAAGC/C/A/CAAAATAAGGCCCTGGCACAAAGTAAGCTCTCC ATTTTGTAGAATGAAT
WI-11466	26	C T T T T A T T T G C A	TGAGAAGCCA TTTATTTTGCA	GTTTATTGTTA TAAAAATGAC	ACTTGAGAAGCCATTATTTGCAG/C/TCTTCAGTCCAAAAAAGTCAACATTTTCAGAAATTTTT TATATAAGTTGAGGTCAATTTTATAACAATAAACTTCTATTATCTATTATCTCTCACATACATTT CATGTATCCTG
WI-13364	35	A G	TTTTCTTTTGTGCTCTTTTGTAGTGAAGC/A/G/GGAACAGTTGTCAATACTACCTTCTGTGTTGG TCCTCTGTAGACAACATACCTTTCTTTGAATGTAAAAATGTCA
WI-11276	41	A G A G C A G A C	GGCAGCCAGG AGCAGAC	TGTACTGAGGA GCGGCTG	AGGCAACACTGCTTTATTAGCGGGGCGAGCCAGGAGCAGAC/A/G/CACCGGCTCCTCAGTACACATT CCCCACCCCTGCCGTGGTGTCTCCCACTCAGGGCTGGGCATGGAGGGGCGAGCTAGGTCTGGAA
WI-12210	76	A G A	ACTGGGAAAA CAACTATTGC	TGCTAGTTTGC ATATGTTTTCC	ATTGGAAACAACCTTAATAATTTGCATCTACATATAGAAAGCTGCTTTGAATAACTGGGAAAAACA CTATTGCAT/A/G/GGAAAAACATATGCAAACTAGCATATTGTCTCTAGA
WI-14186b	88	A G	AATGGTCTGGTTTATTGAGAAGCTGTGGTCAATTTGATGGAAAGACACATACGGGTACAAAAATTACA GGTGGTTTAGTTCAATACATG/A/G/TACAAATCATTAGAGTCTTTACAAGTCTATTAGAGTCTTTGGAT TTT

WI-14186a	52	C T A	GGTCATTGAT GGAAGACAC	AACATAACCA CCTGTAATTT GTACC	AATGGTCTGGTTTATTGAGAAGCTGTGGTCAATTTGATGGAAGACACATA[C/T]GGTACAAAATT ACAGGTGGTTTAGTTCATTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66	A G	GAGAACACTT GTGGGGCTT	GGACCTATCAG TCCATGTTTGA	ATTTTTTTTGGCTATAGGTGAGTGGTTCTAAACCTTGAGCTTGCAAGAGAACACTTTGTGGGGCTT[A/ G]TTCAAACATGGACTGATAGGTCCACCCAGATTCTTAAGTGGTGGTCTGGGGT
WI-12345	37	C A	GTGGCAGGAA AAAGAGGAA	TTGACAGGGG TTCAGG	GGAAACAGACCTGATCCACGTGGCAGGAAAGAGGAA[C/A]CCTGAACCCCTCTGCAAGTATTCTCT TTCCTGACCAGCTGGGCTTGGCACCTTTGTGAGATTTGCAAAA
WI-13416	71	C A	AAATTTTGG AAGTTTTTCAG	AGTGTATTAG TTCAATGAATA ATTTCAA	GAAAAGGCTGTAATTTTATTTCAAATTTTGGAAAGTTTTTCAGAAAAAATAAAATGACAAGAACA CATA[C/A]AAATATTGAAATTTATTCACTGAACATAAACACTTAGCAGAGGAAGGACTTTTGAT
WI-12310	46	A A	TTATCCCAAG TATAATTTTA AAAAGC	TGTTTAAATAT GTTTGGTCT AAA	TTTGAAGATGCTGAAATTTATCCCAAGTATAATTTTAAAAAGCT[G/A]TTTAGACCCCAACATA TTTAAACATCTCTTACACATACAGAAATTTTCAGTTTACAATAATCCAGAAAGGCAATTTTCTTAAGCAG T
WI-12086	72	C T	CCGGGAAAC TTGGATT	GGAGTCTCGG GTCTGG	GAACCGAGCTTTATTGGAGCAAGAGTGTGGACACTGTTTACAACAAAAACGTTTCCGGGAAAACTTG GATTT[C/T]CCAGACCCGAAAGACTCCTCCAAGTTCTCACTGTTAGTAAGGTCAATTTGGGGGCAGA ACAGGAACATGCCTTAGCT
WI-11549	102	T G	GGCATAAAGT TCATAATATTC TTTATG	GGAAAGTCTGT ACAAATCCCC	ATGCTTTCACAGGTGTATTTTGTTAAGAGTTTGCTATCTAAATTTTCATATTTTATGGCATAAAGT TCATAATATCTTTTATGATCTTTTAAATATCTG[T/G]GGGGATTGTACAGACTTTCCTC
WI-11585	79	T C	TGGGTTTGCA AAACAAA	CCATGCTTCA TGATCTTCC	TTAGAAGGAAAGAAATAAACACCGTAAATGGGAAATCAGTTTCAGAGTAGGAAGGAGCTGGGTT TGCAAAAACAAAAT[C/G]GGAAGTATCAGTGAAGCATGGCCTAGAAAGTCCAAGAGCAGGGGTAGAGT TT
WI-11604	68	G C	---	---	TTAGTTGGTTTCTGAAACCTTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTACCAGCATTT G/C]AGAAGTACGGACTTTTCCATGAAAAATAATTAGAGCTAAGGAATTTCTGACGCTCACCATTTC TTTGTTACTCTGCAGT
WI-11614c	108	C A	---	---	CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAATCCAGAAAGACTCAGCTGCTTGAGGCAT GTTCCACCCCTGGACTTGCCAACTTCACTGTGAAACTGCA[C/A]ATTAAGTATTCAGCTAC GGACTTCGT
WI-11614a	60	A G	CCAGAAGACT CAGCTGCTTG	AGGTGGGAAC ATGCC	CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAATCCAGAAAGACTCAGCTGCTTG[A/G]GG CATGTTCCACCCCTGGACTTGCCAACTTTCAGTGTGAAACTGCAACATATTAAGTATTCAGCTAC GGACTTCGT
WI-11626b	83	T C	---	---	TTGATTTTACTAAGGCTTCCACTGGAACATGAAGGTAGGGATAAGTGTACAGGATAATATCTCAG ATATTTTAAAAATAAA[T/C]TACTTAATAATAAGAAATTAGCCATACCACATTGTTCCATTGCTAC AAGAACAATTTGGCAATGA

WI-11626a	39	G A G	TCCACTGGAA CATGAAGGTA	GTGGTATGGCT AATTTCTTATT ATTAAGT	TTGATTTACTAAGGCTTCCACTGGAACATGAAGGTAG[G/A]GATAAGTGTACAGGATAATATACT CAGATATTTTAAATAAATACTTAAATAAGAAATAGCCATACCAATGTTCCATTGCTAC AAGAACAATGGCAATGA
WI-11627	23	T C A	CCCTTCCTCC CATTGCTCTC	CATTTGCAACC CATCTCAAG	ACCCCTTCTCCATTGCTCTC[T/C]CTTGAGATGGTTCAAATGGGAAGTAAAGCAAAAGGG AGATGAGAAATACATGATGCTTTTGTCTGGCTTACTTCCATTGCGATGTCAGTCCATCCATG
WI-11636	61	A G T	GGACTTAAAA AGATCTGCTTA TCCCT	AGAACTTGCT AAATATTTTAT GTAACACT	TCAGAAATGTTGCAAGCAAATACTATTTGTAAAGGTGGACCTTAAAGATCTGCTTATCCTT[A/G]TA TATCCACATAACTCTAGTGTACATAAAATATTTAGCAAGTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCTTTTTTGGTA
WI-11537	119	C G T	ATTGCTCATCT TACTCTGACCA	GACCCAGCAA AAAGAATGAT T	GTACCATTTCTTATGGTGGCAAATAAGCAAACCTGTGAGTAAACGAGGCGAGCTGAATAAATTTACAG TATACAATATTAGAGAATATTATGTTGCAATTGCTCATCTTACTCTGACCATTC[G]ATAATCATTTCTT TTTGCTGGGTCCAGGACC
WI-11654	37	G C T	GCCAAAAGAC TATTCAGCAA CTG	GGCTCTCCAG GACAGTTT	AGTAGAACATCAGTGCCAAAAGACTATTACAGAACTG[C/G]AAACTGTCTCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTTCTGTGGTGTTCATACTCTACAGAGTTCACACTCATATTTTCATATTTT ATTTTGGGTGTTGGGT
WI-11656	28	G A A	ATTGATTTTAG AAGGAAGTGC	CAAGGCTTTGT CCTCAAGTAAA	ACCTGATTGATTTTAGAAGGAAGTGC[A/G]A]CTTTACTTGAGGACAAAGCCTTGCTGCAGTTGTTT AAATGTCTGTAACAATCAGATTCCAGCCTGGAT
WI-11680	55	T C ...	TTATCAGAGC AGGGGACAG	...	ACAGATACTTTTCCACGCAACATTTCTGAAATGAAAGCTTTGATTCTCCCTTTT[C/J]TGCATAAA GGCTGGGAAGGTGGTTTGGCCAGACCCGTACATCTTTT
WI-11696	47	T C	TTATCAGAGC AGGGGACAG	GGCATTAGAGA AGCCAACTT	GTCCAAGAACAAAGATACTTTGACATCTTTATCACAGGAGGGACAGT[C/J]AAGGTTGGCTTCTCTA ATGCCACCATCTGTGTTTCAGAATCTTCCACTTCGCC
WI-11702	69	C T	GAATAATACT GAAATAACCA T CAGCAG	AGAACAACCT AAGCAAATTAT ACTGAAA	TTACATGTGGTCAATGGTGACATACTTTCAATAATTAAAAATCGAATAATACTGAAATAACCCACAGC AG[C/T]TTTCAGTATAATTGCTTAAGTTGTTCTAGAAAACACTGCTAATTTTGTCTGTCAG
WI-11706	60	C T	TGGCTGGAATT TTCTCTCTT	ATCACCAAAG AACAATTTCCA	TGCTGATTGCTGCTTACCATCTGGCTGGAATTTTCTCTTGTGACAAATTTATTTG[C/T]GGCTG GAAATTTGTTCTTTGGTGAATTTGTCCTTGGCTGCT
WI-11709	105	T A	AGAAGCTTGC TTTCTGTTGC	TCATTTCTCT AATTTTACGGG A	AATATCATCACTCATATCAGGCATGTTTATAAAAATGAGAGATTAATGTCCTTTTGGCATACTTCATC TTCTTCAGGACACAGAGAGAAGCTTGCTTCAGTTGCT[A/G]TCCCGTAAAAATAGAAGAAATGAAT GGCCAGATGGATGGAAA
WI-11710	103	C A	GCACCTAGCCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACCTGTCCCGAGCTTCCAGCACAACAGCCAGCCACACTCTAGACAGGCTTCAC TCCAGTGCCATCTGGCACTAGCCTCAGTCTTCAC[C/A]CTCTCCCTGCTCCACACACTCTCTC

WI-11715b	123 C T	AGCTT	AGGCTGGCTGC	TCCCATCCTG TGGCT	AGAATGGAGCTGTTGGGGAGGGACATGCACACAATGTAAACAGACAAAAATGCATTACAACTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAGAGGAAAGAGGCTGGCTGCAGCTTCTTAGCCAC AGGATGGGACTGGGAAGA
WI-11715a	49 A C A A A	A	GCACACAATG TAAACAGAC	CATTACACAC AGTTGTAATGC	AGAATGGAGCTGTTGGGGAGGGACATGCACACAATGTAAACAGACAAA/CJTGCATTACAACTG TGGTGAATGTGGCCACTATGAATCCCTATGTATAGAGGAAAGAGGCTGGCTGCAGCTTACGCCAC AGGATGGGACTGGGAAGA
WI-11727	43 G C T C A A C A		AACAATCCTT AAAACAATA	OCTGTGGTTG TGTTGCAG	CTGGATTTCTTATACCTAACAATCCTTAAACAACATATCAACA/GJCTGCAACACAAACACAGGC AAAATGAAAAACAGATGCCAGACAGACACCCACCACATGGCACAC
WI-11728	16 C G ---			---	TTTTATTATCAAACTG/CJCAATTCATTTCCAAATGTAAATATCATCAGCTCCCATCCACTTT CTCCCATCTTCTATCTTTCCACCCCTACACTTCTCTCCCTACAACCCGGGTTCCAAA
WI-11758	61 A G T C G C T G		ATCTGTGGTTT T C G C C T G	TGATTGGCCCT GTGGTCTA	TTTTCTCTTTTATTAGTCCGCTATACTAACTAGAGGAGAACTGTGGTTTCGCCTG/A/GJTAG ACCACAGGGCCAATCACACAGCTTCTGTAGAGAACATGGAGTGCCAAAGATCACCATCA
WI-11295	37 A G A A T A T A A		GCCTCAGAA GTATTTCTAA	AAAAGTGCTCA TCTGTGAATC	CCGGCTCACAAGTATTTCTAAATATAATTTGCT/A/GJTAGAGTTCACAGATGAGCATTTC CATTAGGTGATATGCAACAAATCACTATTTGGCTCAGCAGGAAACAGACTTTT
WI-11773	93 T C ---			---	AGCACATGATATCTGCCTGGAGTTTCTGTAGCTCAGCAACAGCAGAGTCAGAGATTAAAGATT ATTATTGCCTCCTTTTTTTCCCTT/CJGTGATTGTTAATAGGGAGTCAAGGCCAAGTTATC
WI-11282	42 C G G C A A G G G A A		GGCTCAGAGA G C A A G G G A A	AAAACTCAGA CTGTAAATTTT	CATGACAACTCTTTATTATTAATGGGCTCAGAGAGCAAGGGA/CJ/CACACAAAAATTTACAGTCTGA GTTTTGCGGCGCAGAGACCCCTCTCCACCTTTTTCATGCTGTGTACACACACACTGTCCAAAGCCTC AGA
WI-11790	28 A G A A C C T C T G		CCCAACTTACG A A A C C T C T G	CGGTAGCGAG GCTAAGC	TAATCACCCCACTTACCAACCTCTGT/A/GJCTTAGCCTCGCCTACCGTACACATGCTCAGAGCAC TTACATTAACTACAATGGGCAAAATCATCTAACACAAAGC
WI-11879	61 C A A G T A T A C A		TCATCTAATCT GTGAGGTATTT	GATAGTTGAAC CTCTTCACTTT	TTTTAATCCCAAAGCTTACAACCATCTTTTCATCTAATCTGTGAGGTATTAGTATACAG/C/AJAGT GATTTTCTCTCTTTCTTTTATAAGTGAAGAGGTTCAACTATCCAGACAGTCCCATCTA
WI-12469b	91 C T A A G T T A A A		GTTTTTAATGT GGTATTAGAA	CAATTTTCAGA TTGCTATAGC	TTTACTAATTTCCATTCTCCCTTTTATAGTTTTTAAATGTGGTATTAGAAAAAGTTTAAATTACAT ATGTGGCTTATATTCTATTCTA/CJTTGACAGCAGACAGTTCTTCAAAGTTTGTATAGACAATCTGA AAATGGGTTCTGAAT
WI-11906	52 A G A T C T G A A		TGTTATAACAT CAAAGAAAGA	TTAATTTCTGC AGTCCCTCA	ACATTTGAGTAGGAATGACTTTGTGTTATAACATCAAGAAAGAAATCTGAAT/A/GJTGAGGGAATG CAGAAATTAACCTTCAGTCTAATCTCAGAATGCCAGAGTAAGATGAACCCCTTTACAG

WI-11909	78 A G	TTTGTTGGG TGGTCAAG	CCTCCTCTGAG ATTTTCTGAAT AG	GCAGTTCTCTGAAAGACAATGGATTGTGGAGCATACTGAAGACTATTCCCTAAATGGCTATTTGTGTG GGTGGTCAAGTATGCTATTAGAAATCTCAGAGGAGGACAAATGATAGTGCACCTGCAGCCAGCTCG GACTGGCTTGCAGAGTC
WI-11806	60 T G	CATGAAGAGT GGGAGTTCA	TCCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTAGCATCAATTGCCCCAAGTTTGGCAGGCATGAAGAGTGGCAGTTCA/T/GJGTT TTATTAGTATATAAATTGGCTTTACAGGAAGCATTATGG
WI-11946	31 C A	---	---	CCCTAGTGAATACAAACCTTTGTCTGGAGAC/C/JCCAGCTAGTCTAAGAAAACCTTCTAGGCTGAG CTCTCTTGGGAATCTAAGATAAAGAACTGAGATCTCTGGGAAGGGAA
WI-11965	65 T G	TGAAGATCAG ATCTCTGGTT GATT	CAGCTGTGGTG AATGTTGAT	ACAAAAATTCACAAGTACAACACTGCTTATTTCTTGCTTGAAGATCAGATCTCTGGTTTATTAA/T/ GJATCAACATTCACCAAGCTGAAGGAAATTAACCTGAACCT
WI-11027	90 T A A	TGCCCTACTAC GCCTTTAAAA A	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTTGAACCTGCAGAAAGGGCAGGACAAAACAATCACTTCATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTAAAAAT/JAATAAAAAATCTGTAAACACATTTCTCTCATTTCTTACGA ATACCTCTTTTGATATGCAAAATCTATGGCATACACAGAGGCACCTCCTCAATGCCCTG
WI-11049	95 C T	---	---	TTCTGCTGAAGATCACAAAACAATTTCAACCTCTGTGTTCAAAATAATTAAGGATCTGTACCTTT GTGTTTATTTCTGTTTCAACTAAGGA/C/JTAGACTTCAGAAAGGCATAGCTTCCCTTGTAAAGGTTTT AAACATCTTTTTCATTGTAGGAAGGAACATTTCAAAAGCCCAA
WI-15488	69 C T A C	AAAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCATTTCTG TAAC	CAACATTTATCAACATGGTAGGGAAAAGTTCTCACTCTGCACTATAAAAAGGACAGCCAGATATCA AC/C/JGTTACAGAAATGAAATAAGATGGAAAATTTTAACAAAATTG
WI-13654	49 A G CGT	AACAGTTAAT GAAACACATC	GGCTGGTGAAA TGATGTCAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAAACACATCCGT/A/GJGTATGACATCATTT CACCAGCCAGCTACTTCATGTGGCAGAAAAGTAACCTTTTCCCATTTTACAGACAAAACCCAGT
WI-11070b	135 C T	---	---	ATGAGACCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAAAGGAGCTAGGACAATTTCTTGCTT TCAAGTAAAATTGTGACTGAGCAGAAAATCAGCCAGCTATCTT/JGTGTCAGAGAGGTACTCCAA C/C/JGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCCAACAGAAAGGAA
WI-11070a	110 G T T	CAGAAAATCA GCCAGCTATCT	TTGGAGTACCT CTCTGCACC	ATGAGACCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAAAGGAGCTAGGACAATTTCTTGCTT TCAAGTAAAATTGTGACTGAGCAGAAAATCAGCCAGCTATCTT/JGTGTCAGAGAGGTACTCCAA GTACCGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCCAACAGAAAGGAA
WI-12020	121 T C	---	---	AATCTTTATATTTCCAGCTGTTGAGACAGTATTTTGGGGCTGATGTTACCTCTAGCGCGGAAACC AGAGCCAGCTATTAAGCAGCCAGAAAGCTACAGTAATGAATACATGACCATT/CJCTCTTTTAGC ACGTTCTTTGTTCTCTC

WI-11076b	142 G A ---			---	CATGGTTCTGCCAGCTTACAGGAAGCATGGTCTGGCATGGCTTATCTTCTGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGGAGCAGGATGTACATACCCAGAGCAGGAGAGAG AAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCAT G
WI-11076a	106 T C AGCA	AAGGGGAGC	TOCTGCTCTGG GTATGTGAC	GGTTATTCAAA AATTAGTATGG GACA	CATGGTTCTGCCAGCTTACAGGAAGCATGGTCTGGCATGGCTTATCTTCTGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGGAGCAGGCA[T/C]GTACATACCCAGAGCAGGAGAGA GAGAAAGAGAGGAAGTCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCAT G
WI-14263	49 T C	CGCAGAAAA GGCATAITCA			ACCTTTAAAGTTTCTCCCACTTCTCCCGCAGAAAAAGGCATATTCAAT[C/J]GTCCCATACTAATT TTTGAATAACCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA AATTATTGCTGAATAGGAAGGAGCA[T/C]TGAATGGGAAGGGGAGGTTAGAGAAGACAGAG ATTTAAAGAAGCAAGTACCATTTTCCAAGTATAAACTCGTA
WI-14267	28 T C ---			---	GATTTGTTTATTCAATTCGCTTTTCAATTTTGCCTTTTAAATAGAAC[A/G/A]CTTTGATTTTAGTA TATGACATCATCATGAATTTTCTCTTACTTTGATTTAGGCTCCACCTCAGTAGTTTGACAA AGGTAGAATGAGTTCA
WI-15288	108 C G	CATGAGAGGA TCCCTCTCTC	AAAAGCTTCTT TCCCTTGA		ACCTCTTCTGATGACACTTGACCTGTAAAGGGTCTAGAGAGAAAGAGTAGTACTCTACTTTGC TACAATTCAAGGATGAGGATGAGAGGATCCCTCTCT[C/G]TCCAAAGGAAAGACTTTTGGC AATAAATGGAAGAGGAGTGAACAAAGTAATGAACAAACAGACCCAGATCAGAGGAAGAGATG GCCTTCTTGTTAATTCTGGAGCA[G/C]ATTCAAGCAGCAAAATATTACTGAACACTTGCTATGTGCTG G
WI-13951b	88 G C ---			---	AATAAATGGAAGAGGAGTGAACAAAGTAATGAACAAAA[C/T]AGACCCCGATCAGAGGAAGAG ATGGCTTTCTTGTTAATTCTGGAGCAGATTCAAGCAGCAAAATATTACTGAACACTTGCTATGTGCTG G
WI-13951a	39 C T CAAAA	GGAGTGAACA AAGTAATGAA	TTCTCTGATC TGGGGTCT		GAGACCAAAAAAGGCTCTTGCCCAT[G/A]ATTCCCGTCTCTCCCTCTGACTGACCCCAAGTGTCTT ACAATGAACATCCCTCAGCCCCATGGCATGGTGCATCCCTTCTCTTGGGATCTGTGAATATAACCA ACTGTCTTGTCATTTGGC
WI-13264	25 G A TTGCCAT	AGCAAAAGGA AGTTAAATAC	CATGAAAGGA CAAATTTGCAT C		TTATTTGTCAATTAGCAAAAGGAAGTTAAATACTGATAG[A/C]GATGCAAAATTTGTCTTTTCATGCA TTTGTGGAGCAAGTACTAATCTGTTCACTGTCAITTTCCCTCACAAGGAGTTGAGCCCTAGATGAC
WI-13960	39 A C TGATAGA				AACTCTTTATTGTTTAGCTAGCCCCAGTACTTTATGCATCTTATAACCAAGACCTTCAG[C/T]JAG AGCAAGTCTGAGCCAGAGGTTTATCACACTTTGTCTCAGGGTCCACCAGGAACCGGCTTGGCT
WI-15843	62 C T CAG	ATCTTATAACC AAGAAGCCTT	CTCTGGCTCAG ACTTGTCT		

WI-13983	52	G A	TCTCTCCCACT CCTTAAACCT	CAATACCTCT TAGCCAGTGG	TTGTGATCTGATTTCCGAAACATAGAAATCTCTCTCCCACTCCTTAAACCTT[G/A]CCACTGGGCTAA GAGAGTATTGTACAGAAATATGCACTCACTGACTTAACAGAAATTAGAACATCCAGGCACCTCACTGAGA
WI-13850	51	A G T T	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTTGTA	CATGAATCTCAGGGTCACAGCTTTATTTATAGATTTTAAACACAGCCAT[G/G]TTACAAACATTTGT CAGGGAACATTTACAAGAAATAATAAGATGGACTTGCAGGTGTAAAAAGATTACACTTCA
WI-15295	27	G C A	TGTCAGTTTGA ATGTATTCTCG	TGAATAGTTGG CAAAGGAAAA	AGATGTCAGTTTGAATGTATTCTCTGAT[G/C]TTTTCCTTTGCCAACTATTCAATTATTGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCACAAGAAAAAGGCCCGGAAAAATATGAGTGAGACTCA
WI-14284	55	C T	ATTTCAAAACAAATCCAGAACAGGTTCTCACACTTTGAGCCCTTTAGTGCAAAAAACA[C/T]TATGCCAT GCGGGAAATAAAATGCTTATCCAGTGGAGCGCTCCCTGATGCATTGA
WI-14288	85	G C	CCGCTGCTATT CCCAGAT	GGTCTCTTCC ACCAAATCTT	ATGACCAGACCAGAGCCCTGTTCTATATGAAGACAAACAGGTGGCCATACTTGGGTGGAGGGGATA CCGCTGCTATTCCCAGAT[G/C]AAGATTTGGTGAAGGAGACCATGACAGATGACAAAAACGG
WI-13522	33	C T	TGATGTAGTTA CCCCACTAAT	CATAATATTG AAGTCAGTGGT	TTTATTTGATGTAGTTACCCCACTAATAACAAC[C/T]GAGAACCCACTGACTTCAAATATTATGAGAG AAAATTACTCCAGGGAAATTTTGCAGAGAAGATAATA
WI-13529	42	T C	CACAAACATT TATTGAACAG	TCTATACACTT CTCACTCTCTT	AAATATGATTCCTATCCACAACATTTATTGAACAGTTACCAIT/CIAAGCAAGAGAGTGAGAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGTCTCGAGGGTTTATAGTCTAACAGGGGAAACAACCTCTC A
WI-13859	84	G A ...	TTACCA	GCCT	TTATTTGTCAGAAATTTCCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAAGTTTACTAC TTTGAAAAAGGAAACTAT[G/A]ACAAACAAGTATATATTCAGGAAAGGGAGCTCCTAGAACTTTGAGCA ACA
WI-13536	29	T C	TGAAAGGATACAGAAAAAACTCAGCGAAGT[C/G]GAAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACCAGCTCCAGTTGTCTCTCCAGTCCCATTTACATGGAGTACACTTAATTTTCTCAGCA
WI-13373	52	G A	TTTATTGTTTGGTAGAAAAACAGGCTCTTTAACACTGAAATAACATCTCAC[G/A]AACTGTGCGCTC CTAGATTACAAAAAGTCAAAACCAATTTCTTTGACGCCGGCCCTTGAATCTGACATTCAAGTCAC CGTAATAGAAACCAGAGCT
WI-13477b	61	A G	TTGGTTTTTAATACCTCTTGTGGATAAAAGGACATTTTTCATTAGCTTGTCTTCAAA[G/G]GAC AGAGAAATAAGATAAATACCTTAAAGAAATTAATAAGAAAAATTAAAGGAACATGTACCAAGGTGG TTTAGACTCTCCTCAGTT
WI-13477a	32	A G AAGG	TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA	TTGGTTTTTAATACCTCTTGTGGATAAAAGG[G/C]ATTGTTTTCATTAGCTTGTCTTCAAAAGAC AGAGAAATAAGATAAATACCTTAAAGAAATTAATAAGAAAAATTAAAGGAACATGTACCAAGGTGG TTTAGACTCTCCTCAGTT

WI-15625	40 C T ---		---	GTTCCTCCCACTACTCCCGCAGAAAAAGGCATATTCAA[C/T]GTCCCATACTAATTTTGAATAA CCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA
WI-13367	84 C G A	CCACACTGAA GACTCACCAG	TCCCAACCCCA CCCT	GTCTCACTTTCTGTCTAGGCTGTAAATTTTTCAGTTTAAACAGTTTCTTATGTGATTTGTGGCCACACT GAAGACTCACCAGAA[C/G]AGGGTGGGTGGGAATACTTAATCAATATTTGTGGAATTTACCCGAT GAAATCCAGTTATTCTCT
WI-13600	26 G T AAGCATCCAT	TTAATGAGCC	TGATGG	CTCACATTTAATGAGCCAGCATCCAT[G/T]CCATCATCTAGTAACAAATTTTCAATATATGCACATTATAT TATACTGGAAACAAGAAATACGGATTGTGTAGGGAAGAGCATAGAGGACCACCATCAGCAACCCCTCT TGATTCCCTTCTCTACCC
WI-13602	89 G T GACAACACA	TCCATTCTGGA	GCATACCTCAT GACAAATATTTA ATATTAAT	GATAGGAAAAAGAAATGAAGTCAATAGTCTTTAGCAAGCCCACTAGCTCAAGGAATAGACAGCCC CTTCCATTCTGGAGACAACACA[G/T]AAATCTATTATAATTAATATTTGTCATGAGGTATGCACCT GCCCC
WI-13650	76 A T TTTAAAC	AAAGATTTCAC AATATTTCACT	CAGGCTAGGAT ATGAAGAGTA GTTTT	GCATTAACATTTAAAAATTTCTGAGGATATTGATGAGAACTATGATGAAGATTCAATATTTTCAC TTTTAAAC[A/T]TAAAAACTACTCTTCATATCCTAGCCTGATGACTTAAAAAGTTACCGG
WI-14319	83 C T A	CAATTC AAGG CACAAAGCTA	CCAAATCATCT ATATTGTTGCA TG	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAAGGAAATAGCAATT CAAGGCACAAAGCTAAG[C/T]ACATGCAACAATATAGATGATTTGGGGTGGACAGTACAGAATT
WI-13528	80 A G AAAA	CAATACATTT GCATTTTCCTA	CATGATACCAC AGTTTTCTCTG AA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAAACTGTAATCAATACATTTGCAATTTTCCTAAAA AAAGAAGACATTT[A/G]TTCAGAGAAAACTGTGGTATCATGCAGGAAAAAGCAGAAAAAAATTT
WI-13909c	93 A T ---		---	ACTTAAACTGGCTTATCTTACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCATCTTCTCACACT CTCTTCAAACTCGAATATCTTTTCT[A/T]GAGATGTCCTAGTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80 G A C	TTCTCACACT CTCTTCAAAC	GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAAACTGGCTTATCTTACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCATCTTCTCACACT CTCTTCAAACTG[A/A]AATATCTTTTTCAGAGATGTCCTAGTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86 C A ---		---	TTTTTATTGAATCCAAATGTAGCAAAATCATTAAAAACAAATTTATAAAGGGACAGAAAAATTAAG AATCAACATCATCTGGAC[C/A]ATGGGAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACATA
WI-14323a	78 T C ACATCA	ACAGAAAAAT TAAGAAATCAA	GCCTTTTCAAG GTTCCCAT	TTTTTATTGAATCCAAATGTAGCAAAATCATTAAAAACAAATTTATAAAGGGACAGAAAAATTAAG AATCAACATCAT[T/CT]CTGGACCATGGGAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACATA
WI-15389b	104 G A AAA	AGATAATGAA ACATCTGCGA	GATGAGGTGAT TCCACACACTT	AAAAATTGACAAATCAACTAGCTTGCTTTTGTGCTTTTGGGAAGACTACCATTTATTCAAATTTTATGT AATACACTCATCCAGATAATGAACATCTCGGAAA[G/A]AAGTGGGAATCACCTCATCTGTGC

WI-15389a	33 G A T C	AATCAACTAG CTTGCTTTTIG	TTTGAATAATG GTAGTCTTCCA AA	AAAAATGACAAATCAACTAGCTTGCTTTTGTGTC[G/A]JTGGGAAGACTACCATTATTCAAATTTATT ATGTAATACACTCATCCAGATAATGAACATCTGCGAAAGAGTGTGGAAATCACTCATCTGTGTC
WI-15747	88 T C A G T G T T	TGCTTCATTT AAACTAAATTT	CATAATTCAAC AAAAGTTTATA TAATTT	TGTAATCTGCTTACAGTCTTTGCAAAAGACAGACATATGTTTTGCATAAAGATATAAAATGCTTCAT TTTAAACTAATTTAGTGTTT[C/J]TTTAAATATATGAACCTTTTGGTGAATATGAACCTGTACCAAAC C
WI-13752b	117 C T ---		---	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTCTCTCGTTAAGTGCTGGATATAC[T/C]JGGCTTGCAACCGGACACCTTTTACG GAGGGATTCCGGACAAC
WI-13752a	106 T C A G T G T G A	CCCTCTCGTTA CAGTACATGA	CCCTCCGTAAA AGGTGTCC	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTCTCTCGTTAAGTGCTGGATATAC[T/C]JGGCTTGCAACCGGACACCTTTTACG GAGGGATTCCGGACAAC
WI-14339	102 T G T T A C	CCCAATCAAA CAGTACATGA	TCCAGATTTCT GGAAACCG	AATCATTAAATGAATGTTCCAAACACACCCCTTCACTGGGCTACAGGTAATTTCACTGGGATGGAAG CAGATGAACCCACCCCAATCAACACAGTACATGATTAC[T/G]GGGTTCCAGAAATCTGGATAC
WI-13744	115 C T A A A A C T G A A	TGGTGCTGAAC TAAACTGAA	AATCAGGAAA GATAAGCACA GC	TGGATGGATGGATGAGGCCACCTGTGTTCAACAAAACACGTAATGGAACCTTCATGCAGCTTTAGAT TTCCCTTTGCCAGCTAGGAGCTTGTGTATGGTGTGAACAAAACGAA[C/J]GCTGTGCTTATCTTTTC CTGATTCT
WI-14061	68 C T ---		---	CCCTTGACTATATTGTTTTTCCAAAATAGGACTATGTGTAGAAGAGAGCCCCCGTACATACTTAT [C/J]JAACCATTTTCATCCACCATTGTGTAATAATCTCATCTTCTGGGCTGGATACTCAAAAACAGAT
WI-15719	69 A C A T T C A G C	ACCCCTTCATC CATTGAGC	TGATACTGGC AAGAGTTTTAA ATT	TTACAGTTGGATTAACTACCACACTACCAGTGAATATACTGAATTAACCTTCAACCCCTTTCATCCATTGAG [C/A]JAATTTAAAACCTCTGCCAAGTATCATGAACTTACGAAGAGGAGATAAGAGATCTGATC
WI-13810	106 T C A A C T T	CTCTAAATCG ATACATCCAA	GAACTGATGCT TGCTGCTAAT	TAATCCATCAATCTAAAATCACACATACATAGATCAAAACAGAAAGTACCACAGTATGCTTTATTTTGCA GGTATTAATTGGTCTCTAAATGATACATCCAAAACCTT[C/J]AGTTAGCAGCAAGCATCAGTTCTTC
WI-15736a	27 G T C A C A	ATTTTATTCAC ATTAACCTTG	GTCTTTTGATA TGTTGGCTTAGT TTT	GGATTTTATTCACATTAACTTGCCACA[G/T]TAGCAAAAAAATCAAAACATAAAACATAAGCCACA TATCAAGAACAATATACATAGAGATTGAAATTTCTCAATAGCATTTGGAAGGATTTCCATAAATA
WI-13785d	72 G A ---		---	TCAAACTGCACACTATAAAGTGTCTTTAAATGCAGCAGCAGGAGATGTGAAGACACAAATGAAC AAGTGC[G/A]TAGTGACACATAGCTGTCAACACACAGT
WI-13785c	56 A C ---		---	TCAAACTGCACACTATAAAGTGTCTTTAAATGCAGCAGCAGGAGATGTGAAGAC[A/C]CAAAATG AACAAGTGGTAGTGACACATAGCTGTCAACACACAGT

WI-13785b	40 C G ---	---	---	TCAAACTGCACACTATAAAAGTGCCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACACAAATG AACAAAGTGGGTAGTGACACATAGCTGTCAACACACAGTG
WI-13785a	27 T C TGCTT	AAACTGCAC ACTATAAAG	TGTTGTGACAG CTATGTGTGAC T	TCAAACTGCACACTATAAAAGTGCCTTT[C]AAATGCAGCAGCAGGAGATGTGAAGACACACAAATG AACAAAGTGGGTAGTGACACATAGCTGTCAACACACAGTG
WI-13793	88 C G ATAGG	GGATTTTACAT TCAGCCTAGAT	GGGCAGGAGGA TTTGTACT	AGAAACCAAGTATATCATAGGCAAAATAAAATAGTTTTTACCCCATTTGATACAACATAAGGGATTT TACATTGAGCCTAGATATAGG[C/G]AGTAACAAATCCTCTGCCCATAAATCTATGACTTG
WI-13794	52 A G TTCTTTCTC	TTCTCACCCT	AGAATGGGCTC TTAACCTTGT	TAGTCTCCTACAAATCCTTCAATCCATTTTCTCTCCTCACCCCTTTCTTCTC[C]AGTACAAGGTTAAGA GCCCATTTCTTCAACAAACAAACAAACATAGAGCAAT
WI-15729	35 A G GTGTAGACTGC	CTTTGAACCAT	CTCAGCTTCTT TCTAAAGTGCC	TCATTTAAGTGCACCTTTGAACCATGTGTAGACTGC[C]AGGACCTTTAGAAAGAAGCTGAGACTGAA AAGTCTGTCTTGACTTCCAAGGAAGGTAAAGTCCCTGTTTGCAGCCCCGGGCTGCTCATTTGTA
WI-13424	66 G A C	TGAGGTTTTTC ACCTATTCTT	TTTTCTCCCC AGGGTCTA	GTCCTTTGCACAAAGTCTCCCAACTGGTTTGGAGTTTCCCTTCTGAGGTTTTTACCCCTATTCTTC[C]G/A JTAGACCTGGGGAGAAACACATGTGTAAAGTGGCTCAGGACATGAGGCAGGCCGTTTCAACAAGAT GCTGGCTAAGCGGCTTC
WI-14065	29 T C AATT	TCTTATAAAA GGTCAGAGGC	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAAGGTGAGAGGCAATTT[C]GAGATCCAGATTGAGCTTGTCTCATAAAAAGAT TCAACTTCAAGTAGCACAAATTTCTGTCTGCTTTTAACTCTGAACATTTCTGAAGCACGAA
WI-13446	22 G C TCACTCATCA	GCCATGTTCTT	AAGGGAATCA AAATCAGAAG G	TGCCATGTTCTTCACTCATCA[C]CCTTCTGATTTTGAATCCCTTCTGCTCTGTATTTTTTCTTC TTCCCTTTTAGGGCCTAGTCTGTTTAGAAATCTGGTTTTTGAGAGTAGTGAGCCCTTTTACTTTTT CTGACTGGCTAAT
WI-13725	56 A C TGGGTGOC	TGAGCACATA	CCTGCTGTCTC GGGC	TCACACAAGGCATTTGGAAATGTCACTTACACATGGTGAGCACATATGGGTGCC[C]GCCCCGAG ACAGCAGGATAAGTTTACAAAACCTTGACCAGGCAGGTTAGAAAGCAAGGCATGGTTCAGGATG
WI-15702d	107 T C ---		---	CAAATGTTTTATGAAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACCAATACTAA[C]TGGGTTCTTTGAACAAATAGTTT TGA
WI-15702c	101 T C ---		---	CAAATGTTTTATGAAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACCAATACTAA[C]TGGGTTCTTTGAACAAATAGTTT TGA
WI-15702b	90 C T ---		---	CAAATGTTTTATGAAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACC[C]TGTGTAACCAATACTAAATAGGGTTCTTTGAACAAATAGTTT TGA

WI-15702a	48 G C A A A G	A C A A A A T A A A G G C T T T C A A	C C T C A C C C C T T T A C C C C	C A A A T G T T T A T G A A G A G A C T C C G A A C A A A A T A A A G G C T T T C A A A A A G [G/C] G G G G T A A A G G G G T G A G G A A A G C A T G T G A G A G A A A C T G T A A C C C T G T A A A C A A T A C T A A T A A G G G T C T T T G A A C A A A T A G T T T T G A
WI-13831b	113 T C		---	T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A A G G A G A T T C A C A T A C T T C A C T G A T C C T C C G G G T A A G T T T C C T T C T C T G T A G A T G T C C A T G T T A A G G T G A C A G T C A A C T A T A A A C A T G G C T C A
WI-13831a	56 G C		---	T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A A [G/C] G A G A T T C A C A T A C T T C C A C T G T A T C C T C C G G G T A A G T T T C C T T C T C T G T A G A T G T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13806	62 G A		---	T G A T T G A C T T A G A A A G G A A G T C A T G T T G A A A T C A G A G A G G C C A A A A C T A G G C C T C A G G T [G/A] C C C A T T A A G C A T G C T G T G A A T G C A A A G G A A A A G C T T A A A A A A T T T T T A A G G G T G A C T C C A G T A A A C A T
WI-14372	86 A G		---	C A C A T T T C A G C A A A C A A A T C G A G G T G C A A A C A G G T T A T T T C A C A T T A A T A T A T A A C T G G A T T T T T T G C A A A T A A A T A G G G A [A/G] T T C T C T T A A A T A A C C A T C T C C T C A C T T C A T G G C C A G T
WI-14373	95 A G		---	A G G C T G T T T T T G A G G C C T G A G G C C C C A C A C A T G A C A A C G T A A G A C T G T A A C C A T G G T C A T G T G A G T T A T G A G C T A G G A A C C C T G G A C G A A A C C A [A/G] C A C A T A T A C A A T C A T C T C C C A C C T C C C A A C G C C T T T A C T T T C A C A G C C T C T G C A
WI-14078	61 C T	A A A G A A G T A A A T T A G G A A G A	T G T G T G C A T G T C T C T T A C T G C	A G A A A C C G A G A A C T C A A A G A A C C A C A C A T G G T G T A T C A A A G A A G T A A A T T A G G A A G A G C A A G A [C/T] G C A G T A A G A G A C A T G C A C A C A A A T C G A A A C A A G G G C A T G G A G G A A G G A C T T T A G A T G G T C A C G
WI-14083	47 C T	A G A C T T G A G A G C T T A A A A C A	G C C T A C T G G A C C T C T A A A C T A C T G A	T T G C T A C A T A C A C A T T A C T C C A G A C T T G A G A G C T T A A A C A A C A C T [C/T] A T T T G T T A T T T C A C A G C T C A G T A G T T T A G A G G T C C A G T A G G C T T G G C T G A G T T G T T G C T T A A G G T C T T A C A A G G C C A A
WI-14085	31 A G	C A T T T A T T T C A T G T G T A A G A	C A G T C A T G T T C A C G T G C T A G T T	T G C A T T T A T T T T C A T G T G T A A G A A G A A A A A C [A/G] T A A C T A G C A C G T G A A C A T G A C T G C A T G G A T A C A C G G C T C A G C A C G A G G C T A A A G T C A G A A G T G A G T G A A A A C A A A A T A G C A T G T T G A T T T A A G T G A A A T A A C A G A A C A G G A G G C C T T T
WI-12169	121 G C	A A T A A A A C T T C C T A T T T C T T	G G G T T C T G A G G T G A A A G A A A A A	G T C A A A G G T T G G C A A A T T T A T T T C C A C T T A T C A G A A C T T A C A A A A T A T T T T G T T C A T T T C T A A A T T T T C A C C T T A T T G C T A G T T A A A A T A A A A C T C C T A T T T C T T T G C T T [G/C] T T T T T C T T T C A C C T C A G A A C C C C C T T A
WI-15705	50 A G A T C	G G A G G G A G A T T T T A G A C T G A	A G C T G T A G T C G T C A A A T A C T C T A G A A	T T G T T T T A T T T G G G G A G A A T G A A G G A G G A G G A G A T T T A G A C T G A A T C [A/G] T T C T A G A G T A T T T G A C G A C T A C A G C T C C T C T C T T T G T A C T A C G G A G A C C C T G C T T A T A G C C C C A C A G A A A T C C T C A T C T G C G G T T G C C A G A C A G

WI-14379	102 C T	TCTATTAACA GGGTATGTCA CAAC	ATCATCTGTTT TGAGGTTGACA ---	TTTATGCTGTTGTTTCTACTGGTGGTCTCGCTCACTAATATCAATCCTAGTAGATTTTCTTT TACTTGTGTCTATTAAAGGGTTATGTACACC[C/T]TGTCACCTCAAAACAGATGATACT TAAATAAAAACAAAGCAGAAA[C/A]CCACCATTTAAAGAGGACACTGCAGAGGCTTATGTACA ACACGTGTCGCCGAGGCTGGCGAGGACTGCGACTCACTCCAAAATTTCTTTGGAGCAGAG
WI-14102	22 C A	CGCAGAGCTG CTGTATTTAAA	GCAGAGATCCA GACGCTGT	ACCGCAGAGCTGCTGATTTAAAAA/GJACAAGCGTCTGGATCTCTGCAGGGGCTGGGACCAGCTGC AGTGGGGCTCCGGCACTGCTCTCTCCAGGACTCTCCACCACCCC
WI-15937	24 A G A	AAACTGAAAC GTATTTCTCTCC	GGCCTTTAAGT TTCTACGGTG	TGAACTGAAACGTATTTCTCTCC/A/JACACCGTAGAACTTTAAAGCGCGAAAAGACTCACACCC ACCACTAGCGGCGAAAAAAGGAAGTTTCAGGTGATACAAGATGTCTCTGCCATCACACCTGAAGGAT GGTT
WI-15944	24 A C A			ATGTTTTATGATCAATTCCAAACATACAGTACAGGGGAGGTGAAATGAGTAAGAAAAAATCAT ATTTAAGTCCCGGTTAACACTAAGCC[A/G]TATTATTCAAATGTGTTTCAAAATACTCAGCCAGAT CACCAAAGCTCAGTCACTAC
WI-14124	92 A G		---	GACAAAGCGTCTCTGGT
WI-14125	88 C T	GGTTGACCTG CATAGATTTT	GGATGGCATG GOCAC	GACAAAGCGGAGTTTCTGTAGTCCAGCAGGGCCAGAGGTTATCAGAACGGTTGGTTGACCT GCATAGATTTTTCAGCAGT[C/T]GTGGCCATGCCATCTCTGTAAGTGAATTAATGAACA
WI-14136	120 G A	GCTTCTCACC ATGTCTTCACA	CTTGTCTGTC TCTTTGGGC	GTTTATTTCTCACAGTTCTGGAGGTTAGAACTCTGAGATGAGGATATCACCAGCATGGTTAGGTTCT GGTGAGGACTCTCTGGCTTACAGCTGGCTGCTTCTCACCATGTCTTCACAT[G/A]GCCCCAAAGAGAC AGAACAGCTCTCTGGT
WI-14138	23 C T	TGTTGGCACCA GAAAAGCT	CAGTATGTACA GTGACATAACA TAGAACA	TTGTTGTTGGCACCAAGAAAGCT[C/T]ATGTTCTATGTTATGTCACTGTACATACTGTAAACAAGACT GCAITTAATATTGTTTCTTATGATTTGTTTCAATG
WI-13551	74 G A	TCCTCAGTAG TAGTATATTC A GACAATC	GCTCATTTCTT TTAGTGCTAAG TAATATT	GGCAGGTTTATTCATAATTTTCAAACCTTGGAAAGCAACCAAGATGTCCTTCAGTAGTAGTATATCA GACAATC[G/A]AATATTACTTAGCACTAAAGAAATGAGCTATCAAGTCATGAAAAGACATGCAGG AACCTTAAATGGATATTACT
WI-15953b	59 C T		---	TTTTTAAGAGTGCCTTCACATCATTTATTTGATTGTCACACAAACCTTTTAACTC[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCCAGTGCTTTTGGAGATAGAAGCCTTCTTCAGAATCA CCTCC
WI-15953a	26 T G A T	TTTTAAGAGTG TCCTTCACATC	TCATCTGTTCT TGTTGTTTTG A	TTTTTAAGAGTGCCTTCACATCATTTATTTGATTGTCACACAAACCTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCCAGTGCTTTTGGAGATAGAAGCCTTCTTCAGAATCA CCTCC

WI-14631	82	G A ---			---	TGAATCAATGGACAGTTTGGCTCTGTTTGTAGTAAACCCCTCACAAGCAGCTCTGTCATAGTCGGCTTTCTGTCTTTTAACTG/AJTGCCCTGGTTCCCTCTGCCAAACTTTTAGGATTGGCCCTCCTCAGGGCCTTGTCTGTA
WI-6053	24	A G ---			---	ATCACCACCGTGTCTAAGAACAAC/AJGTCTTCATGTCCAACTCATATCCCGGGGACTTTGTCAACTGCAGTACACTTCTGCAATTGAACCTGGCTTCTGGAGGGAAGCCTCTAGAGGCCAGGTAAGGGGGTGCAGCAGTGAGGGGTATATCTGGCTGGCCAGTTGGAACCCAGGAG
WI-15964	99	T A CTGGAGGTA	GCTCTGTGC	GACTTCTCCAC	OCCTCTGC	CAGAAACCTCTTCTGTGTATTAAAGCTGATGCTAAAGTCAGAGCAGTCCAAAGGCAGGAGGCTGCCTTGGGAGGTAGTAAGCTCTCTGTCCCTGGAGGTA/T/AJGCAAGAGGGTGGAGAACTCTTGGCAAG
WI-12075	103	G A GGCAC	AGCAGCTGGG	CCCTTCTTTC	TCTTCTTC	CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAGCAACAAGCCAGGCCAAATACCCATCAGAGCAGTGACAAGAGCAGCTGGGGGCACGGGGGAGGC/G/AJGAAGGAAGAGAAAGAGGGGAGGAGCCT
WI-12179	96	G A TGGAGGTCA	GGAGGTACGG	TGGAATGACCC	TGTAGATGC	TAATTTAAACACGCCCTTCCACATAGTGCCTGAGGCATCTGCACATTTCTCTAGAAGGACATGATAGTGATGGAGGTACGGTGGAGGTCA/G/AJGCACTCTACAGGGTCATTCGAGGGGAACAG
WI-14651	49	C G ATTGT	CAAGAATCAT	GGAGATATTGA	CTTATT	CACAAATAGTGAAATATCTGAGCAAGAATCATCTCTATTTAAATTTGTC/GJAAATAAGTCAGAAAGATCAATATCTCCCTGCTTCAAAATGACACTCCCAATTTTACAGGTAACCACTGTTA
WI-14666	105	T A ---			---	AATGTGGACTTCAACAAGGGTTTAAACATAATCTAATAACAACCTCTACAACACATTCAGAGCATATAACAAGAATTTACAGGCAGCTAATGTATTAAAT/AJAAACCATGAAAGAAAAAATTTG
WI-13473	31	C T ---			---	ATCTAGATGTCAGCAATGGCTGAGACTGTC/TJGTCTGGTAGATGCAGTGTGTATGTTTCTACCTATTACAAAAATTAACAGAAATATGGCTTGTGCAAAATGTTTATATCACAGTC
WI-13967	103	A C AAATAAAAA	AAAAGACTAC	TTGTGTTTCA	TG	AATTTAATAGCAGCTGTGTGTGATTTTAAAGAACAGATAAAATATGTCATTTCAGCAGTCATTTAAAAATAAAGACTACAGATACAAGGAAATAAAA/AJ/CACCTTTAGGAGATGAAAAACACAAA
WI-14408	60	T A G	GCAGACACAC	TTAATTGTGTA	TTACTTT	TTAATATTTACGCAAAAGTTATTGCAACAGGTTGAAAATGCAGACACACTATTACAGGCTGT/AJAAAGTAACAAATGAGTTTACACAATTAATAATTAACACATACCTTATGGGATTTGTTGAATGA
WI-13683	47	C G ---			---	TTTTGTGTTAAGAACAGCATTTTGAAAAATAAAACCTATCTGCCCATG/CJGTTTTACAGCCTTTTAAATTGTAATATTATATAGTCGTTTATGGTACATATTGATTGC
WI-13910b	63	C T CGTCT	CACCATGGCA	CATTGAGATAA	CAC	TTAGAAAACCTGATAAAGCAACACAACTTTTGGGAAAGCACCATGGCACGTCCTTTGTGCTA/CJTGTGATAAGTGTGCTTTATCTCAATGAAGCAACCCCA
WI-14635	22	G A ---			---	ACATGGCAGATACAGAGCTGTG/AJGTCTTGAAGACCACCACCTGACCAGGAAATGCCACTTTTACAAATCATCCCCCTTTTCATGATTGGAACAGTTTCTGACCGTCTGGAGCGTTGAAGGGTGACCAGCACATTTGCACATGCAAAA

WI-16002	59 T	GATAACATAA AATGATCATG CAGAAATTC	GCCATCTCTC TTTGACTTTT	CCAACATTTTAAACCTATGACTGGTCATTGATAACATAAAATGATCATGAGAAATTCATTC/GTGA AAAGTCAAGAGGAGATGGCTAATGTCATGCTGGCT
WI-15361b	101 A G A	CCCACTGAAC TCAAGTCATC G A	AAACTAAAC CTTTGTGCTA AAA	GTGGAATTTTAAAGCCATCAAAATTCCTTCACACTCAATACTGTTGAACAACAAGATAACACAT CTTCTGTGCTATCCCACTTGAAGTCAAGTCATCA/GTGTAGGCACAAAGGTTTAGTTTTCTCGG GAAATCAAGTTTTAACCA
WI-14759	73 T C	GGGTTGACTT GTGGG	TCCACACTGC OCC	TGAGTTACAAATGAGCAACAAGTTAGAAAAATGGTTTTATTCAAACCTCCTAGCGTTGACTT GTGGGGTTC/GTACTCAATGGGGGAGTGTGGACGGGAGGATTGCAACCCAGAGTTTCATACTG CAA
WI-12535	50 A T T A T	CTAGGAGGTT GAGGTGTAGA TAT	GCTCCACGAGA AGAGAGGAA	TCCCTAACATTTATTCAGGTGGTGACTAGGAGGTTGAGGTGTAGATATATCTTCTCTCTCTC GTGGAGCCTTACTGAAGACAGGATCGCGTTCTTGTTTATCAGCTGAGAAGGCGAGTCTCGCCATC TTAAAGACCTGCCCTCC
WI-13805a	112 G A G G G A A	AAAGGCACAC GGGAA	CTCAGCCTGOC TTGACC	TTCCATTATTGCTTGGCTTTACCAATTTTTATAGCTATTGGGAGGCGAGGAAATTTTGGC CCCAGAAACCATGAGATTTGGTTCAGAAAGGCACACGGGAA(G/A)GGGTCAAGGCAGGCTGAG AGTCACATTTCCAGACCTC
WI-12340	18 T C	---	---	ACACAATAATTCATTC/GCAGTGATTAAACCTATTTGTGTTTAGAACCAACAAAACTAC AAGAAAAATTTCAAACCTTTTTTTCAGGCTGA
WI-14808	52 T A C T A C C C T G T	ACCCACCACA CTACCCGT	GAGGCATCACA ATGTTAAGATT TT	CTTTGAAACACTTTAAGCAACAGTTAAAAAGTACCACCACTACCCTGTT/AJAAAACTTTAAC ATTGTGATGCCCTCTGCATCAATTTTAGAAAAACAAGAAAAACACAACTGAAGGCCCATGTA AGTTAAAAAAAATCGAGTCAGCATTTATT/AJAAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTGTATCCCAAGCCCTGAACATGAAAAAATATTACTAAAGGAATGTTG ATTACCAGCTACGACTTTC
WI-14816	29 A T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGGCTCTAGATC ATG/GTTAGGTGATTGATACAAATACGATCCATAA
WI-12542c	71 G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGGCTCTAGATC ATG/GTTAGGTGATTGATACAAATACGATCCATAA
WI-12542b	70 G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGGCTCTAGATC ATG/GTTAGGTGATTGATACAAATACGATCCATAA
WI-12542a	45 C T T T T A A A	GCTATTAGGC AAACTGAACA TTTAAA	TCTAGAGCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGGCTCTAGATC ATCATGGTAGGTGATTGATACAAATACGATCCATAA
WI-12173	57 C T C A A A A A	GGATACAGCA GTAAAGAATA	CCACCTCTAGA ATGTATGCTCT	CACCTAAATCATCTAGAAACTGGGGATACAGCAGTAAAGAAATACAAAAATCCTGC/C/TCTTATA GAGCATACATCTAGAGGTGGGAAAGAGGCAATAAATA

WI-14836	28 T C ---		---	TCITTTGGAGGGATAGAGGACAGAGTGTTC/CJGTTGATTTTCGTTTCGGTTTCAGITTTGGTTGTCATT GGTTTTTGTTTTTGCTAATTTTGGCCCACTATAAAAAGCAGTGGCCACCCAGAGGCAG
WI-14856	60 A T A A	TGGTGACAG GAAAATACTT	TTTGTTCGTA CTTTTACAAA CTTT	ACATTTCTTATGATAGCAACAATAATATGATGGATGGTGACACGGAATACTTAAATATTTAA AGTTTGTAAAGATAGCAACAATAATTTGAGTATATACTATAAGTGATAGAGGATGTATATGAAAAA GGCTATAAAAAGCTCCAAAA
WI-14863	61 G A ---		---	ATGGCAATTTTACTTTATAGCAATGAACAAATATTTGTCAAAAGGGCAAAATATTTTGTCTG[G/A]AG TTAATAAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCACATATTATTGATTGGCCACT ACCTGGC
WI-14867	46 T C A	GACATTCCAA GGCTCTCTAAC	TGGGCTGCAG ACACTC	TTTTAATTAACGTAAAAAGGCGAGACATTCCAAGGCTCTCTAACA[T/C]GAGTGTCTGCAGCCCCA TTGGCTTTGAGATGTGAATGTGTTAACCCAGGTGGA
WI-14733	98 G A A	CCAAATTGAC AGATATTCTGC	GATGAGGTCAG GCCATTTATT	ACGGAGTCGTCTCTGATGATTTCTTTGTCAAAAAATGTTTGCCTGATTCTAATCATGAAAGAACAAAT AGAAAAATCCAAATTGACAGATATTCTGCA[G/A]AATAAATGGCCTGACCTCATCAAAAAACATCA ATGTCATGAAAAACACAAAA
WI-14898b	79 A C ---		---	TTTTGTACCTATTCCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCTATAAGGTGCCACTAAGGAAA ACTTCTCCAT[C/A]AAGCTGCCTGCTGTGCACGTTGCCTGGGCTTTGCTAACCCCTGGTGTGCATCT GCCTGTGTTCTGCTT
WI-14898a	50 A C C A	CATGTACAGG AAGAGTTGTCT	AAGTTTTCCIT AGTGGCACT	TTTTGTACCTATTCCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCTAT[C/J]AGGTGCCACTAAGG AAAACTTTCTCCATAAAGCTGCCTGCTGTGCACGTTGCCTGGGCTTTGCTAACCCCTGGTGTGCATC TGCCGTGTTCTGCTT
WI-14907	48 G A	GGCACACATT GGACTCTGAC	TCTGCTGCAAG GGGAAT	TGGTATTTATTTCCGACATTACTGTAGAGGCACACATTGGACTCTGAC[G/A]ATTCCCTTGCAGCAG ACATTTGTGAAGCTGCTGGTGGCACACACCATCAATCAGTGACTCTGCTGACACTGAGAGGGGCCACATG CAGCATGCTCAAGTGTG
WI-14911	52 G A C	CCAATACATT CAGTTCTGTT	CAAAACCAGGA AAAGGACCTT	CTAGAATCTGGGAAGTCCAAGCTCAGTGCACCAATACATTTCAGTTCTGTC[G/A]AAGTCTCTTTTC CTGGTTTGCAGACAGATACCTTGCTGTATCTCTCACATGGCAGAGAAAGAGAGAGTAATCT
WI-14913	88 C A ---		---	CTGATGCTTTGACATCTGGGGCATTGCTGTCTCTAGAGAGACTACTTCTCTCTGGGACCAGCCAAATTC TAGTGATAGTAGAGGACTCA[C/A]CCTGCACGTGCACCTTTCTATATACAGATCAACCAATCCAAAAAC CTACACCTCCAAACCCT
WI-14914	66 G C A	CTGGACACAG TTTTCTCTAGC	CAAGCCAGGA CAATAAATTC	ATTTCTTGTATTGGCTGTCGTAAGCCTGTGAAGTCATGCACATCTGGACACAGTTTCTCTAGCA[G/ C]GAATTTATTGCTCTGGGCTTGATGGCTTTACAGC
WI-14926	49 T C ---		---	GTTTATTTTCAAAATGACACATCCACAGATTGAAATGGGCACCTTAGCGAA[T/C]ACTTTGTGGACCACA AGACTTGTCTGAGAACATGTTCAAAAGACAGTTTTCAAATAAAAAATTTTCTTAATCAGGTCCA

WI-16083	89 C T	ATGTTTAAACA CAACATATC AAGGAT	TGGAAGAAGATT CCAGGCC	GCATCTTTATTACCAGAACTCATTTATGTCCTTAATCATTTGTTTAAATATATATAAGCATGTT TAACACAAACATATCAAGGAT[C/T]GGGCTGGAATCTTTTCCATTCTATAGAAAAGCACTAACCATC CATTAAAGCAG
WI-14930	55 C T	GGAGGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTCTGTGTTCTGGAACAGCTCTCTTTCCACAGGAGGAGTCCCTCATGGAT[C/T]GCGGTATTG GTTGGTTGTGGTATTGGGGAGCAGAGGGAGAGCAA
WI-14946	47 T C	---	---	TCAATCTGAAGGTGTCAAAGTGGTCTATTGCCCCCAGACATAACAT[C/T]CTCTAAATCATCTCTA GATCAGGGAGTCTATAAGGACCATTAAAGGCTCATTACACACAGTACTTTATGGAAGGATT
WI-15987b	80 A G	---	---	ACATTAAACACAGCACAATTAAAGGGGTCCCAACGAGGTGGTAGTGCCCTCCACTATGTGAGGACAC TAAGAAGATGGT[C/A/G]TCTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-15987a	32 C T	CACAATTAAA GGGGTCCAA	GGAAGGCACTA CCAACCTC	ACATTAAACACAGCACAATTAAAGGGGTCCCAAC[C/T]GAGGTGGTAGTGCCCTCCACTATGTGAGGA CACTAAGAAGATGGTCACTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-14948	56 T C G	AGGGAAC TG CTAAGTTGCA	GATGATCTTAC ATCAGTTGTTG	GAATAAAGTCTTATTGCCGTTCTTCAGGGAACAGGGAACCTGCTAACTTGTGAGT[C/T]CCAAACA ACTGATGTAAGATCATCTCTGACCATAGCGAACCTGTAAAGGCTTGCTTCCCTCCAGCTGA
WI-16100	52 A G	CAAAAGCTA TTTCTACAC	ACAGGAATGTC AGAAAACAGT	TTGTTTAAATTCATCAAGGAATTGACAAAAAGCTATTTTCTACACTTGAC[A/G]GTAATATACTG TTTCTGACATCTCTGTTATCAACTCTCTGAAAAATC
WI-14958	83 A G	AATAATTTAT CTCTTCTTTT	AATGCAATTCAT TTGGGTTTTT	GTGATTGATCTGTAATTATTGGGATTATTATTCAACTCAAAATCCAAAGTAAAAATTTATCT CTTCTTTTCAAGGG[A/G]AAAAACCCCAATGAATGCATTTTCAAGTTCTCCAGGCCCTTTGAACTGC AGCAGAAAAATTCAGGA
WI-14976	35 C T	GTTGATTTGCT TCGTTCAAAG	TCAAACATAAT CTTCCATTCTA	TATTTTTTAATTGGTTGATTTGCTTCGTTCAAAG[C/T]GCTTAGAATGGAAGATTAGTTTGAGGAG GGCAGGTTTGGGGTAGGCTCAGCGGGCATAGTGGCCACAAAGATGCCCATCTCACACCTGGAG ACGTCCATGAGCACTCG
WI-14981	31 G T	TCAGTGGTGT TATTGGATTT	CACCTCTGACA TAATACTTAGC	TAATTGATTCAGTGGTGTATTGGATTTT[G/T]TTTATGCTAAGTATTATGTCAGAGGTGGAGAAT AAAGAGGAAAAAGAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTACAGGAAGTTTTTGA GAGCTCACAAA
WI-14992	80 C T	TGCATTAAAT GAAGCTGCAG	GCTATGTGCTC AGCTTTCTC	TGATTACATTTTTTAAATATCATGCCCTACCAGCCCATCTAAGCCAAATTCAAAACACCCTCTGCATTA AATGAAGCTGCAG[C/T]AGGAAAGCTGAGCACATAGCACCCCAACTGATCGGAAAGAAACGTA
WI-15002	72 T A	---	---	AAATCTCTCTTTCACACACAGATGAACCTTTAATAAATTACAAATGCACCTGAAAAATGCCCTCTTGA TTTCC[T/A]TTCAGTTTAGGCCTCAAATGGGCTCTCCTCAAGGCTGGACCTCAAAGGCCAGTT
WI-15000	90 G A	GACAGAAAA GACTCAGACT	GTTTCTAGTTC TGCACAAACTT	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAATAAACAGATGGATAGACAG AAAAAGACTCAGACTGTCTAAGTA[G/A]TGAAGTTTGTGCAGAACTAGAAACAAAAATCCACCT CA

WI-12323	68	G A	CACAATACCT CATGTACCTAT	CACTGGACATA TTCCCTACCTG	ATTTGTTGATGTTGGTTAAATCTTATCTCTTTTATACACAATACCTTATGTACCTATGAATAA G/AJACAGGTAGGGAATATGTCAGTGCAACACAGAGGACTCACACCTGTGCTAGACAGCACC
WI-14683	91	A T A A C A	AAGGGACGAT TTAGTATCTAA	GGCATGTCCCA GTGTTTT	CATAAGTTGCATTTATTCACGCTCCAGCCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTTAGTATCTAAACAA[A/T]CAAAAAACACTGGACATGCCCCCTGAATTGCAAGT TGGAGTTCGTAAGAATCTAC
WI-13470	100	C A T	CTGCCCTTTAT ATTGGAATTC	GGGAGACCATG GGTCTCT	ATTTGTTGTTTATTAGCACCTGAATTTAGGCAAGAGAAACATTTCTACCTGAAGACTCCATGCAGT CAAAATTCCTGCTTTATATTGGAATTTCTA[C/A]JAGAGACCCCATGGTCTCCCCAAGTGAGGAAGCC AGGCACCTAGCCCTTC
WI-14712	38	T A C A	TGAATGCTTCC AAGTACAAAT	TGAAAGTATGT TGTATATGGTA	TTTGGTGCTACTTTGTGAATGCTTCCAAAGTACAAATCA[T/A]JCTCACAATACCATATACAAACATACT TTCAATCACAACTCAAAATATAAAATAACCTACAAAATCACATTGC
WI-13712	40	A C T C T A T T G	TTTACITTTGT GTCAATTTTAT	CCATAAGGTCT CACACTTTTCT	TGGGATACCCCTTTTACTTTGTTGTCATTTTATTCTATTG[A/C]JATTATAAGAAAAAGTGTGAGACCTT ATGGCTTCTGCTTATGGGCAATATGCAATATAATTTGTGTTGTTAAAAATTTATGCAT
WI-16163	35	C T A	TCTGGTGATGC AATTGAAATA	GCTGCCAATTA CATTAACCTTAC	TCTAAGATTTTACTCTGGTGATGCAATTTGAAATAA[C/][A/T]GTTAAGTTAATGTAATTTGGCAGCATT GCCCAAAGTTTAAGAGGACTATTTCTTTAAACAAAAGACAGTGTCTGACATTTATTTCAGGT
WI-13453	88	T A T C	AATGCACAAA ATCTTGCTCT	TCAGATTTTAA CATCTCTTCT	TTTTTTTATTGCAATTTGAGTGCTTTATTATATTGGGAATTTGCAGTGATATTAAACATTTGTACAAAT GCACAAAATCTTGCTCTCTCT[Q/T]A/JTGCTAGAAAGAGATGTAAAAATCTGACCTAGTTGAACAGTCTT AATGAACCTCATTGTCCAT
WI-16167	58	T C G A T T T T T	CGCACTCTAA ATTAGAGATA	TGCTCGTGGTG AATAAGATG	CGGATATAATTATGTACCGCACCTCTAAATTAGAGATAGATTTTTTCTGATATACATTT[C]CATCTT ATTACCCAGAGCACACCACACGACAGTAGAACAGITCCACACCTGATAAAATTCACAAAGATG
WI-14482	17	G A ---	---	---	GCAGAACCAATTAA[A/G/A]AATCTGCAAGTTTTCCCAAGAAACTCTGGAACCATAGTGCCTAAT GCCCTTTAAATCGATACTAAAGGAGAGAGATAAAAGGAGTGTCTGATGTGACAGTCACTGGT
WI-15069	81	T C ---	---	---	TGTAGTTCTTCAAAGACATGTTGGCAGATAGCCAGGCCATCTATGTGTATCCCAGTATCATGTAC GCACTAAAAAAAT[C]GTGTGCTTGTCTGCTGTGTGAGTGAACCATTTGCTTAAGATAAA
WI-16156	97	A C	TGAAGATTAA CCAGAGTCGC	AATGTGTGCA TTTTGAAGAGA	ATCTGGTATTGTGTATCCCAACAGATATACAGAACTACTCTATAAAACCAACCCACCCCTTCAATA TTACACTAATGAAGATTAAACCCAGAGTCGC[A/C]TCTCTTCAAAATGCACACAATTAAAGACG
WI-15012	59	G T A T G T	GCAGCAAGAT TACATCAGTA	CTCCAAATAGC CTAGAGTATAG	CATGGCAGCAAGATTACATCAGTAATGTAATATAATACAGCTTTTTTTCATTGAAGCTTT[G/T]TACCT TACTACTCTAGGCTATTGGAGTGTCCCCAC

WI-15100	74	G A ---			---	TCATTTCACAGCCAAAGAAAAATACCCAAATTATTTCCAAATAAAGCAAAAAATTGGAACAGACTGGA GTGAGAAAC[G/A]GGTTCCACCACCAAGCCCTCAAGACAAGATGGACACGGCAGCTGTTCTGGGGT GCATTTCTAGTGGACTTTAT
WI-14492	92	A T AATTACT	CCTTATTTC CCAAATATAA		GTCACCATGTT ATATTTCTTT TAAGAC	TGGTACAGAAATGTTTAATTACAGCAGGGCAGTGATTCCAGTTAAATAAAAAACCTTTATTTT CCCAATATAAAATTACTAAATTAA[AT]GTCCTTAAAGAAAAATATAACATGGTGACAGCTTT
WI-12002c	89	T C ---			---	TCCTTAATTTTATCGGAATCCAGGACACAACAAGAAAAACCCAAAAACCCACATGGAGACAGAAG AC[G/A]JAGACACAACCTCTCCCCACTGCCCTCCTGCTCTAGAGTGGGGACAAAAGTGGGGTGAGAC AG
WI-12002b	68	G A ---			---	TCCTTAATTTTATCGGAATCCAGGACACAACAAGAAAAACCCAAAAACCCACATGGAGACAGAAG AC[G/A]JAGACACAACCTCTCCCCACTGCCCTCCTGCTCTAGAGTGGGGACAAAAGTGGGGTGAGAC AG
WI-12002a	30	C G GGACACAA	TCGGAATCCA		TGGTTTTGGG TGTTTTCTT	TCCTTAATTTTATCGGAATCCAGGACACAACA[G/G]AAGAAAAACCCAAAAACCCACATGGAGACAG AAGACGAGACACAACCTCTCCCCACTGCCCTCCTGCTCTAGAGTGGGGACAAAAGTGGGGTGAGAC AG
WI-15116	96	C T GTTGACGTAA	GGGAGCCCTA GTTGACGTAA		CCTGAATATGC AATTATTTATT ATGACA	TTTTCATTTATTTCCAGAAAAAGAAATCACATTTTCAGTAACAACCTACATATAGAAATTAACCTTTG TTCTGGAATGGGAGCCCTAGTTGCAGTAA[C/T]GTGTCATAATAATAATTGCATATTCAGGATTTTG TGAAATAGGTGATTGGGA
WI-12578	37	C T AATGGGAA	GGCTAAAGG		TCAAGCGACCA CCAACAC	GCAAAAGCAAAGCTATGGAGGCCCTAAAGGAATGGAA[C/T]GTGTTGGTGGTCGCTTGACTTGGT GCTTGTCATGGATGGAGCAGAAAGTCTTCTGCTCCATGCAGGGGGTCACATATTTTAAGTGCACATAAT TTGGGCAAACTGTCAATC
WI-15153	40	A G GCATTGCA	CCCTTATGTTG GCATTGCA		AACCTCAGATA AGTGCAGTGT T	ATTCACGTTGGCCAAAGATCTCCCTTATGTTGGCATTGCA[G/A]JAGACACTGCACCTTATCTGAGGTTA GAAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATACCATTTCCTAA
WI-15215	84	G C TCAAATGGG	TGGCTTTAGAA TCAAATGGG		CCAACAGGGGA AAAAGTCA	CCTTTGCTCTGAACTGGGACCAGGATGTGAATAATTTTGAATCTGATGCAGGTCGAGGTATGGC TTTGAATCAAATGGG[G/C]TGACITTTTCCCTGTTGGTGGAAAACTCTGTGAGGGTTTGGCA
WI-15225	80	C T C	CTTGAGGACCT AGAAAGCAAA		TTTGATTGGCA TAATCACTCC	AGGAAAGAGTGTGAAGCAAGGGCATCTTGGATGGAATGATTATGTGTCCAGGACCTTGAGGAC CTAGAAAGCAAAAC[C/T]GGAGTGATTATGCCAATCAAAATTCGAAGTTGGAGATATGCTAAAA
WI-15152	51	G A ---			---	AATTTGCTAGTGCAAAATGGACCCAGAAATGGAAAGGGCTATGTAACTACACAC[G/A]TATGCACACCCAC AGCCATGTCAGTGTACAGATCCTCTTGTGCATTACGCTTTCTTAAAAACACATCAAAAGGCTGCA
WI-15123	55	C T TAGGATG	TGTTAGTGACA GACAGATAAA		TTGCTTAAGGG CAAACAGAC	TGACTGTATACCAAAATGCTGTGCTTAATGTTAGTGACAGACAGATAAATAGGATG[C/T]GTCTGTTT GCCCTTAAGCAATTTACAACCTCACTGGGGAAGAAACAGACATGCAAAACCGAGATAAAACACAAT

WI-15182	49	C A	GCACAACCAG GGCAAAATA	GCATGGGTAA TCCAGCA	GAGACTGCCGTGTGACACAACACTAGCTAGCTGACACAACCCAGGGGCAAAATAC/AJTGCTGGATTAAACCC ATGCTAATGGGTACCTTATTAGTAATCATGGGTCCCTCATAGCATGGTCCAGATCCG
WI-15198	38	T C	GGGOCCTGGC ACTATG	ACTTATCCGTC AGCAGAGTAG	GTGGACCTCTACAAGTACCATGGCCCTTGGCACTATGTC/CJCTACTCTGCTGACGGATAAGATTGGC ATATGGTTCAGATTGCTGTCTACACAGTCCAGTTTCCCTAGAGACTAGTCCGACTCTCTT
WI-12601	42	T C	TGAT	GTGTAGTCTT ACATGCTTACG TAGAC	TCAAGTGGTAAATAGCCATTATTAGTATTTCTGCTTTGATTC/CJCTACGTAAAGCATGTAAAGACT ACAACATTACGACCCCATCTCTTCAAGAGGAAGTCTGGTATTATGGAAAAACAATTTTGTCATTCAGAT T
WI-14510	104	A T	TGCAAAATA TGCATAACAA AA	TTGAAAATGGT TAAACTGGCA	ATGTTGAGAGTAATAATGCCCTACATATTAGTGTAAAGTACACCCACAGATATTTTGGGGAGAAGAG TTGTTTGTCTTTTGTGGCAAAATATGCATAACAAAATATTTGGCCAGTTTAAACCATTTTCAAGAGT
WI-15239	57	T C	CAATTGCAAT AAACACCATC A	GGACCTTATCT GTGGACTCAGG	CAGTGTGATGACATTTCAATGGGAAAAGATTGTGCATTTGCAATAAACACCATCATTT/CJCTGAG TCCACAGATAAGGTCCCGGAGAAAGGGCTTCCCTCTCTTCTCGCTGGTTGACGTTCCACGGAGT
WI-12634	52	T C	AGT	AAATAGC	GAAGCCTTTCTGGAATG
WI-15249	34	T C	AAAGTTCTAA AA	GGAAAGCCAG AGATTTTAAAC	ATGAGTTTATAAACTGGAGACAGCGCATCATATGAACCTGTCTAGCAGTATTATTC/JGCTATTAGCTA TGTTTACAAATTTGTCTGAAGGGGTCTAGATGTGTACACCCAGAAAAGTGGTATTCTCTGA
WI-12159	28	C T	GCAAAATGC	GTGCACCTT	TTTGCTTGAAGGGCTTGACACAAGTTCTAACTTT/CJTTGTTAAAAATCTCTGGCTTTCTGGCTGG TGAGAGGCACAGGCTGGGCTCTTCAGGTATCCACTGGTGGCCCGCATCTGTTCCTCCACTCCCCAG CCACATCTTGGCTCT
WI-12648	41	A G	TAAGGATGC	AGTGGACATCC T	CTGTCCGGGGAAGACACCGTGCAATGC/CJAAAGTGCAGTGAAGAGAGGGGAGGGTCTGTGACTC CCAAACCCCTCGAATATTTATGATCTAAGAGTCCAGACGCAGTTTCATCCACGGAGATCTGC
WI-12684	64	G T	ACAGCTGTGC	AGCCTAAATGG	TCCCATTTAGGCTTTGTTTCCATTTAGAGAGCACAGGAGGAAATTTAGCATAATCTT
WI-15260	75	G A	GA	AGCTTGC	TTTATAAGCTGAATGAAGAGGTGACACAGCGGACACTGTCTATAAGTGGAAACAAAGGATGAAGCT AATCATGGA[G/A]GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAATGAGCTGGAGAAATTA TCCCTG
WI-15325	39	T C	GAGGC	GATTGTGA	AAGTTTAAATGGACTCACAGTCCCATGTGGCTGGAGGCTTC/JTCACAATCATGTGTGGAGGCAAAA GGCACATCTTACATGGTGGCAGTCAAGAGAAATGAGAGC
WI-13936	123	C T	C	CATGGAGTT	TATTTGAGTATTTTCATCCATGGGCTTCTCACTCCCTATACATTTCTCCAGGGTTGAGGTAGTCTACCC CCATAGGTTTCAGAACCTATGACCTGTATCTTCAGTTGGCATTCATAGCCTATCTC/JAAGTCCATGT GGGAGTTTCATAATAA

WI-14528	62	T G T A A A T	TCTGGATGGTA	TTTTAACTTTT	CTCGATTAGCA	TATGCTTTATTGAAGAGAAATAGGCTATTAAATATATTTTAACTTTTCTGGATGGTATAAAAT/GJTT GAATATAAAATTTTAAATTTTATAATAAGTCTAATCGAGACATCACTGGGTATAATTGA
WI-15347	74	C T A A T T	GAAAGAACCA	GACTTCAAAG	TCACCTCCCCA AGTCTTTG	TATTTCTTTGCGTTTCGGATGCAAAACAAAAATTTTAAAGAAAAATGTGACTTCAAAGGAAAAAGA ACAAATTT/C/TCAAAGACTTTGGGGAGTGAAGGCAGAGCCTGGTGCAGATGGACGAGGTCTGCAGA CG
WI-14546	95	C A G G A C T C A	TGATAGTAGA	CCAATTTCTAG	AAGGTGCACGT GCAGG	GTATTTCTGATGCTTTGACATCTGGGGCAATGCTGTCTCTAGAGAGACTACTTCTCTGGGACCAGC CAATTTCTAGTAGTAGAGGACTCA/C/A/CCTGCACGTGCACCTTTTCATATACAGATCA
WI-15353	37	G A ---	---	---	---	TTTATGGCTGTCTCTGTAATACAATGTGGTGAACAC/G/A/TCTTAATTCAGGACATCTTCCACCTTG TTTTGGCTCCAGTTGTAAGACACAGTGTGAGGCACATAGGCTGATTAATCAGTGG
WI-14580	100	G A G T C T G C A	CATTCCCATCT	CCGACCAAGAT	CCCTCC	AGAATTTTTCCTTTTAAACAGGACAAATGTAACAGATTACATCAAACTTCAGAACTTCTCAAAATAC CTAGTTATTATACACATTCCTCTGTCTTGCA/G/A/JGGAGGGATCTTGGTCGGCTTAACA
WI-8540	73	T C G G C T T A	GGCTGCATTT	GCCTTCTTTT	TCAGGCAC	CCAGCTGGAGGTGAATAATGCGGCAACACAGAAAAACACACAGCTACACACAGGCCTGCATT TGGCTTAT/C/JGTGCCTGAAAAAGAGGGGCGACCTCTTGATAAAGAAATGTCT
WI-8039b	97	T C ---	---	---	---	AAGTAGAACACAATAGATGGCTCAAAAATATCAGAAATGCACACTACGCACATCACGAGTAAATACTG TTTGGTAAACTTGTTCAGTTAAATATGAT/C/JGTGCCGTGCATGTGATTAATATCCTTCT TACCACAGTCACCTAAAGAACCAAGCTTAGGACTAGGACACACACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGTTGAGATGATGATTTAATGCCGACGCCACACCCACA
WI-8039a	87	T C ---	---	---	---	AAGTAGAACACAATAGATGGCTCAAAAATATCAGAAATGCACACTACGCACATCACGAGTAAATACTG TTTGGTAAACTTGTTCAGTT/C/JAAATATGATGTGCCGTGCATGTGATTAATATCCTTCT TACCACAGTCACCTAAAGAACCAAGCTTAGGACTAGGACACACACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGTTGAGATGATGATTTAATGCCGACGCCACACCCACA
WI-8044	107	C A ---	---	---	---	CACAACATTCAGAAAGTTTCTGCAATGTGTCTCTCTGATGTCTAAAAAGATTTGAGCTTTGACTAT AGGATTTCCACACTGAACGCATTATAGGTTTCTCC/C/A/JAGTATGGATTCCTGATGATTAATA AGCCCGAATTCGGCTAAAGGCTTCCACATTCAGACATTCAGAGTTTCTCCAGTGTGGAC TCTCTGGTTGTCACAAGATGGAATCGGCTCGGCTGAATGCTTCCACACT
WI-8550	32	G A A T G C A C A A G	GGGAACATCA	AGTTTACAAAT	TTTGGGCTTG	CTTACTACATGGGAACATCAATGCAACAAGT/A/G/A/JAATTTGTAAACTCAAGCCACAACTTAGTTA ATAATCATGGTTAAGGGACATTGCCAAAGAGCAACTGATGCCTCAGTGAA
WI-8057	87	T A ---	---	---	---	TATTAGATAAAACCCCTTTGTTCCCGATTCCAGGATGTTTAAATTTGCTTCTTTAAACTCTGTGACTTTT CCTGGTTCAAAGGACAGT/A/JGATGGACAGCAGCAGAGGAGTGGGGTCTGAAAAATGTAATCTTT GTGTCAGGCACTCTGTGCCCTCACAACTGCCCTGTGAGGGATGCTGCCCTCCAGGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGGTGTGAAGCAGCCAGATGGTAAGG

WI-6192	91	A G	GACTGCTAAG GATTTAAATTTG TAAAA	TGAAGTGTTAG ATGGCTAAGTA TAAAA	AAGAGGAACAAATTAGCTCAGTCCAACATGATTGGCAGTTGGCATAATTCAGTGAAGCAAGTGTTCT GACTGCTAAGGATTAAATTTGGATAG/ATTTAATACTTAGCCATCTAACACTTCAAGCATAAC
WI-6194	105	T A GAAA	CACATGGCAA TGATAATAAA CA	TCTATCCTCAG AGTGTAGTCTG CA	AAGTGATGTCTCTCACAATAACATTTCTCAAACCTCAAACATCATGCTTGAATAATCAGTGAACCT GTCACCAAAGAGTCACATGGCAATGATAATAAAGAAAT/ATATGCAGACTACACTCTGAGGATAG AGCTCAAAGAGTAAACAAATGGAAATTTGGAAAAAATAGGAGTAA
WI-6213	164	C T ---		---	CATATGCTGCTTATTTCTGTAAGGATACACTGAAACGTTAGATGATAATAGCTAATGACAGAATGT AGAAATGAGGCATCAGCTTCTTAACCACCTCTACAAAGATGTTAGTATGTATTGTCATTACATGTT ACTTTTGATAATTGCTCATTATACATATGTTC/TATATAATAATGTAGAATACAGTAAGTAGGTGATCC TGCATTTCAGGTAAGCGGTAGGTGGAATCCAGATTTCTCTTGAGGAAAA
WI-6217	131	C T ---		---	CGGGTTAAGAAATACCTTTAAATTTAGGTAATAAAGCTCAAGGAGTGGGGCTGTCATCTGTGGTG TCAGTCTTCTGGCCCCCTGGCTGTCAGTGTGCTCCAGGGCTTGACAAGCAGCTCATTCAG[C/T] GGCCACCATGGCCCTAGGGTCGTCACAAGTCCAGCAGCAATCATGGCGTTCTCGTATATCTGATCC AC
WI-6238	175	G A ---		---	ATAGTCTTTATTTGTCAACGAAGGCTACACGGGATCACTCTCGTTTGTGTTTTATGCTTTTTTTTC TAGAAGGTATCTACATCTGCATTATTTACAGCCTTGTGGTATTTACACAGTCAAGATACAGTGTTA GAAACACAAAAGTGTTGAGAAAAAACTTCTCAAATTTG/ATGTTCCAGACTTCAGGAAAAATGATT TCCACATGGTAAGGCCAGAGTCCAGTGTTGGTCCATCCAGAAGCAGCTTG
WI-6272	86	C T TAA	GCATTTATTCA GGGAAAACCTT TAA	CTGTTTTTGA GAAGACAAAG AA	CTTGATTTAATCAGGGCTTTGGGGTCATAGGGGATTAGTCACTGTCAACAGTCAATAATAATGCATTTA TTCAGGGAAAACTTTAATC/TTCTTTCTCTCCAAAAACAGCTGCTGGAACACCTCAAATTA GGGATGTTTCATCTAAACACCTTTACTGAAACTTGATTCCTTGGGCCAGAGGAGGTTCTTTACTGTAG CAGAGGACTTAATGCAATGCCTATTCCGGGCAATAAATGAATCTTGATGCATTCATACAGGCAAGAA TCCCAGCATCCAGAGAAAGCTGTCTGCG[G/ATG]GCAAGCCATGGCTGCAGACATCAGGGAAGCT GGTGAGTTCTAGTCTCGCCTCTCGATTTCCTGCCAGCAGTCTCTCTCTCATCTCTCTGCGCC
WI-6303	96	G A CTCTGCTGC	CCCAGAGAAG CTCTGCTGC	CAGCCATGGCT TTGCAG	TCTG ATGCTTTTGCATGATTCTAATATTGCCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGGTGCCATACA AACAGTCCCTTTTCAAGCCCGGCTGTCATGCATCTGCCAATCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAACTGGATAAAGAGTTGCTGATAGTGT[C/TTCTGGTT CTTCCCTTACATCTTTGGGGGA
WI-6315b	193	C T ---		---	ATGCTTTTGCATGATTCTAATATTGCCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGGTGCCATACA AACAGTCCCTTTTCAAGCCCGGCTGTCATGCATCTGCCAATCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAACTGGATAAAGAGTTGCTGATAGT[C/TTCTGGTT CTTCCCTTACATCTTTGGGGGA
WI-6315	187	T C ---		---	ATGCTTTTGCATGATTCTAATATTGCCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGGTGCCATACA AACAGTCCCTTTTCAAGCCCGGCTGTCATGCATCTGCCAATCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAACTGGATAAAGAGTTGCTGATAGT[C/TTCTGGTT CTTCCCTTACATCTTTGGGGGA

WI-6375	28 A G A A	GGTTTATTGCA TATGGAAATC	AATGTGAGATC TTTATTCTAAG CTTTTT	AAGGTTTATTGCATATGGAATCAATAG/AGTATCTTTTACAAAAAAGGTTAGAATAAAGATCTC ACATTTGTAAGGCACATATGAACAATTTATAGCAAGCACAAAGGCGAGTGAGACATCAACAA
WI-6409b	112 T A ---		---	TTGTCTCAACAGATGAAATTCATAACCTTTCTGATAGACAAATTCAAACATACAAATCAAT TACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTAA/T/A/GCAACTGACAGTTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73 A T ---		---	TTGTCTCAACAGATGAAATTCATAACCTTTCTGATAGACAAATTCAAACATACAAATCAAT TACAAC/AT/ATGTGCTTATCAGCTCCCTCCACCCCTATATTTAATGCAACTGACAGTTTTTGAAG GACACCAAGACAATAGGGCT
WI-6523	165 G T C T G	GCTAATCCAGT AGAGACTGAA	AGATGCTTAGG GAAGGTTGATA	CTAATAATCTCTGGGCACATGGATTCCAAAGAGAGATTTTGCAGCAGATTTTATTATAGTTACTTAA CAGCTAAATAATAAGGGTGATTTAACTTACTTACAGAGTCACTAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG/TTATCAACCTTCCCTAAGCATCTGTCTGGTCCG CAGC
WI-6554	195 C G ---		---	TCTCTAGCCCTATTAGGCTACACTGTAGTCACTTCTATGAGAGCAAGGAAACAGAGATGGGC TCTGGAGTCCAAACAGGATGTGGACGTCCTGGTAGTCTCTCTTTTACACAACTTTTCCCTGAGA ACTGTCCAGTCAAGTGGACCTTCAACAACACGACGCTAAACTCTGAGAGAAAC/C/G/CTG ACTTTCAGAAAGCATAAAGCTGAGAAAAA
WI-6558b	68 C T ---		---	ATTGTAATTAATAATACATGGGCCTATTATTAAGGACATGTGTAATGTTCCACTTTGTTTTAAA /C/TTAATTAACAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAGTTTGAAAAATGGGCG
WI-6558a	42 G C ---		---	ATTGTAATTAATAATACATGGGCCTATTATTAAGGACAT/G/C/TTGTAATGTTTCCACTTTGTTTT AAACAATTACAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAGTTTGAAAAATGGGCG
WI-6629	75 T C G T C A T A	TCITTTTCAGAG AATAAAAGTT	TGACACAGCAT CCATTGCT	AACCAACAAAACATAAGAAATGGGAAAAAGAAATGGCAGTGAAGAACTCTTTTCAGAGAAATAAA AGTTGTCTAT/TT/CJAGCAATGGATGCTGTGTGAGAACATACTGCCAATAAATTTAAGAAAAAAGGA ACTCAATGAAGTTACTGTATATAAACAAGGAGCTCACAGCAGGGATGTAAGAGTTAATGGAAGAT ATCGTGAGCCAAAAC
WI-6644	134 T C ---		---	CTGCCCTGAACCAATCAGATTTAGTTTAAATCAATCAATAAATCCAGCTGTTTCTCTTGTCTTT TTACTTAGCAAGGAAAACTTTAGTGAATGCTACTTGACAAGAAAGAAAAAGTCAATTTCTCAAGCACA/ T/C/ACCCAAACTTGAAGGTGATTGAACCCCAATAATGGGTGGGAAACACCAAAATGAGGTGGAGGA ATGAGAAAGATGTGTGGGCCAAAGCTATCTGGTTATATTTGATGTTGCCAAT
WI-6690b	106 C T A G C C A C A G C	CAGACTCTGG	ACATAAAATA TTGCAGTGTAT TAGCC	TGCTAAACACCACCAATTATTAAGGAGAGTACTAGGAAAAACTACCAACACAGCATGTGAAACAGT TGGGCACGGTGGTAAAGGGCACAGACTCTGGAGCCACAGC/CTGGCTAATACACTGCAATATTTTA TGTTTAGCAAAATTATAGCTGGTCTGTGTATTAACCAGAGAGCGGTATCTGG

WI-6690a	28 T C	AAACACCACC ATTATTAAGG AGAG	GCTGTGTTGG TAGTTTTTCT	TGCTAAACACCACCATTATTAGGAGAGT/CJACTAGGAAAACTACCAACACAGCATGTGAAAC AGTTGGCACGGTGTAAAGGGACAGACTCTGGAGCCACAGCGGCTAATACACTGCAATATTTA TGTTAGCAATATAGCTGGTCTGTGTATACCAAGAGCGGTATCTGG
WI-6770	53 A G	CAACCCCAA AACATCACA	GCTTTGGAGT GTATAATAGTA TGAATAA	GATGTTTAAATGACACAGATCTTCCCAAAGTAATCCAAACCCCAAAACATCACA/A/GJAATTATTCAAT ACTATTATACACTCCAAAAGCAAAATACTTCAACTGCAATCC
WI-6686	151 A G A	GCATTCTCCA AAACAAAGA	CCTTGTAAGTG ACTATTCCAAT GTT	ATTCTGTAGGCAAGGTCAGCAATCAGGTAGCAGTCACTAATCTTGACCAATGGGTAGTCAGCCTCA TCACAGAGATTTTTTTTTTAATTAGATGAAATTTACATTTAAAAACATGTTAACTCCAAGCATTTCT TCCAAAACAAAGAAT/A/GJACATTGGAATAGTCACCTTACAAGGAC
WI-6761	32 C A G	GATCTAACAG CTGCAGAAATG	AAAAGCTGGG AAGGAAGAAG	CCTGAGAGGCAGATCTAACAGCTGCAGAAATGG/CJACTTCTTCTCCAGCTTTTGTGAACAAAC AATTCTCTAAGGCATCAGAAAGCACTGAGTGCAAAATGGTTGTTTCAGGTACAAGTCTC
WI-6844	225 T C ---		---	TAAATACTGCCAACTAGCATTACGTCCTCTTGCAATCATTAAAAACAAAGGATTTCTCCTCTTG GTATTTCAAATGATGATTATACAATAACGAAGTTAGAACTTAAATGCACCTGATTAATTATG TAACTGGTAATTTGTTTTAAAGCATAATAATTTGGTCTCTTCTCATAAATGGAATTTAA TATTTCTGTAGTCTGAGGTT/CJATCATTATGATAGTAGTCAAGTG
WI-6824	112 A G ---		---	CGGTTTGTACACTTAAATGGTTTTTTTTAAGGATTTTTTTCAGGCTTTGTCAGCAACATCAA ACAAAAGGTACTGAGTACTCCACAGGTCACAGAGTCTGCCAA/A/GJACCTTAGAAAAATTACAT GACACGGAGAAAATGCGCTCTTGTCTTGAAGAGCTACAGTACAGGATTTGACAACTCAGAT CTTAGGAACTGGGCAAGTAAGGCAAAATCTTCATCCCTAGAGCTATTG
WI-6889	139 T C AATC	GAAAAATGAG ATGCAGTTAA	TCACTTTGTGG CTTTTAATTAT TCT	GTACAAAAAAGCTGAGAAAGGCCAACATGGAAGTGTCAAGAAAAACATTTCTGATAGTACGGACAA AAGAGCTCCTCAATCAAAAGGAGTTACATATTAGTTCTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTCT/CJAGAATAATTAAAGCCACAAAGTGAACCTGTTGTTCTGGGGCCCTATGTTGTAGATT CTCT
WI-6911	216 T C ---		---	TCCCAGCTCATATTTTGGGCACAGTGGGCACTCAAATATCTGATGAACITGTGAACGTAA AAGAGGTCTCCTTAACAAGATATCATCTCCGAGAGAGAAAGTCCCAACCATATAAATGTATGAT CAAGTCCCAGAAAACTTGCCTCCCAAGGAATGTGTTCTAATTTGGTTTCAAGCACACTGGTTCC CACTTTTACCACCTT/CJCATGACATTGGACAATAGTACTACTCTTTCTAC
WI-9413	112 G C ---		---	GCCAGTCTCTAGTAAGTCTCTAGGGACATGACAGACAGAGCCCTGTTCTATATGAAGACAAAC AGGTGGCCATACITGGGTGGAGGATACCGCTGCTATTCCAGAT/GJAAAGATTTGGTGAAGGAG ACCATGACAGATGACAAACGGAACAGTTTCTCAAAAACAGAGGTATGA
WI-9557	74 C T ---		---	AAAAGCTTTAAAAAAGTGGTGTATCTTTAGAAACACTTTCAGCAAGATCAAGTAGCCCCAGCT ACAGCCTC/TGGTGCATCTTAACCCCTCTCTTTT

WI-9617	37	G T	---	---	TGCTCTTTTATTCACGTTTCACAACACACGCGCTG[G/T]TGGCAGAGTCTACAAAAGTGCCCGCAG CGCCACGCTTGGCCGGAAGGTCTCATCTGTTGGTCTCTATGGACTGATTGAATTTGGGATGGCCAG CTCCAGAATGTTCCACGTGGGGCACTCTGTGGGCAGAGAGGCTGAGCCCTTGCCACACTGGCACCA AAGAGGTTCACGATGACGCTTGCAGTGGGTCCAAAGCCGGTGTGCTGTG
WI-9657	121	T G	---	---	AATGCTGGAGAAACATCAACATTGAGTTGACATTTGTTTGTGAAGTATAGTACCATCCACTAT CATGAATTTTGTTCATTACAAATGATAGAAAGCCAGATTCTCAAAATAAAGT/GJATAATTCTT TGTAATAATAAATGTTTATAAATGTTTATGAAGCTCATTACATTATCTTTTTTAAAAAAGTAAAA TTTTAGACATATGACGCTTTTCATAATTAAATGCTTTTGATATAGATTGAGG
WI-13119b	114	G C	GCTGGGA	AAAAATTAAC CAGGTGTGGTG T	CAGGGTCTTGCTCTGCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTG/CJACACCACACCTGGTTAA TTTTTTAATTTTTTGTAAAGATAGGGTCTCACTATGTTGCCCGCTCTCAAAAAACAACCAACTAAC
WI-13119a	51	C G	---	---	CAGGGTCTTGCTCTGCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTC/JJACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCACACCTGGTTA ATTTTTTAATTTTTGTAAAGATAGGGTCTCACTATGTTGCCCGCTCTCAAAAAACAACCAACTAA C
WI-13112	71	C T	AGCTTTTT	TTAGAAATTTT TGATAAAGAC TACAGACTTA	ACAGGAATCTGAAAGTTACCAAGGCAATTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTT/C/TCTTTTCCATATAATACACAAAATTTCTAAATATCCTTTAAAAAGAAAATATAAATAGT TTCAGTATGTTATGTAGAGTCACATACATATGGCAAAAATATTTTAAATTGAGGGAATAGGCCAAT TT
WI-12988	36	C A	CTCAGTACAA	CAAAGTGTA CTACTGATGCT GTTT	TGTTAACATTTTATTGGTACGTGCTCTCAGTACAA/CJAAACAGCATCAGTAGTGACACTTTGAT AAAAAGGAATTTTAGCTTAGTAGAAAAAGAAAGCCCAAGGTGAGAGTATAATGAATATGTACAT CTTTATGGAAACTGTTTGTGTGACCATCTTTATCTTCCCTGTGGATGAGATGTATGCACACACAAGT AAA
WI-13020a	108	G A	CTTT	CTAATAGTGG AACCCTGAGA CTTT	TGCTATTTCATGACAGACACGTGAGACAAATATCTTATTTTACAGATGGAAATAGACCCAGACATTA TTCAGTACTTTAACCACTAATAGTGGAAACCCTGAGACTTTA/GJATCTGCAAAAGGGTTTAAATAAT GCAATATACATATATTTCCATTTTACACCATAATTAAGTTTTCCATTTTCTTAATAGAAAAATGA TAAAAATGTTTTCCCAATAT
WI-12837	87	A G	AAAGTCCA	CCATATACAT ATATCAAGGT ATGCTGTTTTT	TGTATAAAAAATCCAACTTGTTCACAAGTACATATGTCCTATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAAGTCCA/GJATACAAAAAACAGCATTTCTATGGCCAGTGTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAAAATGAGATTGCACACTAAGGCAGGATGAGGCAGAAAGCA AGTGTGTCCA

L42611b	50 GC ---			GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTCTCTCAGGTTGCCTGTG[C/G]CTCTCCTGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCTCCTCTCTCTCTCTGTATACCT GCCCACTGTAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATGATGATTACCA CTGGAGCTTCACITTTGTTAC
L42611	34 TC ---			GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTTT[C/G]CTCAGGTTGCCTGTCTCTCCTGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCTCCTCTCTCTCTGTATACCT GCCCACTGTAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATGATGATTACCA CTGGAGCTTCACITTTGTTAC
WI-1172b	179 C T A	TGAAGAAATG GCTGATACCA	ATGTGCATTTT TCACTGCAG	TGAACGTGTGGTTAAACTAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCCCTAGAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCAGCTCAGATTATGTTCTTGAATACCATTTTCTGCTTTC AAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAG[C/T]CTGCAGTGAAAAATGCA CATGATGAGCCTGGAAACATGTTGT
WI-1172a	17 C A ---			TGAACGTGTGGTTAAAC[C/A]TAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCCCTAGAAACA GTGACCACACCTCAAGCAATGATTATCCCTAGCAGCTCAGATTATGTTCTTGAATACCATTTTCTGCT TTCAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCCTGCAGTGAAAAATGCA CATGATGAGCCTGGAAACATGTTGT
WI-1177	35 G C A	GCAGATTGGA AGTGTGAAAA	CACCTACATTT CTGAATATTTA GACTCTTT	AGAGGCAGATTGGAAGTGTGAAAAAATGAAAGAA[G/C]AAGAAAAAAGAGCTCTAAATATTTCAG AAATGTAAGTGTGCTGCCCTCACTGTCTTTACCCACTTAATCTGCAATTTTGAAGAACTAGATTGAAT TCCCTTGCAAAAACCTTGCATCATGGATACCCGAGTTAAACCGTTAATTTAAAGACATTTAAACATGG CCTGGTG
WI-1231b	141 G A ---			TCCATGGTTTGGTTGCTACTGACTTGTAGCCTTACTGCCCACTATGCATTGGAACATTCCTCATATTC CAACTAAGCAGGAGTGTTCACAATAAACACATAGGCTCTTTATCTCCTTCTTTTCAATTTTCTT TCAC[G/A]TTATTCCTCACCTGAACGCCCTTCTCCTTCGTAGTACATTTTAAATCCACTTTAC ACATCGGACC
WI-1231a	126 T C A	GGCTCTTTATT CTCCTTCTTTC	CGTTCAGGGTG AGGGAATAA	TCCATGGTTTGGTTGCTACTGACTTGTAGCCTTACTGCCCACTATGCATTGGAACATTCCTCATATTC CAACTAAGCAGGAGTGTTCACAATAAACACATAGGCTCTTTATCTCCTTCTTTTCAATTTTCTT CTTTCAGGTTATTCCTCACCTGAACGCCCTTCTCCTTCGTAGTACATTTTAAATCCACTTTTACA CATTCGGACC
WI-472	114 G C ACAGAAAAG	ACATACATAT CCATTATACA	GACCTTTCCTT TCCAGCCC	GAAAGCAGGAGTGTGTTGGAGGACAAAAAGTAAATCTTTTATATCTTTATTTTAAATTTTATT TTTTTTCAGGCATATAGACATACATATCCATTATACAACAGAAAAAG[G/C]GGGCTGAAAAAGAAAG GTCAAGTGAGATTTCAGATATCTTAAATGCAAGGCTGACAAATTTGGGCTTGATT

WI-478	46 C T	GCATGCTGTG TTACTCTATTT TGTTC	AAATGCCACAG GTGGCT	AAACCACTGCAACCTTCAAGCATGCTGTGTACTCTATTTTGTTC/CTAGCCACCTGTGGCATTT CAAAATATGATAATCTCTGCCACCATACTGCTTTAAACACAAATAGAATCTGGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAAGGCTACCATCAGTACCTTAGCACATTTAAAAAATAAAAAACCAAC ACTGCCCA
WI-533	29 T C A A C T	ATCACAGCAG AGTACCTTTCT	CCTTCCAACCT CTACACAATCT T	AGCCATCACAGCAGTACCTTTCTAACTT/CJATAAGATTGTGTAGAGTTGGAAAGGAGGACAGGA CTGTCTGTGGTATAATGACCCTGTGTCCAGTTAATCCA
WI-601b	112 T A ---		---	TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAGCGCAACAGAAAGAGGTTTCATTGACTCTCTAACTGAGTAC/T/ACAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-601a	74 C T ---		---	TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAG/C/T/GAACAGAAAGAGGTTTCATTGACTCTCTAACTGAGTACTCAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-863	107 A G C C T C A C C A	CTCCTTCACAA CCTCACCA	CTTCCCGGTAA GCCAAGT	AACAAAAACAGACACCCCTGGCTCTCTCACAGTCCACATGGTGCCAAACAAATCCCACATTCTCT ACATCTCCCCACTGGCTGCTCTTCAACACCTCAACA/GIACCTGGCTTACCGGGAAGCATAAA GCCAAAGCATTTAGTCTTTTATGCAACATGGTCTGGCTGCAATAC
WI-919	36 G A C	ACTGCTTGCTT GTTGATTTAAT C	TTATTCTAATC CCACATGACAG C	ACTCACTGCTGCTTGTTGATTAAATCAACCTAGCC/GA/GCTGTGATGTGGGATTAGAATAAATA AACACAAAAATGAACACACACGATTGCTAACAAAGCAGATTCTTTTCAAGGCACACGCTAAAGAT AATAACTTCAA
WI-991	37 A T ---		---	TGCATTCAATATGCACCAATAATACTTCTGTACAT/AT/CATTATTGTATTTCATTATCACAAAAAT TATGAGTGAGGGATGATTGTTATCCCTATTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCT TTCCCAAGTCACAAAGTTAGTGACAGAGCCGGATTCCGAATCCATCAACTTGAATCCAGAGAAAAAT GTTCTGCATCACTGTACAACTGACTCTCTTTCTCTCTTTGAAAAACAAGGC
WI-1011	70 G C C A	CAGTATCTGA AGTTTTGTCT	AGGAACACCTA CAAAATGACTT CT	CTTCTGACCTGTTTGCAGTGGATACTGTTTGAAGGCTCTGTCTCAGTATCTGAAGTTTGTCTCC A/G/C/JAGAAAGTCAATTTGTAGGTGTTCTGGCGTGTGTTGCTACGTTTCCATTTCTCTAATACACTGC CGTCTTAAGGGAGGGCTTGACAGCATTTATCAGATGGCTGTTTGTGCTGCTGTGCACTGAAG
WI-5381	178 A T ---		---	TTATGCAGAAAGGTCCATGAGTTTACAGAACTCAAGGAAGAAAGGCCCTAGAGATGACACCCAGAA ATGAGAGTGGCTGCTCATGAATAATGGACAGCATGTTCCAAAGCAGAGGGAACAGCATGGAGAAGA AAAAATCACTCTATCCACGTGCAGAAACTGGCAATTAGTTTGT/ATTTACTAAACACACAAATGT TTAACTGGGGTCCACAAACAGGATA/GTTGGCAATGGIATTTCTGTGATG
WI-5791b	76 G A ---		---	CTATGTATTCATCTAGCAAAAGCAAGACTATTGGATAAGTTTCAAAAGATGAGAACAGGTCTCTA GAACCTCAG/GA/JATCGAAAGGAAGTTTCATCTAGTCCATAGACCCCTATCTCACTGACCCCAAGGTA AAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTTCTTATTTGCCACCCCTGTTTGT TAGGAA

WI-5791a	44 C G ---			CTATGTATTCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTC/GJACAAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGACCCTATCTCACTGACCCCAAAAGGTA AAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTTCTTATTTGCCACCCTGTTTGT TAGGAA
WI-5406c	120 C T ---			CACCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACC/CJTATGAGCCCCAC ACTTCTCATTTCCCTTAGAATTTCTTGACTCTGTGAAGAGGAAAGGAAAGGAAAGGAAAGAGAGGCAA GG
WI-5406b	118 C A A	CCAGGATGTC AAGGTGAGAA	AATGAGAAAGT GTGGGCTCAT	CACCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACC/CJCTATGAGCCCCAC ACTTCTCATTTCCCTTAGAATTTCTTGACTCTGTGAAGAGGAAAGGAAAGGAAAGGAAAGAGAGGCAA GG
WI-5406a	42 A G ---		---	CACCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAGGAGCCACTTCCACAGATGCAACAG GCCCTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCTATGAGCCCCAC ACTTCTCATTTCCCTTAGAATTTCTTGACTCTGTGAAGAGGAAAGGAAAGGAAAGGAAAGAGAGGCAA GG
WI-5798	48 G C TG	TTTATTTCCC TTGTTTCTTT	ACTGTTAGAAA ACCAGTATTT TCAAT	CCATTCCTTCTTCCCTCCTCCCTTATCTCCCTGTTTCTTTTG/CJATTGAAAAATACTGGTT TTCTAACAGTGTGCTGATGGATACTATGTTATAACATGCATGATCTATATGGGTATCA
WI-5415	54 T A TTT	TCATCTTTTCAG TTT	GGACTAATTCA TGATCCGATCT	CCTGCTAATAATAATTTAAGCACGATTTGCTTTCATGAATTCATCTTTCAGTTT/TJATAGATCGGAT CATGAATTAGTCCAGGCTTTTAGTTGTAATCGAAATTGGA
WI-5437	41 C T G	TCCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAAATATG GTTTAAG	TGTTTTAACCCAGGCAGACCTCCAGAGAGAAAAATCCAAGAG/CJCTTAAACCATATTTTGTGTTTA GAAACTCCTGTGCCAACCACTCTTGATGTGAGTGAC
WI-5481b	131 A G CTGCAGTCG	TGTCATTTATG	TTACTTCCAGG CTCCAAGTATT	AAGCCAAATTCACATTAGTTGATGAATTTGAATTTTACAGTATCTAATGCATGGGCATCTGTTTCAAC TCTCTGTTTTTCAAGAGGATGATATGCTGAAAAATCTATTTGTCAATTTATGCTGCAGTCG/A/GJA ATACTGGAGCCTGGAAGTAAAGACTTGGCTATTTTCACAATTA
WI-5481a	29 G A AATTT	CCAAATTCAC ATTAGTTGATG	CCCATGCAATTA GATACTGTAAA ATT	AAGCCAAATTCACATTAGTTGATGAATTTGAATTTTACAGTATCTAATGCATGGGCATCTGTTTTC AACTCTGTTTTTCAAGAGGATGATATGCTGAAAAATCTATTTGTCAATTTATGCTGCAGTCGAA ATACTGGAGCCTGGAAGTAAAGACTTGGCTATTTTCACAATTA
WI-5492	38 T C ---		---	TCATGAGTCTTTCTTCAAGATGCTTGTAAAGTCCCAT/CJCAAGAAAGGATGCCCATGGCCCTAAT GAAGATGTACCTCCACCTTAGGATATTTTGCAGACCAA

WI-5826	134	T C	---	---	TATTTTTTTTCTCAATTCCTGGAGCACACCATGCTCTTTCTATTTCTATGCTTCACATTTATTTTTT TTTCACTTAGTTAAATGCTTTTCCCTTGATCTAGCAATGGCCAGTTTATACATATTTCTTTAGT[C] TTTCAAAATTAATGCCACCATAGAAATAATTTCTAACCACAGGCCAAACAGCCTCACTCTTCCTT CCTTGGTGCAATTACTCTTTACAC
WI-5546	40	C T	A	CCCAATACTTT TTCAGGTGAA	CCTGTATTTTA GCAAAACATGGG
WI-5552	97	C T	T T T T A G A G T	GGCACCAGCCT T T T T A G A G T	TGTCACAAATGG CCGAGG
WI-5836b	161	C T	---	---	TGTTGTCTGCACCTCCCAACAAGTGGTCAATGAGCCTCAAGGGTTTGTGAGCGGGTATGGGT GGGGCTATCGGCACCAAGCCTTTTGTAGATCTCTCTGGGCAATTTGTGCACCTAGTGTGAGA TAAGTTGATTTAAACACTCTGTGCTCAATTTTCTCACCTATAAAATAAGATAAGTATCTAAAA AAAAAGAGAGAGAAATTAAGTGGATAGACATGAATACTCTGATGATCTGTTGTATCCCTGAA TCCTGCAATATACACATGATTCAATGAT[C]TCCATTTTGAAAAATTAAGCTTTTGAATTTTTCCTCA ATG
WI-5573	58	C T	G T T C A T A A G G A G G T G G G A	TGAACAGTTGG AGAGTAATGTG TC	TCGGGTATTAGGATGCGTTCAACCTCGATGATGATGGCGTTTCATAAGGAGGTGGGGA[C]TGACAC ATTACTCTCCAACCTGTTTCATCAGAACACTTCAACAGCG
WI-5850b	134	G A	---	---	CAGGACCTTGGAGCCTTGTGTTGTCTTCCACCTCACTCTTCTGCTGCCCTGCCCATGGGTGGAGC CTCTCTCAGGCTTCTCTATGCACGCGTCTATCTTATATGGGCAATATCCAATGTCCCATTC[G/A] TTTTGCCATTTCTGTATATCAAAACAGAGAGCAGAGGGTGG
WI-5850a	92	C T	---	---	CAGGACCTTGGAGCCTTGTGTTGTCTTCCACCTCACTCTTCTGCTGCCCTGCCCATGGGTGGAGC CTCTCTCAGGCTTCTCTATGCA[C]TGGCTCTATCTCTATATGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCTGTATATCAAAACAGAGAGCAGAGGGTGG
WI-5612b	125	A T	C T A T T A A T G A G C A T C G T G T C A T T C	TTCTCTTGAGA AACCTAAAAAG ACTG	TGCTGATTGACACATAGTTATCTGACAGTAATCATCTTAACATCACAATAATCTTATTTCTGCCTG TCACACTAAATTTGCAAGCATTCATTTGATTGACTATTAATGAGCATCGTGTCAATC[AT]CAGTGT TTAGGTTTCTCAAGAGAAATATGCTGTTCTTCTGTAACCTCAAGTA
WI-5612a	44	T A	---	---	TGCCTGATTGACACATAGTTATCTGACAGTAATCATCTTAACA[AT]A/CACAAAATATCTTATTTCTGC CTGTACACTAATTTGCAAGCATTCATTTGATTGACTAATTAATGAGCATCGTGTCAATTCACAGTGT TTAGGTTTCTCAAGAGAAATATGCTGTTCTTCTGTAACCTCAAGTA
WI-5636	26	A C	G C C A A T T T T A T C C G C A A T A A A	CATCGAGGACT TTGGGA	TGAGAGCCAAATTTATCCGCAATAA[A/C]TTCCCAAGTCTCTCGATGGAGGCATTTCAGAATCGGG GCAGGGAGGAGCAAGGTGAGACAGATGTGAAGAAC

WI-5865c	103	C G ---	---	TTAGAAACCTCCATTATTCTGCCATGGTAGACATCTTTTAAAGATCTTTTTTTCATTTATGCAATC ACTGACTCACTCACTGCTCTATCAAAAATTAA[C/G]AAATATTAATATTTTATTTACAGAGGAA CTCAGAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCTTCA GAGAAGACAGACAATAAATCCAGG
WI-5865b	99	T A ---	---	TTAGAAACCTCCATTATTCTGCCATGGTAGACATCTTTTAAAGATCTTTTTTTCATTTATGCAATC ACTGACTCACTCACTGCTCTATCAAAAATT[A/J]AAACAAATATTAATATTTTATTTACAGAGGAA CTCAGAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCTTCA GAGAAGACAGACAATAAATCCAGG
WI-5865	165	T A ---	---	TTAGAAACCTCCATTATTCTGCCATGGTAGACATCTTTTAAAGATCTTTTTTTCATTTATGCAATC ACTGACTCACTCACTGCTCTATCAAAAATTAAACAAATATTAATATTTTATTTACAGAGGAACTC AGAAGCCAGAAAAATGACCAAGACACAGT[A/J]CCAGTCTCCATCTTCAAAAGGTCACAGTCTTCC AGAGAAGACAGACAATAAATCCAGG
WI-5874	76	T G ACAGAAAA	CATAGCATGG ATAATATTAT ATATGT	CTCAGACATTCATTTTCATTAGTTGTTAAATTTTGTGTATTTTCATAGCATGGATAATATTACAGAA AAAAAATTTGTTACATATCAAAATGACTGAAACCTTACTAGTAGCAATTTGTTTGTCAATTTGCT CATGGAGCCGACGTTCCAGCTCTCAGTTTTTCCATC[A/J]TTTTTTCATAATTTACTCTCTTTTCTGTC ACAATGTTCTGCTCTGATTTCAACTCTCATTGCTGATGGATGGTAGTCATAAAATATGGGTGATTC AGAAAAAAGTAAATG
WI-5752	36	A T TTTTCCATC	GACAGAAAAAG AGAGTAAAT ATGAAAAA	TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAGTGTTCCTCCGATAAAT[A/C/G] CATTAGGTATTAGATAAGCATCCCATAAACATTGTTGAAACGAAAGCCGAGTTTCGATTTCACACA GTTGCTGTTTAACTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCCACGAAA CATTGTTGAAACGAAAGCCACGTTTCCGATTACACAGTATTGTCGT
WI-5760b	61	C G ---	---	TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAGTGTTCCTCCGATAAATACCCAT TAGGTATTAGATAAGCATCCCATAAACATTGTTGAAACGAAAGCCGAGTTTCGATTTCACACAGTT GTCTGTTTAACTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCG[G/A]TCCCACGAA ACATTGTTGAAACGAAAGCCACGTTTCCGATTACACAGTATTGTCGT
WI-5760	187	G A ---	---	AAATCTGGCCTTTTCTCTTAGGAGGAGATTCTCACCATTGGGAATCTTG[A/G]TGCAAGTTAGAT CCCACCTCACTATTGAGAAGCTAAAGTGAAGACTACTCATTTCTCAGTCTTCTTCTGCTG
WI-5944	52	A G GGAATCTTG	TTCTCACCATG AACTTGCA	GAGTTTAATGAATCTGTTCCCTCTAAACCTCTGTTCCCCCACTTCACATTTCAGCAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCTGTAATTTGATGATTCATTCAAGAGTGTGAG TAATGCTTGGT[A/C/J]TTGCTCTGTGCCGATCTGCTCCCAATCACCATTCCACTTTATTTCCTATTAT GCTGAATGAAACGGTTATTACAG
WI-5967b	148	C T ---	---	

WI-5967	165 C T ---				GAGTTTAATGAATCCTGTTCCCTCCTAAAAACCTCCTGTTCCCCCAACTTCACATTACAGAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTAATTTGTGATCATTTTCAAGAGTGTGAG TAATGCTTGGTACTTGTCTGTGCGGTATC/TJTGCTCCAATCACCCATTCCACATTTATTTCCCTATTAT GCTGAATGAACGGTTATATTACAG
WI-6093	53 G C ---				GGGTAAGATCCAGAGCCACAGGTGAACCTGCCGGTATTGAAGTCTTTGGGCCA/GCJGTCTGTAATG ATCTGACTTCTCCAGAACCCCTCTCTCTGGAAGTTCCAACTGTGCACTGAGGCCATTGTAGGGA GCAATTTGAACCAAAACCCAGCAGACTGCTGACATTTGACTTTCAGCAAACCTTGATTGACGGTGAC ACACATGCTTCGAGAAGGAATGAGG
WI-6141	80 T C AGGTACTT	CTTCTTAATTA AGCATCTACA		TGAAAACCCCA GAACAGTG	GACTCTGTCTCAAGAAAAAATAAATTTGAAAAATGAATAATTAAAGCACTTCTTAATTAAGCAT CTACAAAGGTACTTAT/CJCACTGTTCTGGGGTTTCAATCCTCTCACCTTTAGACTTCAGGAAAT CAGAAAAATGCATGAAAAACAGGATTGTTACATGCAGAGAAATAGGGGGAGATAAAAAATTTGTCTTTT CTC
WI-6450	45 T G TGTCACA		CCAATGACTT ATTCATATCT	TTGTTTGAAT GTGTGGTACTT CT	ATAGGACAGTTTTTCTTCCAAATGACTTATTCTATATCTTGTACAT/GJAGAAGTACACACATTTCA AACAAGAGCCAGGCTATGCCAGGGTGGATTATTTTCACGGTCATGTAATATGCATGTAAAGACTA TTTTACTGGCCTCTTTTATGCATAAACAAGGATTGGTCTATTCAACAAACATGTGTCAATACAG CAGTTGTCATGTCCTCTGCTGACTAGAAATATAGTCTTTATAGAATATGGTTTAGAATAAAGCCACA AATTATTCTATAAACAACA/CJJAAGGAACGAGGCTCAAAAGTGGAACAAACGGCCTTAGTTTC TAAGTGAAGACTAAGACGATATAGGAAAAATATAATCCGTGACCTCTTA
WI-6461	88 C T ---				GAACTATCCTTTAGTGGTGCCACATTTTCTATTCTGATTCTTTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCTATTTCAGTGAAGTATCATATAAAGACATGCAAAACCTTTTCACAGTCTTTGT CCTGG[G/JAATATCTCACAAAAATTAATTATAAATTTGGCATGCGACTTTCTGATTTAGCCTGACAGG ATTGTCCTTT
WI-7466c	141 G A TTGTCTGG	TTTTCACAGTC		AGTCGCATGCC AATTATAATT	GAACTATCCTTTAGTGGTGCCACATTTTCTATTCTGATTCTTTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCT/JAATTCAGTGAAGTATCATATAAAGACATGCAAAACCTTTTCACAGTCTTT TGTCCTGGGAATATCTCACAAAAATTAATTATAAATTTGGCATGCGACTTTCTGATTTAGCCTGACAGGA TTGTTCCTTT
WI-7466b	80 T C GTC	GACTTCTGGG CTATGAAATA		ACTGAA	GAACTATCCTTTAGTGGTGCCACATTTTCTATTCTGATTCTTTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCT/JAATTCAGTGAAGTATCATATAAAGACATGCAAAACCTTTTCACAGTCTTT TGTCCTGGGAATATCTCACAAAAATTAATTATAAATTTGGCATGCGACTTTCTGATTTAGCCTGACAGGA TTGTTCCTTT
WI-9814	104 C A ---				TGCTTTTTAAAAATAACAATGACCACCACTGACACCATAGTGTGCTCTCCATTTGCCACGCTTCCTC AGTAGAATAAGACAGGGACTTTGCTGGCTGCTATCTC/JA/TCTCTCAGAAAGACACTTGGCCCT CATAGGCATTCATAGATATTTGTTGAATGAATGTGCTTTTTCATATTTGATTCCTACATTTGATACA TTCTCAGGAGGGACATTTGGCCTAT
WI-9720b	55 A G ---				CCTCTAACAGAAAACTTGACTTCTCAACTCAAAATACCTTCTCTAATAATTTT/JA/GJAGTAACCA AAATATCTCTCAAAATAAATTAATCTTTTAATTAGAAAGAACACAGTGTAGAGGTAGTACATTCA CCACC

WI-9720a	47 A G ---			CCTCTAACAGAAACTTGACTTCCTCAACTCAAAATACCCTTCTCTJ/GJATAATTTAAGTAACCA AAATATTCCTTCAAATAAATTAATCTTTTAATTAGAAGAAGCAACAGTGTAGAGGTAGTACATTCA CCACC
WI-9825	123 A T ---			CACGCTTAAGGCAGGATGTGGCTTATGAGATACCTTTCATTGCTGTCTGCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTTACCTCTCTGTGATGTGCAGATGAAGGCTAGGGTGTJ/JGAGGATTAG TAAGATCTCTTTCTAAAGACAGGAGAGATTATTTACAAGAAGAACTCACCAGGGTTTAGTTGCATT TAAGAAATGCCAGTCTTTTGTCTGCATCATCTTGAACATTATCCACATG
WI-9748	74 C G ---			CCACTTCAGTAAATCAATTTGTAGCAGCTTATTTCTAAAGATTTCTAAATTTTATATGTTTACCCTTT GTCATTJ/CJTCAGACCAAGTACATGTTTTCACACAGCCATCTTCTTTCTCGGAATCTTTCAGAAT TACAGTTATGATGTCTTTTATATTCCTCA
WI-9943	91 T C ---			TGAGGCTATGATGCAGATTTGTAGTGACTAATACTATTAAAGCAATTTCAATGTTGTGGCAGCTGTT CGTTGTGTTTATATCCATCTTCTJ/CJATTTTAAATTTCTACTGAGCAGAAAAAATAATGTATACATT AACCTTTGTCTCCCTATTGTACCTTTTAAATTTGCATTTCACACCTTCTCTTTTGTCTATTAGGGA
WI-9891	39 T C ---			AGGGCTTTCACAGATCCGTAGCTCAACACTGCCTCTTJ/CJAGTGAGCCTGTGAACACCCCAAGAC GGCTGGTCATCAGTGTCTCTCTTCTTCCGGACACTATCTTTAAAGAAAAAAGAGTGT CTTTGAATGATCCATTTATCCCCAAATAATCTTGTGTTTAAATAATCCCTTATAGGCCAAATCCAAT GTGCTGAATATCTGCCAAGCATGTCTATTCTACACAAAAGGATTTGCAAA
WI-9897b	84 C T ---			CTCAGAAATTATCAGATCTTCCCCAAATGTCATGATCTTGTCTCAACATCCTATTTTCTCTCAAAC ATTTATCTAGCCTGTJ/JAAGTCAATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9897a	83 A T ---			CTCAGAAATTATCAGATCTTCCCCAAATGTCATGATCTTGTCTCAACATCCTATTTTCTCTCAAAC ATTTATCTAGCCTGTJ/JAAGTCAATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9935b	115 C A ---			AGATAACCCCTGGAAAACCTAGAAGAAATTAATAACGTGTGCAJ/CJACCTCACCAGAACTGGAAGG CTGACTGTGTTCTTATGGGTGCTTGGACTGGCAGGGGGAGTTTCAGACACAGCCAGAAAAAGCC TGATATTAAGAGGCACCTTGCAATTA
WI-9935a	42 C T ---			AGATAACCCCTGGAAAACCTAGAAGAAATTAATAACGTGTGCAJ/CJACCTCACCAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGTGCTTGGACTGGCAGGGGGAGTTTCAGACACAGCCAGAAAAAGCC TGATATTAAGAGGCACCTTGCAATTA
WI-9983	146 C T ---			CCGTGTTAGGTGCCAGAGTCCATGCTTGTGGCCACAATGTTAGGCTGCCTCCCATTTCTTTGTCTTGA TTCCCCAAACCCAAAGTTCTCACCCCAATCTGATCAAAATGCTGACTAGGTGCTGCTGAGGGTAA AGCATTATGAJ/CJTAGACACAAAGACAAAGAGGTTAAAGTTGCTGTCTCAAGAGAGAGACATAA /AAACAAATGGATCTGGAACTAAGTAAAGGCTTCGAGGAGGAGGTGAGCAAAGG

WI-10019	139	A	T	ATCT	TGATGTAATGC TATGTAGCAA	TTGATTACTGT GCTTAGGSA	ATATCAGTGGTTGAGTATACAGCAATCTATTGTTTATTTATGTGTGCTATAAAATCAATGGTTCTA ACATTCAAAATAGATCTTTTTCCTCTGCTGCTCAGATGCTTTCATGATGTAATGCTATGTAGCAAT CTA/ATTTCCCTAAGCACAGTAATCAAGGCCCTCTACCCCA
WI-10020b	122	T	A	TTT	GCGAGAAAAG AAATCATGAC	GACTGTTAATT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATATTGTTAACTGGCTCTGAAAAGAAATTTAGGC ATGCATAGAGAAATAGCAGTGTTTTATTGGCGAGAAAAGAAATCATGACTTTT/TA/AAAAATACC AGACTAATGATTAAATAAATAACAGTCTAGGGTCCGGAAGTGGCCTAAAGCACGTTAGTAGCCCT CCTTAGA
WI-10020a	39	T	C	ATAAAT	TGTCATCTTGA CTCGTATTA	AAATTCITTTT AGAGCCAGTTA AC	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAAT/TC/TTAACTGGCTCTGAAAAGAAATTTA GGCATGCATAGAGAAATAGCAGTGTTTTATTGGCGAGAAAAGAAATCATGACTTTT/TA/AAAAATACC AGACTAATGATTAAATAAATAACAGTCTAGGGTCCGGAAGTGGCCTAAAGCACGTTAGTAGCCCT CCTTAGA
WI-10064b	170	C	T	TTTACATG	OCTTTAGATAT ATTGTGATTGT	ACCTTTCTGAA GCCAGATTTC	TCTGAGTCTTTCTGAGACACTTGCCTGGTCAAGGTAGCAGGATCAGGAAGGCATTATAATAAAT ATAATTTGCAGAGCATCTCTCTCTATGCACAGATATTGTTGAGACTCTGTTTAAATCCAGTATCC CTACTCCTTTAGATATATTGTGATTGTTTACATGTC/TA/AAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10064a	54	C	A	CAGGGAAGG	GTAGCAGGAT CAGGGAAGG	GAGATGCTCTG CAAAATTATATT TATTAT	TCTGAGTCTTTCTGAGACACTTGCCTGGTCAAGGTAGCAGGATCAGGAAGGCATTATAATAAAT AATAAATTTGCAGAGCATCTCTCTCTATGCACAGATATTGTTGAGACTCTGTTTAAATCCAGTAT TCCCTACTCCTTTAGATATATTGTGATTGTTTACATGCGAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10289	29	T	C	CAAACTCTT	TCTCTGTCCC CAAACTCTT	ATTCTTGTGT ATTGAATGGAA TTAA	CCAGGGATTCTCCTGTCCCCTAACTCTT/TC/TTAAATCCATTCAATACAACAAGAAATTTATAGAA TATGCCACCATGCCACAAAGACACCCCTTATATTAGT
WI-1319	40	A	T	ATTCTTT	TGGCACTTAG AACATAGTTT	GCCACACACC CTATGGT	AAGAAAATCCTTGTGGCACTTAGAACATAGTTTATCTTT/TA/TAACATAGGGGTGTGGCTTATCT TTTAACCTGGCATGGCTTTAGTCTGTTTATAATTTGGTATCTTTTGGCACAAGAGTCTGTTCTGAC AGTCTTATGATCTCTATTTTAAACATTAACACTGGTCAGATGTGTTTAAACTGTTGAACCTGCAGC
WI-10316	104	T	C	CTCTT	CTGTTGATTT CTACCTCTATT	GCTTTGGAATG TATCCAAAAGT TT	AGCAACGTGTACAACCTTAGTGGGTGTAATCAGAAAGCATCTATATTATTCACCAGTCACCACCCTG GACTATAGTCTGTTGATTTTCTACCTCTATCTCTT/TC/TAAGCTTTTGGATACATTCCAAAGCAT CATGGTCACTTCCAGTTATGAAAGGATGTTTAAAGCCCGCC
WI-2572	61	C	T	---	---	---	AGTGAGTTGTGCACAATTTGGAGACATCTGTGACCCCACTTAAACACCTCTCCCCACA/CT/AC AAAGTTAACACTTCAGTTACCAGGTGATGAGCAGA

WI-10368	31 C T	TGAAGCAACC T AGGCTTGTT	CAAGATATTAT ATTTATTCCT AAGAGGGG	GAGGAAGCTGCCTGAAGCAACCAGGCTTGTTGCTACCCCTTAGAGAATAAATAATATATCTT GAGATAGGGAGGAGCAGCCTGAGGACAGTCTGGGTTTTGTTCTACCCACTGGAAGCAGAAATATCC TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCCTGATGGATTGCTTTTCAGGG T
WI-10391	32 A G	CTGTCTCAGGT ATGACTCCCA	GGGAGTTAGGA GTCAAGAAGTT GA	CTCCCGTTCTGTCTCAGGTATGACTCCCAAGGTTCAACTTCTGACTCCTAACTCCCATCTCGGTG TCTGTTCCAGGGGACGCATCTGACACAGCCTTTTGCTTGCTGTGACAAACAGAACATTCGAGAAG TGATGCTGGGTGACCTCCAGGATA
WI-10567c	146 A C GCAA	GTACCCAGA GTCTTCTAATA	TGCCGCTTCCA GTAGCT	AGGATGAAATTTATATGTTATGCTGACTAGCGGGTGCTCAATAATATATCTTTTTTCATATT TTCCAAATTATTAATACTAGAAATTTTACCACACAGAAATTTTTTAAACATTTTAAAGTTACCCAGATCTT CTAATAGCAAGCAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-10567b	82 A C	AGGATGAAATTTATATGTTATGCTGACTAGCGGGTGCTCAATAATATATCTTTTTTCATATT TTCCAAATTATTAATACTAGAAATTTTACCACACAGAAATTTTTTAAACATTTTAAAGTTACCCAGATCTT CTAATAGCAAGCAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-10567a	60 T C TTTT	GGGTGCTCAAT AAATATTATT	AAATTCGTGT GGTGAAATTC TAG	AGGATGAAATTTATATGTTATGCTGACTAGCGGGTGCTCAATAATATATCTTTTTTCATATT ATTTTCCAAATTATTAATACTAGAAATTTTACCACACAGAAATTTTTTAAACATTTTAAAGTTACCCAGATCTT CTTCTAATAGCAAGCAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-11153b	84 C G TACTTTA	CAAACTCAA ATTGCTTTAAG	AAATCCAACA GTCAAGGCTT C	CGTTGGGAATTTTCTATCTCACCTAAATATGCGGTGATTAATAATATACATTTTAAACAACTTCAAA TTGCTTTAAGTACTTTACGAGACCTTGACTGTGGATTTTGGATTTTTCATTTTCTTTTCTTAATA AAACATGTCATATTTAAGTTGTCAGCAAGATGACTTATATGTTAATATCTGATATCAGCATCCCTT TATGTATT
WI-11153a	33 C A AATTATG	GGGAATATTC TATCTCACCTA	GCAATTTGAAG TTTGTTAAAT GTAT	CGTTGGGAATTTTCTATCTCACCTAAATATGCGGTGATTAATAATATACATTTTAAACAACTTCTC AAATTTGCTTTAAGTACTTTACGAGACCTTGACTGTGGATTTTGGATTTTTCATTTTCTTTTCTTAATA AAACATGTCATATTTAAGTTGTCAGCAAGATGACTTATATGTTAATATCTGATATCAGCATCCCTT TATGTATT
WI-2616	125 T C ATCC	CACAAATGTA ACAAGAATTG	CCATGGCTGTA GTCCAGT	GTTGTGAAACTCCAGTATCATTTCCCTCAAACCCAGCTTAAATCACAATCAAAATCACTTTTCTTCTCTGTA GAGCTCAAACCTCAGTCTGAATGAAATTTGCTGCACAAATGTAAACAAGAAATGATCCTATTC/ACTGGG ACTACAGCCATGGAGAAAAGCAATGTAGTCAGCAAAATGTTAACAG
WI-11163	58 C T TGAGA	CAAGTGAATT ATGACCAAAA	TGCTCTTTCA TTTGAGGTTTT T	TGACTCAAAGGAAACACACACAAAAAGTTTACCACAGTGAATATGACCAAAATGAGA/CT/AAAT TTGTTAAAAAAAACCTCAAAATGAAAGAGACAAATATAGTTCAAGATTCAGGTTCAATATTTGT ACCTACAAAAATAGGGATAGTCATGGTGTGGCAGACTTTTCTTTCTTTTCTTTTGT/G/CTCTTA GAATCCATTTGCTTTTGGCCAGCATTCCTCTCCCATATTTTAAAGGAGAGAAATTCACCTTTTCT CTGTTGGATGATCACAGGTTCTGCTCTTCCCAATCCAGAGGCGAGGTACTATTACCCCATGGGTGAT AGAGAGGATTAAACAGGGGTGATGCTGCAATGGGAATTTTGAACACC
WI-10656	59 T G	

WI-11169b	154 T G T T T T	TTAACCAAGA GTTTTTCATTC	CTAACTTAAAA ATCCTCATTTCA AAATATAA	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTTGAAAAAATAAATTAAGCCTAAAGTAGTCTTTTAAACCAAGAGTTTTTCATCTTTTT TTTAAAAAAGAGCAGACAT/GJTATCATGTGTTCTGATAAATTTTTTATATTTTGAATGAGGATT TTTAAGTTAGCAT
WI-11169a	95 A G T T G A A A A	AATAAGTGAA AGTAACTGAC	AAACTCTTGGT TAAAAAGCAC TACTT	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTTGAAAAAATAAATTAAGCCT/GJAAAGTAGTCTTTTAAACCAAGAGTTTTTCATCTTT TTTTTTAAAAAAGAGCAGACATTTATCATGTGTTCTGATAAATTTTTTATATTTTGAATGAGGAT TTTTAAGTTAGCAT
WI-10685	25 A G ---		---	CAAGTGCTTGACCTTGATAGGTG/GJACCGGCTGAAGTTGGACAGTTGTTGGTTAGGTTGGAG ACCAAAATTCAGTCACTCTGTAATATAGATCTTGTCTTTGGGTTTACCACAGGGTCACTAAAG AGAGATGGGAGACAGTCTCAATCTTGTCTAAATAATCCAAAAATAGCCATGGGTTTGGACAAAATAC AAGTTAGTGCTCTCTAACTTTAATGGGCATA
WI-10686	133 C T A A G G	TGCCCTGTGC AAGG	CAATCTCTAAA TTCATGTGTAG ACACA	AATAACCTGTGGCACATAAGGCAATACTGAGCCCCATACAGAGTGTTTATGTTAATATTATGAAA AAAGTCAAGAGAAACAGATGATATAGTTCTGCTAGAAATCTGAAATCTGATGCCCTGTCCAAAGG[C/TJTGCTACACATGAATTTAGAGATTGAATGAAATGGCAAAATTCAGAAAAAGG
WI-11175	77 T A A	AAATGATTCCT TCTGCTCAAG	CTGTTCTCACA TTCCTTTTGAA AA	GGTAGGATGATCTAGAATGCCACTTACAGCCACTGAAATATATTGCCCTCCCAATGATCTTTCTG CTCAAAAGAGT/AJTTTTTAAAGTTATCTACTTATTTATCTGCTTTTTTCAAAAGAAATGTGAGA ACAGTACAAAATGTGTTTCAGTATAGCAAAATTAATAATTAATAAAGTAAGAAAAAGAGCCCAATT TGGGC
WI-10694	144 A G T A T G A G T T T C	TGCAAAATGCTT TGAATTCATCC	GGCATTTTGTA AAGGAGGAAA TCTCTTTTCTC	TAGAGAGGCTTTTCAGTTTCAGGTTGGAGGGTGGTGAGGTGAGATTCATCTTAGAAGCACTGGC TATGTACAGAAAGATAAACTCTGAGAAAGAACTCAGTTCTAAAGTTTCAAGTCTTTCAGTCTTTGCAATGCTTTA TGAGTTTTTCA/GJTTCCTCTCTTACAAAATGCCATCAATTCCTCAAGGAAAAAAGGCTTTCT
WI-2716	23 T C C	AGAAAAACAG TTC	TCTTGTGTCA TTC	GTGAATTCATCCAGAAAAACAGCT/C/GAATGACAAACAGAGAGAGAAAAAGGTTTGTGT ATACGACAAGTGGCTCAAGCAATTTTCTGTCTGCCAGTGCATGGAGCAGTG
WI-10719	115 T C G C C A T T C T A G	TGACTCTCAAG GCCATTCTAG	GCACTGCCAGC AGCC	CAGGCCCAACTCTGTCTAATTAAGTGTTTTGAACACAGACACCTCAGTCACACAAAAGTTTCTCTGTATGT GCCCAACATAAACAGTTACTGGAGGATGACTCTCAAGGCCATCTAGT/CJGGCTGCTGGCAGTGCTT TTCCAGCCTGCTGCCCAATAACTAA
WI-10721	40 A G C T T G C C A	TGGCTCTGCTA CTCA	GAACTCCAC ATAAATAAAT CTCA	CAACCAATTCAGATTTAATTTTGGCTCTGCTACTTGCCA/GJATGAGATTTATTTATGTGGGAGTT TCTGAAGATCCCATGGTAAATAGTATTCCTCTTCCCTGCTTAGGTTTGAAGAGTTGAA

WI-11204b	88 T C ---			GCACACGAAATTGATTAAATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAGAAAAACTTTACACCTTTT/CJATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAATTTTAATTGGGAAGAGATTTAGTGAATCAGAAAAATAAGTCTGAGGAAATTTATTCAGAAG GCAACATC
WI-11204a	80 T A AACTT	GTAAAAAGGG TGAAAAAGAAA	--- TGATCATTAA AATGTACATAA TACCTTT	GCACACGAAATTGATTAAATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAGAAAAACTTTT/CJACACCTTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAATTTTAATTGGGAAGAGATTTAGTGAATCAGAAAAATAAGTCTGAGGAAATTTATTCAGAAG GCAACATC
WI-10732	80 C A ATTGGTCACT	GCTGTGCTTC ATTGGTCACT	AGAACAATG CATAACAGAA CTTTAA	ACATGATTTCCTTTAGTGGTCAGCCCTTCCACCCCAAGAAATATCCCTGGTTTATGCTGTGCTTC ATTGGTCACT/CJTTAAAGTTCTGTATGCATTGTTCTTGAGTCCACATAGGTGTTAATCATTCOA CACCACCTGTGTTAACTGTC
WI-11206	127 A T ACTC	GGTTGTGTTTT CTGTATGTACA		TAGTCTTTTCTTTGTACGAGTGTCAATAAAGAAATACCACCTCTGTACATTTGTAAAGATAGCACAG AGAGAAGCATTACAGGGCACAGCACAAACATGAGGTGTGTTTCTGTATGTACAACTC/A/TJCCAA CCATTAGGATTGTCACTCTCATATATAGACAGAAATTCAGTGGTGGTGAATTTGAATCCACACATGGA ATAAGTCTA
WI-11215	68 C T ---		---	GAAAAAAAGTTTAAATTGGATTGCTTAGTTTGCTTAAATTTGACCTACTTTCAGATTTATTTTAGT [C/T]ATTTTCTATAATATTTCTGTAGTGATGGATTTCTATAAATTAAGGAAACAGATATTT ACACAGAGAAGACAGGATTGCTTGAATTAGTATAACATTTCTTATCCAAAGCCCATTCACCATGT TTT
WI-11219b	89 G A AGAGAA	GAGAGAATAT TCCAAAAAGT	GGTCTCTAAT TTTCTCACT TTCT	ATGAAAAATGCATTAGAAGAATTGGAGGATAAAATTGAGAGAATATCCAAAAAGTAGAGAAAA GAGACAAAGAGATGAAAAATAGGA/GA/JAGAAAGTGTAGAAAAATAGAGGACCATCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAACATCTC
WI-11219a	18 G A ---		---	ATGAAAAATGCATTAGAA/GA/JAATTGGAGGATAAAATGAGAGAATATTCAAAAAGTAGAGAA AAAGAGACAAAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATAGAGGACCATCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAACATCTC
WI-11222b	136 G A GGCTGG	CATACCACTGC	CCTGGTAGCCA AGTTGTGA	AGCCACAGTGAATCAATTTACACTACCGAAATCAGCAAAATGCTAAAAATGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCACCGTTGAACATTTGTTAAACATTTACAGCATACCACCTGCGGCTG G/GA/TCAACAACCTTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTTGCTTTCACAGGCTACTGG AAAGCC

WI-11222a	25 C T A	GCCACAGTGG AATCATTTAC	TTTTAGCATTT GCTGATTCG	AGCCACAGTGGAAATCACTA/C/C/GAAATCAGCAAATGCTAAAATGGGGCTTTGGATTTT TGTTTTGTTTTTCCATAGACCCACCGTTGAACCTATTGTTAAACATTTACCAGCATACCACCTGCGG CTGGGTCAACAACCTGGCTACCGAGGAGAACCTGACACAGACTTCGTAATTGCTTTACAGGCTACTGGA AAGCC
WI-10775	39 C T	TTTATGCCATA TTAATTCATTA	CTAGATGTATT TGCTAAGAAA ATATGATG	TTGCAAGTTTGTTTTATGCCATATTAAATTCATTACACTC/C/CACATCATATTTTCTTAGCAAAATACA TCTAGACACCTGGCACTCAGTAAGGGATATTCCTGGCAGATAATCATTTGTTATCATTAGACATTGCA GGAACCAACCATATGGATGATAAATGTGTGTTTAAATGAAGGCAAGCAATTA
WI-11226	165 A C ---		---	TTGCATGCATTTATACGAAAGGAATTAATAATATCTTCTTATAGTTGAATTTAAGTAAAAATAAA GTTATACATATAATACAAAAAGTTGTAAGTATAGTAACAAATGAATTAAGAAAAATGTCAGTGGTTGC TAGTACAGGAATCAAAATTTGGACTATGAACA/C/CAGACATAGTTGCTAAGGATATTCACAAAAATTAT TTCATGA
WI-10778	62 A G	GCAAGGGAGG AACATTTACA	CTGGTGACATC AGAGATGGAC	CAGTGGCTGGCTACTGACAAAACGTAAACATCGTGGCAGGTGGCAAGGGAGGAACATTTACAG/C/G/G TCCATCTCTGATGTCACCAAGCAGGGCCAGGAAGGTTGATCTGGAG
WI-10789	21 C T	GGGACACACT GCTCTAGACC	TTGAGGGACCC TGGGA	TGGGACACACTGCTCTAGAC/C/C/TTCCAGGGTCCCTCAAAGGTGGGTGAGAGGCCCTACTGCCCT GCCCTGGGGACGACAGGACATCAGGGCTTAGTCTCTCTGGGACAGTGAAGGGGCCACCAAC
WI-10810	58 C T	CATCTTCATGG GCAGGAATT	CAACCCCTAAG AAACACAGAA ATG	ACAGAAAAATGCCTAGGTCTTGTAGCAAGAGAGAAAGCATCTTCATGGGCGAGGAATTC/C/TCATTT CTGTGTTCTTAGGGTTGTGGCTGGCCATCAGTTCAACTCAGCCCTGTCCCTGTATCCAGCAACATT TCCGTAACCTACCCCTCTAGAAATCATGCAAGAGAGAAATGATGA
WI-10828	23 T C ---		---	GGACCAACAGAAATTAATCTGGCAT/C/JAGGGTTTCTTAAACATATTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCGAGGAATACAGTTAGGGAACATGTGGATGAATATTTCTTTAGTAGAG GACTTCTAAAGGCTATAATATTTGGATACATTAGGCTCATTATGAATCTCAAAGGAGGCATGTAGT AGGGCATATCTAA
WI-10832	91 G C	CATTAATCTGC AGGCTCTCC	CCTAACTGCAG GTGACTTAGAA A	TATGCCCTTCCCAACGAGCCATCCACGCTGCTCTTAGCACAAAAAATAGAAATACATCATCTGAAATG GGCACATTAATCTGCAGGCTCTCC/C/G/TTTCTAAGTCACTGCAGTTAGGTCTGCAGACACTGTGTA TACCATATAAATCTGATTTCTGAGCAGGAGGGAGGCAGATGAGAGAGGGCTGCTCCGTGAAATAC TAGTTCGG
WI-10834	96 C T	AGAAATTAAT GTTCAAAAGT GTGTTAAT	TGGCCCTATAA AATTGGTATTA AG	GATTTGAGTATTATCAAAATGCCCCAAGACCATTACAAGATTTAATAGTTAAAGCCAAAACTATA AAGAAATTAATCTGTTCAAAAGTGTGTTAAT/C/TTCTAATACCAATTTTATAGGGCCACCATTAACTT CTGAAGAAAGGTGAGCATATGCAACTAAATTTCTAAAGTCCAGT
WI-2287	24 T C ---		---	GGATGATGTTCTGTGGTCCCTTTAT/C/JAAAGCCCTCTTGATCCCAATGTGTAAATTTATTTATCT TGGTATTTCTCGCTTACCCATAGTCACCTGTCAAGTGTCCACCT

WI-2296	81 A	G	TGTTACTTTGA TTCTTTGCTCT	GCAAATCACAC AGCTAACTGG	TGGAGGGTTAGAAATCAGGTGGCATCCTAGAAAGGTCTCAGGCTTTAGAATAAGTTGTTACTTTGA TTCTTTGCTCTGAC(A/G)CCAGTTAGCTGTGTGATTTGCAGAAGTTACATTTGTTTGTG
WI-2300	77 G	T	GGCAGAGAAG CCAGTCATAC	GGTGGGTCAA TTTTAAAGCA	TTTCATCATGCTGCTCTTCCCTGGAAATTTCCCTTATTTAGCGGGGCGAGGTGGTAGGCACAGAAGC CAGTCATAC(G/T)TTCCTTTAAATGACCCCAACCATTTACTAAGAATAGCATTCA
WI-2371	55 G	T	GTCTTGTTCTT CCAGCTTCT	CAAAGATTGAC AGCCACCAC	CAATGATCCCCCAACATTTCCAGGGAAGGTCTGGTCTTCTCCAGCTTCT(G/T)GTGGTGGCT GTCAATCTTTGACATTTCTTGTCTTGACGCTGTATAATTCGAATCCTTGCCTCCAGCTTTACATGATGT TCTCTCCGTGTGTGTG
WI-2395	122 A	C	GAACATATTT GTAGAAAAAT	TCACCTTTCTA TTTATTCTGAA	GGGGGCACAATTTAGCTACAGTGCATATTTAAAGATAACATAGAAATATCATATAAATTAACCTTGGTTTAC TGAAATCTGAAAACTTAGGATGAGTGAACATATTTGTAGAAAAATTTACTATCCAA(A/C)CTGAATTC AGAAATAATAGAAAAAGGTGAATCATCTTATATCATTAAAGAAAGCTAAATTTATTAGTAACAATCTTTA CATTTACACAACCCCA
WI-2437c	192 G	A	---	---	CACCAGCCACCACCTTACAACCTCTGTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACCTTTCTAAATAATAGACACCAAAAAATTCCTCAATGCTCTAA ATAGTGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGACATCACAGTG(A/G)GCTGTG GTGCCAAGGACGCATTATG
WI-2437b	179 G	A	---	---	CACCAGCCACCACCTTACAACCTCTGTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACCTTTCTAAATAATAGACACCAAAAAATTCCTCAATG(A)CTC TAAATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2437a	128 G	A	---	---	CACCAGCCACCACCTTACAACCTCTGTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACCTTTCTAAATAATAGACACCAAAAAATTCCTCAATG(A)CTC TAAATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2440	71 G	A	GCAACCTACT GACAAITTA TTTTAGTT	AACAACCTGTC TATTGGTCTCA C	CAGTAGGAAACGGGTCTTCTCTAGACCCCTCCAGAAAAATAATGCAACCTACTGACAAATTTAATTTTA GTTG(A/G)GTGAGACCAATAGCAGAGTTGTTACCTGCAGAACT
WI-1356	123 T	C	TGTTTAGGAA ATAATGACAA GAAAA	TGGTTACAAC GTACCAACAT G	CTGTAACCTACACACATCCTCTCTGTAACCTCTAGGTTACTTGTAAATACAAAAACAATGTAAATGCT ACATAAATAATTGTACATATAATTGTTAGGAAATAATGACAAGAAAAAGCC(T/C)GTACAT GTTTGGTACAGTTGTAACCAGCCATTTTCCCCCAATATTTTCAATCCACAGTTGTTTAAATCCACAG AAACCACGAATG
WI-2886	46 C	A	CAGAGTCTGG GGGAGAAGA	TTGCCATGCTT TATCTCGTT	ACAGTTAAGAAAAAGGTGACGCCGTTGCAGAGTCTGGGGGAGAGA(A/C)AACGAGATAAAGCATG GCAAGACCAACGCTGAAAGTATCCAGGGTGTGTATGTGCACATAGGAAGATCACTTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAGGTGTGACAGAAACAGAGGAGCGTT

WI-2906b	77	T A	---	---	CCTGAACACCTGGAGCACTCCCTCCCTGGACACCTTCATCTTCTGCTGGAACCTTTGCCCTGGAATGCTCTTTCCCTCTG/AJGAGCTTTGCTTGGCTTACTTTTCTTTTCTTTAGGTTTCAGCTTCAAAAGTGACCTCCTTAGAGTTGGTTTGTGACCAACAAA
WI-2906a	50	A C	TCTTCTGG	AGACATTCCA GGCAAAGT	CCTGAACACCTGGAGCACTCCCTCCCTGGACACCTTCATCTTCTGCTGG/AJGACTTTGCCCTGGAATGCTCTTTCCCTCTGAGCTTTGCTTGGCTTACTTTTCTTTTCCCTTAGGTTTCAGCTTCAAAGTGACCTCCTTAGAGTTGGTTTGTGACCAACAAA
WI-1736	175	C T	---	---	TACTCCTCATTTCTCATGTCCCTAGACGTACTCAGATTTCCATGCCCTGAAACATTTATTTCCCTAAAT TAGATTTCCACCCCGACACTATTTACACAGAAACAGCATGGAGCAGTTTGGAGTCTGGCTCTTAGA GAACCTTACTTAAGGACAGTGGTTTCCATCTGCTCTCCAC/AJTAGAGATCTAGGGTGTCTTTTGGAAACC ACCTTGG
WI-1851	136	G A	GTGTTAAGTA	CACTAGCAATT TTAACTGAAG TTG	AATACCCACGTCCTAACACCATCACACTGATCATCAATCAGGTTTTAACATATTATCTGGGGAGG ACACAAACATTTAGACCATAGCATTGAATTAAGTATAGATGTGTTAAGTAAATTATTAACATGGTA CA/G/AJACAACTTCAGTTTAACAATTGCTAGTGATTCCATGTGGATACCATGTACCTTCTTACATCATG TGA
WI-3000	62	G A	AGAGACCCC	GCCACTATAGG ATTGACTAAGA CTCA	CTGATGTTTGGGAAGCACTGTCTTACATCTCTAAATGTACGACCCCAACACAGAGACCCCG/AJTGAGCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTGCCTGGTGCATAGTAGACACT
WI-1754	177	G A	TAGTC	AAAGTCGAATT GCCTCTGG	ATGGATCTGCTCAATTATAGTCCAGATAAACAGCCCTTCTCCCGCCACCCCGGATTATTTTACT TAAGGGTTTAGCAAAATTCACCTGACAAAGAGTTAGGTTTCAACATTGACCCCTCATAAAGTGATTTT TTCTCTTCTGTTTGTCTCCCTTCTTAAAGAGATAGTC/G/AJCCAGAGGCAATTCGACTTTCTGT AGCCACAAGATT
WI-3167	37	T A	TAGATTG	TGTGATAGTT TGAGATGGGTG	ACAACACAGCAAAATCAACCACAGATCTATTAGATTCT/AJACCCCATCTCAAAACTATCACATCAA AGAAGCAAGGAGACATATTACTGGTGAGGAAGCCAAATTCAA
WI-3208	140	G A	AGATAAAGA	TCACTCAAAC AGGGCTTGG	CAAGCACACATTCAAGCAGTGGGAGGTAGGGAAGGTGGGCAACTTGGCAGCAGAGAGGAGGAAG AAGTTCAAGCCGTTGGGTAGGATAAGTGGATCCAAACCCCTTTGTAGGGCAGGTGGTGGAGTGGGCAG ATAAAG/AJAJCCAAAGCCCTAGTTTGAGTGACACTGTGGGGATTCAAG
WI-1775	47	C T	TTTTCTCTG	AGTTGAGATT ATGACAATGAT GTAAA	ACTCCACCAACAGTTTGTGAGCCAAACCCCTGCATGGTCTTTTCTCTG/C/JTTTACATCATTTGTCATA AATCTCAACTGACACATCAGTGTCTCTGCCACCCCA
WI-3402	55	G A	ACAT	GAGGACTTAA AAGGAGCATTT G	CTGCCCTTTACATCCAAAGCCAGTTACTCGAGCATATTTCATTGATTTCCCTTACAT/G/AJCAAATGCTC TTTTAAAGTCCTCAACTTTTAAAGCGGAAGTTGAGACATGCACAAAATAGATTTCCCTTAGGA

WI-3416	33 C T GTC	CCAAGTTGTA GCATTTCAGAA	ACGAGCACAA CTACCTCTAAG AG	TCTGGTTCCTCCAAGTTGTAGCATTAGCAAGTC/C/TCTTAGAGGTAGTTGTGCTCGTCGTTAAAA TATGTTTTCAAGATAGTATCTCCCTGTTGTCACTTCTCTCCAAACAAGTGTACCAACAGCATTTGTTAAG GAAATGTGAATGCTTGTCTACCTCTGACGACACACATAATTAATCCCATTCCTCTAAAGACCCAGG
WI-3453	70 C T ATCAGAGAA	TTCTAGGCC TTCAGAGAA	TCAATTTTCCC CATGACTTC	TCCTATTCCTACAAACACAGAAATTAACAAATTAAGAAATCAGCTACTCTCTTAGGCCCATCAGAG AATC/TGAAGTCATGGGAAAAATGATGCCATGTGAATTTGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACCAGGACACAATCCCACTCCAGAGCCATCATCTGTAAAGAC
WI-3474b	109 G A ---		---	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACTTAAATCATCAAGTGTGTCAACTGGTTGA GTCAGTTTCCCTAAATTTAGCACAC/G/GTATTTTAATGAGGTGGTGGGAGAAAAATTGATGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474a	90 A G AC	AGTCAGTTTCC CTAATTTTAGC	CAACCATCAAT TTTCTCOCA	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACTTAAATCATCAAGTGTGTCAACTGGTTGA GTCAGTTTCCCTAAATTTAGCACAC/G/GTATTTTAATGAGGTGGTGGGAGAAAAATTGATGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3502	79 C T GGATGTCT	CCTGGGTTTCT GGATGTCT	GGGTGACCTG TCCTCA	TTTGACCCCATACATGAGAAATAAAACCATGAAGTTGGTGGAAAAATAAAACGGGAGAGACCTGGG TTTCTGGATGTCTCT/TTTGGAGACAGGGTCAACCCAC
WI-3600b	146 G C CATCT	GGTTTCTAACC TGGATATAAA	CCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCTGCTGCTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGTGAGCCACCTAACTGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGGATA TAAACATCT/G/GATGGAAGGCTGCAGTGGATGAGGTCACAAA
WI-3600a	78 T G ATAGTTCTG	CCATGCCCCCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCTGCTGCTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGT/G/GAGCCACCTAACTGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGG ATATAACATCTGATGGAAGGCTGCAGTGGATGAGGTCACAAA
WI-3678	125 G T ---		---	TAAATCATGCTTATTTTCAACAAGGTAATCCACTCACAAATAGGCAATGATGTGATCTCTTTCTGTAA GAAAAGCTCTCATGCTCTTCTGAACCTTCTACTTACTGTGCTGTTATGATGCACCT/G/TCCCTTTTGG ATAGATGGTTGATAGGAGATGGTTGTTAAAGACACAAATTTACCTTGTGTTTTCAGGCAGAAATAG ACTCTCTGTGTATCACTGAATGAGTTCCAAAAGCCTTTATGTCTTAC
WI-3687	67 A C ---		---	AAAGCGATGTTGAGATACCACATTCCATGAAAAAGTAAAAACACACACACAAAAATGACATAAAA T/CJAAAAAATACTATAGTTTATGAAAAATGACTTCCAAAATTCAGAGAAAAGTCACCTAAACAGG ATTCTCAATTCATCCAGATACTCCTCTGTGCTTAACTTGAAGTGCACAG
WI-3735	72 T C AAAAC	CCTCAGTTATG TATCAAAATGA	GGCTCACCAAT CATTTGTTTT	TCTAAAATGTGAAACCAAGAAATCTGACACGACCTAACTGCCAGTCTCAAGTTATGTATCAATGA AAAAAT/CJACACCGGTTCAATGAAAAAACAATGATTGGTGAGCCATGTCCCCTTATTTAATGAAAAA GATCTTGGGCAATTAACCT

WI-1819	51	C T ---				GAAGAAGCAGGAAGCCAGGAGGACAAACATTTTGAAGAGTCTTTCAGCAC[C/T]TCGTGGATCOG AATTTAGTGTGATTTGGCAGGCAATCGGGGTAAACATGTTCCAGTGTTTTAACTTGCACAGAATTGC CAGATTAGCGATTGTTTGTGACTTGTCCAAATTAATGAATGTGGAAGAAAAAAGGGTGGTAAGTGT AAGCCTGCTGCAATGTTTAGACACGAGGGTGGGGTGGGAGGTGAATACC
WI-3746	116	G A ---				GGCCTATTACATGACACTGGCCCAAGATCTTGCTCCCTTCTTCAATAGATAGACTAACTAGAAA ACTGCCCTGGCCAGGAAGATGGTTGCTTCATCATCTCTGCTCTG[C/G]A]GCCCCAGGATAAAGCA GGCA
WI-3867	49	T C C A A	ACAGTCATTT AGTCTTCTCTGA	TAAGATAACC ATACTAGGTAC ATCCG		AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCTGACAA[T/C]JCGGATGTACCTAGT ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTGAACAAAGACACAGT CATTAAAGTGGAGAAGCCAGCATTTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG CATC
WI-3898	25	A C G	TGACCAATGTC TTTAGAAGCA	TCGTGGTGTG CTCTCC		CAATGACCAATGTCTTTAGAAGCAG[A/C]JGGAGAGGACACCGACGAGACACACAGGAAGGAGTGAG GTGAAGATGAAGCAGTGTGACGACGCCACAAAGGTGAGGAAGAGCAAGGGTGTGCTGGCCACT
WI-3901	114	A G ---				GGACCATTTGCCCTCAGAAGTACATTCAAGCCCTGGACGGTGTCTCCTAACACTGTGACCTCAGGCA AGTCATGTCTGCTTCTGAACTCGGCTTCTCACCTGACAAAGTGG[A/G]TATCATGTGCTACACTGC AGTGTTTATAATGCTGCAT
WI-3914	99	C T G C	TGATTTCTCTC AAGACTCACA			CTGAGGAGATTGATGCTACTTTACCTGAGGAAACATTTTATACCTCCCTGAGTTTGTGCTTGCCTTGCAA GACATTGCTGATTCTTCTCAAGACTCACAG[C/T]JACCATCCTTCAATTTGCTTCTAGACCTATAACTAG ACTCAAGTCCCGAGGCGCCTTAAAGGTAAGGTACAAAGTGTGACCCATGGGAGGTATGTTACGCTA CAAAAGAG
WI-4019	33	G A A	CCAGAGCGT CCTATGAATC	AACAGCAATA ACAGGAACAA ATG		CCACTCCCAGGCCAAGAGCGTCTCTATGAATCAT[G/A]CATTTGTTCTCTGTTTATGCTGTTACAGAGT GGCAACTCTTGCAAGGGAGGGGTACAAAGTGAATTTTATAGATGCTGCAGGAGACGAAGGGTC
WI-4091	84	A T G T C A T T G C A T G	TTGAGTCTTA GTCATTGCATG	TGAGTTCCTAT TAAGTGACAAT ATTGTT		TAATTCACATTGCTCTGTTTGTGCAATTTATTGCTTCTCTTATGTAACACAATCACCACATTTGAGG TCTTAGTCATTGCAATG[A/T]JTGATAACAATAATTGTCACCTAATAGGAACCTCAAGCATAGTTATGIGT ACATTTATTGCTAACAGCAG
WI-4160	117	A G C A C A G A A	CCTATAATTTA GCAACAATAT	TGCAGGTAGAA TTTTCTAATAT AGCC		TCCTCTTCTGTAATAGGAAGTCTGATTAGATGCCTTTTGAGGTAGTTGGCTTCTAAGATGGTAATT ATCTGTCCAAGTTTTTGTTCCTATAATTTAGCAACAATATCAACAGAA[A/G]JGGCTATATTAGAAA ATTCTACCTGTCATCCCTGGATGTCATGTAACGTTCTTCATGATACT
WI-4168	32	A G A A C A	GGTGAGAGTC AAATTGATAC	ATTGCCAAACA GATTTTCAGA		CGTTGCTGGTGAGAGTCAAAATTTGATACAAACA[A/G]JCTGAAAATCTGTTGGCAATCTATTAAAGG CAAAATATACCAGCAGTGTGGTCTAGCAATTTCACTGCTGGGCATTACCTAACATAAATGAT

WI-5204	54 C T	---	---	TAGATTTTGATTGATGACAATAGGGAAGCCCTTTGTTAAATTTGGGTTTTGAAGAA[C/T]GAAGAAAA TGGAAAGGGAAGAATTGACAGAAACCAAGAGAGTGTGAGGGGCAGCAAATCCACAGTTTGACTGGA ATATAGAGTGATGICAGGGTIG
WI-5215	70 A G C T C A A A A A	GGACCTTAAT ATTTAACAGA TTGCG	AGATAATTTTG TAAAGATAGTT TTGCG	TTTCCCTTATTATTAGGAAGCAAAATGTTTCATACAGGACCTTAATATTTAACAGACTCAAAAA TAT[A/G]GCGAAACTATCTTTACAAAATTATCTCCATAGCAAGTAGACATTTTAGCACATTTTCCT GTAGTCAAGGTTTTAAAGGCCAAATGAAGTTGACTAAAGACAAT
WI-4448	112 T G A T A A A	TTGTATCAAA GAGATGGGT GATATAA	AATTAAGAA ATCTTTACATG GTTCTTT	CCCTGAAATGTGCTTTGCTTCTCTCCCACTCTAGGGAACCTTTCCATGTGAGGTGAAGGTTTTGA AGAGTACTTTAATTAACTTGATCAAAAGAGATGGGGTATATAA[T/G]AAAGAACCATGTAAAGATTT CTTTAATTAGTGAATTTTCATCAGGGCTCTTCCACTGTCTATCAGTAAA
WI-4456	49 C T T A T A G T T C C	AGTTGAATTA TTCAGAAAAT TATAGTTCC	TTTCCTGTTAT GCATGAACITG	ACACATTTCACTTTGCTTTAAGTTGAATTATTCAGAAAAATTATAGTTCC[C/T]CAAGTTTCATGCATAA CAGGAACACCAGGTGGGCAATTGATTGAATTGT
WI-4461	49 A G C C T T C C	TCACTGTTATT TTAAAATTAT GCTTCC	TTGACCTTTC ACCAATTTCA	CTGAAACTAATGAGGTGCTAAATCACCTGTTATTTTAAATTTATCCTTCC[A/G]GTGAAATGGTGAAA GGTCAAGAATGAATTCACCTTTTATAGATTTCTGGAAATTTATTTGCGATGATAATGCAATGGGC CTACTGGATTTTACTTTGCTCAAGCCAGACACACGAAAGTATATAAAGAAAAACAGTTAGTAATCTT TCACCTTT[G/A]TATTCTCTACCTCAGGGAATC
WI-4465a	41 A G A C A C G A A A G T	AAGCCAGACA ACACGAAAGT	GGTGAAGATT ACTAAGTGT TCTTT	CTACTGGATTTTACTTTGCTCAAGCCAGACACACGAAAGT[A/G]TATAAAGAAAAACAGTTAGTAAT CTTTCACCTTTGATTTCTCTCTACCTCAGGGAATC
WI-1949b	160 T C T A A T C	GAGTGAATAA ATGAATGCCA TAATC	TGAGAGGTGGG GACAAAAA	GGGGTTAGGACCTCGAGATCTTTGAGAAAGCACAATTCAAACCATTAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G/C]AAGGCTGCTGACATGGTCATGGCTGAATATATGTTGAAGAAAT GGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTTGTCCCACTCTCACACCTTTCCCTGG CACA
WI-1949a	86 T G A T G C T G A G T	CAGTGGTGAG ATGCTCTGAGT	CCATGTCAGCA GCCTTG	GGGGTTAGGACCTCGAGATCTTTGAGAAAGCACAATTCAAACCATTAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G/C]AAGGCTGCTGACATGGTCATGGCTGAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTTGTCCCACTCTCACACCTTTCCCTGG CACA
WI-4529	64 T C A A G A T G	CCAAGTAAGT CTATCATTCTG	TTCTAAAAATA ACACTTCCTGA AAAA	TGAGAGAGTTTTGGATTATTTCATCCTCTGCAACACTCCAAGTAAGTCTATCATCTGAAGATG[T/C] GAGTTCTCTTTTATATCCTATGATTATTTTTCAGGAAGTGTATTTTGAATATAAACTCCTGGGT CCCATCCAGGCTAGGGTCAATGGCATGCCATCGGTGCTGGACAAGATGGGCCCTAGGATCATTTT

WI-4540	110	A G	GCACATGTGG CATCC	GACAATGCAGC CATGCA	AGCTTTTCCTTTCTTAAAAATTGGTGCCATAGTACTGGCTTCTGTGTGCATCAGGAAGCAAGCCCTAT TGCTCGGTAAAGTACTTTTGCATAAGCACCATTGGCATCC A G TGCAATGGCTGCATTGTCCAGTC AAATGAGACAACCTTCCTAT
WI-4582	226	T C	---	---	AGCAAGCATCTGGCAAGCCTCGGTGACCAGAACATTAAATTCACCAACACACACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATTCAAGGCCAGTTTAACTTATTCTGTATACACA AATAACTTTATGGGAGACAGCATTGTAAATCAATCAATGAATGACTCGGTTTGGCTGTACAAGCAT AAACAGAACGCTTGC AAAATATGGTTC C CTCCTTGCTAGAAACCACTTTGAT
WI-1965	105	G C	AG GCCATTGAGG AAGTGTTAA	GAATGGATGGG TCACTCTCT	CAAAGTTAGTTAACTTGGGGGCAACACAAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGCCATTGAGGAAGTTTAAAG C JAGAGAGATGACCCATCCATTCTCTGG GCTTCTATATGACACCATACTATCCACACAGATGTGGAGTCATTTATTTGGTTGGTGTATGACAGT CATGG
WI-5248b	99	C T	TTG CACTGTTTCT ATTGACCGTAC	AGAAAAAGAG AAGAAAGGAA AAA	TGTTTAAAACCATAACAGTTTGCTGCTACGTTGTTAGAGCAACCCAGAAAAATTAACACGCCTAC CATTTTCACTGTTTCTATTGACCGTACTG C T CTTTTCCCTTCTCTCTCTTTCTG CCCTCTTTAACTATT
WI-5248a	38	G C	AGTTTGCTG CTACGTTGT	TTTTAATTTTC TGGGGTGT	TGTTTAAAACCATAACAGTTTGCTGCTACGTTGTTA G C JAGCAACCCAGAAAAATTAACACGCC TACCAATTTTCACTGTTTCTATTGACCGTACTTGTCTTTTCCCTTCTCTCTCTTTCTG CCCTCTTTAACTATT
WI-4596	69	T A	TGAAGCAGAA AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTCCAACTTCGGTGACATTACTCTGTTGACTTTGCTCTGAAGCAGAAAGCACTGTGA C T A CATTATTAGGCCCATCTCTGCTGAGCCCTGACAGCAATTTGTAACATATGCGATTGGG ACATATCTGTGAGCCCATCACTATTGACAAGATTCTCCTTTTAAACAA
WI-5252	119	A C	---	---	GAAATAGGGCAAAATTAAGACTTCAATAATTAGAAGTCTTGGGAAAAGGATTTGTGATGATCATTTG AATCTGTTTAAATACAGAAATTAATCTGAATACCTGTGTGAATCATTTGCTTTT A C TACCATGTACA TATTATGAATTAACAATGATAATAGTATGACTAAGAAATATTGGGCCCT
WI-4606	61	A G	CT GCAATGCTAG AAAATTATGC	TTAGGTGCTTA AGTTGTCTACT TGG	TGCAAAAAGGAAAAATGATAACCAAGGACTGTTGTTCAAGCAATGCTAGAAAAATATGCCTA A G C CAAAGTAGACAACCTTAAGCACCTAAGGCAGAAATGAAAGTTTCTCTTTGTCAATTAAGTCCTTATTCA ATTACCATTATCGGGGTAATTAACACACTGGAAGTAATGCCAGGCTAATTGTTAGATTATGATAAT TACACGCTTTTGCTATGCT
WI-5257	77	C A	GAGGCATGAA GCAAGAGG	CCAGGGGCAGA TGAAAG	CAATGAGAAGTTACCAGATGCGGGGCAAAATTAAGCATATGAAAAATACCAAGTGTGGCAGAGGCATG AAGCAAGAGG C A CTTTTCATCTGCCCTGGTGGTTTTTCAGTAACCTGCAACATGCTTTTGGCTCC CGGATGAAAAGATACCCCTTCTATGACTCAGCAATTCCTAGGTATGCACCCCTAAACATGGGTG GCAAAAT
WI-4649	50	C T	GAGACCATTTCT TTCCGAATG	TGTAAGTGTG TACTTACAAGA AATCATC	TCAGTGTTTAGAAATTTCTTCTCCTCAGTGAGACCATTCTTTCCGAATG C T GATGATTTCTTGTA AGTACACCTAGTACATCTATGAGCACACAATTAACAAGTACTTGCTACCTGAATTTGTAATTTTTTAA AAAACTCTCCCAATATTG

WI-4650	148	A	G	GCACAAAGAA AGTATAAGTT GTCTCTT	CTGAAGTGTTA AACTGGATTG G	AACTGTGGTATGTAATTGTTGTGATTTTCTGGAGAGTCAGTTACTCTACTAGATCATAAAGGG GACTTGGGAACCAAAAGTATCTCAAGACATTTAATCCTAGAGACACAAGAAAGTATAAGTTGTCTC TTATATTGCTTTT[A/G]CCAAATCCAGTTAACACCTTCAGTAACGTT
WI-4677	82	T	C	TCCAAAAGTG ATTAGGTGAA CTAAA	TTTCAACAGTG TCATTATTCAA CTT	AATTCAGATTTTGAACATACGTGACATTTTGGAAAAAATTTGCCAAAAAGTGATTAGGTGAAAAAAT GAGTTGAAATAAATGTT[C]AAGTTGAATAATGACACTGTTGAAAAATGATGAATCTGCTTTCAATTCA CATGGAAGGAGACTAGAACACACAGCAGGTTTATAGGGGAATACTCAT
WI-4698	135	C	G	---	---	ATGATGCTATCATGAGGAATCTGTAGAAAAATTTACCTGGCAATGATTCAAATAAAGTTTGTCC TCACCTGGGAAACTGCTTATCTTGATGTCAGTGACATTTCTTTTCTTTTGACGGAAGAAAACTTCAA C/GTTGAGAGGCTTAGATTATATCGCTGAAGCCCCATTCTG
WI-4722	88	G	A	TGCATATGG AACACCAC	AATATGGAATC TGCATTGAGTT G	CTTCCATTCTGCCAGTTAGATGACTGCCTCTCCACCAGCTAGAAAAAGATGGGAGATTTATTTTC TGCACTATGGAACACCACAC[G/A]CAACTGAATGCAGATTCATATTTGAATACTGGGAAATCAGTGA AAG
WI-2020	145	C	A	---	---	GCCACAGTAAAGAGGAAAAATGGAGCCATGTAACAGAGGAGAGCTTTCTGAAGATCAGTGTATTGTCA TAAAGGTCAGTAAATCACTTTGATGGTTGAGATTTTCAAGAAACGTGAAATTTATGAGTAACCATGGG TCAACTATGAT[C/A]CCAAAACAGCAGTGTGTCTAAAAAATATGATAGTTTCTTCTCCTGTCCACC GCAATGAAAAGGAGTT
WI-2028	176	T	C	TGTTACGTT CCTGCTCATC	GGTTGGAAC CAAAATTACCTA GAA	GACTACAGCGCACAGACAGGCAATGTGTGGCTTGACAGGTTTGGTTTGTGTTAAGTTAGATT TGAATCCTTTAAAGAAAGAAAGTGGCTCTTCAAGTTTACTACAGACCTCATCTCCTGGTTCTCTTG CACCCAGTCCACTTCACTGTTTACGTTCCCTGTCTCATCT[C]TTCTAGGTAATTTGAGTTTCCAAACC TGTTGG
WI-2033	183	T	C	GGGTGCTAGA ACTAATCCCTC	---	ATGTGTATGAGCTCCACATTCGCAGATTCACCAACTATGGATAGAAAAATATAGTATTCACAGATGG GCAGCCCAAGGATCAGAGGGCTAATTTTAAATTTCCAAGGTTATACAGGACCACTGTTGGAAATTT AGCAATTTCTGGTTTGGCATCCATCAGGGTGCTAGAACTAATCCCTCA[T/C]GGAGAACGTGGAACCC ACTGATATACCAAT
WI-4745	131	T	C	---	---	TTATGGATACATGTTTCTGGTGAAGGACAAAGATTGAAGCAAAAGGACAAAAGGAGATCAACTGGG TAGAATAACTCATCGATCCCACAGGCTCTTCCACCATTCTCCATCTACTTTCTACTCTGAT[C] AGGCAGACTTATATGAAAAAAGGGA
WI-2034	150	T	C	CCACAGTGCA CCAAGGAC	GGGTAAAGAT AGAGTGCAGGT CC	CCACGACTATGCTTTCAGAGTCCCTGGTACTGACAGAGAAGGCTTTGAGGACCATGTGGCGCCAAGA CTCCTTCTCGGTTTTCAGTGAAGAACGATGAACCTCTTCTATCTTCTACAGCAGCTGACTTCACCA CAGTGCACCAAGGAC[T/C]GGACCTGCACCTCTATCTTTACCCCTTCCGACACACAGATGCTGAGATGCC ACACTCTGAGTG

WI-2038	155	C T	ATTAAATTAG	TGTCCTTTAAA GTGTGTAAGT	ATTCCTCTTG AAAGAAACAT	TCAGGTGACAAGAAAAAGTCACATTTCTTCAATCACTCACCATTGCTGTTATTGCTCTTCAGTGT ATCCAAGGATGTCACCTTTTGGAACTCTGTAGATCAGAAAAAACTGTGCTTTAAAGTGTGTAAGTATTA ATTAGATTTCTATTTTGTGATAC[C/T]TGATGTTCTTTCAAGAGGAAAAATTTGTGTAAGAGGATTCCCAATT TGCATTTCCATTGGC
WI-4782	113	C T	AATGC	GATGCAGAAG ATAACTAGAA	GAACTCTCTG GTTATTTTCT	TCATTGACTTTTAGAGTTCTTCACTCTTATGCTTTATTTCTTTAGGAAAAAACTAGGCTAGGAGAA CACAAATTCAGGTTCTCTCCAGATGCAGAAGATAACTAGAAAAATGC[C/T]GAACACAGAAAAATAACCA GAAGAGTTCATTATGGTTTTTTTCCAGAACGATTAC
WI-4788	65	A G	TTCC	GCATAGAATC ATCTTGCTAAG	GGATAAAATT AAAAATTTGGC	AGGAGAGTTTTGGCTCTTTCCGGACTCTTGGAAATTCAGTGCATAGAATCATCTTGCTAAGTTCCJ/G JTGAAAAAAAATTAATGCCAAAAATTTAAATTTATCCAACTTTTAAGTCGAGATTATAATTGATATTT AAAAAACTATATTGAGTCTTTCTTAAAGAGATGGCGTATCACTCTA
WI-5300	38	T C	CACTTCATTC	TCCAGAGAC	CTACTCTTTCT ATTCATAATC	CTTACTTCCAAAGTGTTTTCCAGAGAGCCACTTCATTC[C/T]TTTTGGATTATGAAATAGAAAAGAGT AGGTGTTATTATTCCTCTTTTACCAAGGTGAAATTTAGGGCTCAGACACAAGGTAGATGATGAGCCCA AGGTCAGTGACAGAGCCA
WI-4818b	121	G T	GGCCTGTT	TGATAATGGG	CCTTCCTTTTA TATGTATGCCA	TATAATGTTTTGTTCCATAGTGGCATAGACTAGGTTATGTCCACACATGAATAAACAACTCTTATATA ATAATTTATCAAGAAGGAAAAATATACATATGGGGTGATAATGGGGCCCTGT[C/T]CTCTGGCATA CATATAAAGGAAGGCTAA
WI-4818a	43	A G C		TTGCCATAGAC TAGGTTATGTC	CATATGTATAT TTTCCCTCTTG	TATAATGTTTTGTTCCATAGTGGCATAGACTAGGTTATGTCC[C/T]G/CACATGAATAAACAACTCTTAT ATAATAATTTATCAAGAAGGAAAAATATACATATGGGGTGATAATGGGGCCCTGTGCTCTGGCATA CATATAAAGGAAGGCTAA
WI-5317	139	T C	GTAGCAGGT	TTCCATTTCTG	GATGCAAAGA AGAAATGAGTC	TTTTTCCATTTTGTGTTGATTCCTTTTGTCTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGGTTAAT AATATAATAATATGATGTTATATATTACAAATTTCAACTCAACAGGAATTCATTTCTGGTAGCAGGT ATA[C/C]GGACTCAATTCCTCTTTCATCTATTTCTAGGTTAATTTGCAGCCCCGAGATCTACCCAGG
WI-4888	56	G A	AAAGATAACA	GCAAGATATA AAGATTAAAG	CAATCCACTA CCTCATTTATT	AAATGAGTAACCCCAAGTTACTCGGCAAGATATAAAGATTAAAGAAAAAGATAACAAGA[G/A]ATGAAT AAATGAGGTAGTGGAAATTCCTTGATAACTGGAGTAGTGCCTT
WI-5328	44	A G			---	AACATTTTTTAACCATGCTACATTTAGAACACTGAAAGACAG[G/A]AAAAAAAAGAAATATTTTG CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAGAAAAAATATGAATCAGAAAAAGGAAAAAGAAAT AGAAACACGTGATCTGGAAGGAG
WI-4897	93	A G			---	GCCTTTTGAGTTTAAAGTCTTTTGTGAGTGTCTTTTTCCTCCCACTAGGTACTCTCGGCCCAAT CCCCAAAAGAAAAATAAGCGCTTGG[G/A]GATAAAAACATCTTC
WI-5345	29	G A			---	CCCTGCTATAGGTGAGTTTAAAAATCCT[G/A]CCTGCTATGGTTGCTTGTGTAAGCCACATCCAGT GAGGTATATTCTGCTGCATTTTCTATATCACTCAGCTTCAGATCCACTCCATCAACTTGCAG

WI-5370	143 T C	AATAAGATGG TACCTTAAC TA ATAAAACAA	CAAAGTTGGTA CAGAGAAATTC AAA	TGCATGTTACTCTCTGGAAATCATAAAGGGATCTGAGAGCCTACAGTATATGGCAACATTAACCAAT CTTTTGAATAATTTACCTGTATCCCATCATGGTTCAATTTGCAAAAAAATAAGATGGTACCTTAAC TA ATAAAACAATTCCTTTGAAATTCCTGTACCAACTTTGCTTTTC
WI-9711b	423 T A		---	GATCTCCTTCATCCCTCTCCAGAAGAGGAGAGGAAACACAAGAAACGCCTGGTGCAGAGCC CCAAATCCTACTTCAATGGATGTGAATGCCAGGTGAGGAGACGGCTTGCTGTAGTGGGAAAGCAC TGGACCTCAACAGTTGGAAATGTTGTAGTGTAGCTGTCTCGTATCCTTGAAGCTGTGCAGCAGCTT CAGTTCTTCGCCCTGTGGAAATATTTCCCTGATACCTCTTAAATTTGAATG
WI-9711a	390 C A		---	GATCTCCTTCATCCCTCTCCAGAAGAGGAGAGGAAACACAAGAAACGCCTGGTGCAGAGCC CCAATCCTACTTCAATGGATGTGAATGCCAGGTGAGGAGACGGCTTGCTGTAGTGGGAAAGCAC TGGACCTCAACAGTTGGAAATGTTGTAGTGTAGCTGTCTCGTATCCTTGAAGCTGTGCAGCAGCTT CAGTTCTTCGCCCTGTGGAAATATTTCCCTGATACCTCTTAAATTTGAATG
WI-9702c	345 G A		---	GGAGGAATTCAGGGTGAATGGAATGGAATGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCCTATTACGCAATTCCTACTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATTCTAACTTTAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTTCATCCAGTGTGCTACAGCATCTGATAG
WI-9702b	344 C T		---	GGAGGAATTCAGGGTGAATGGAATGGAATGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCCTATTACGCAATTCCTACTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATTCTAACTTTAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTTCATCCAGTGTGCTACAGCATCTGATAG
WI-9702a	179 C T		---	GGAGGAATTCAGGGTGAATGGAATGGAATGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCCTATTACGCAATTCCTACTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATTCTAACTTTAATGATCTCTGTG CTTTTATACTAGCTTTAAGAGGTTTTCATCCAGTGTGCTACAGCATCTG
TIGR- A003N21	49 C A		---	TATAGTATTTAACGAAGCCTAGAAGCACGGCTGTGGGTGGTATTGGTTCATAGCATATCTTAGGT ATATAATACTTTGAAGCCATAACTTTTAACCTGGAGTGGTTGATTTCTTTTAAATTTTATTTGGGA GGGTTTGGATTTAACTTTTTTAAATGTTGTTAAATATTAAGTTTGTAAAGGAAAGAAACCATCTCTG TGATTACCTCTCAATCTATTGT
TIGR- A004V30	203 C T		---	AGAATGGCTACTTCATAGGGCAGAGCAGCCACTTTTGGGTAATTTTAAACATCCAAAGCTAATAAAT AATCAAGAAGAAATAGAGAACATTAACAAAAATAAATATGTTCTATTGGGAATACCTAATATCAG ATACTAACAAAGTACAGTGATAAGAAATAAAAAAGATAATAATCACACATACCTTCTAGGTTAGTAGA AAAGC/G,CTCTTAGGTTAGTAGAAAAGTT

WI-7593	46 G A ---	---	TTTTGTTGCTCTGGACACCCACTGCTCCAGGATGAAAGGAGAG[G/A]AATGAGATCAGTTTGGG CACTTCTCTTGAATATAAAGATCAACAAGTTACAGTCATGTTGGGACTTCTTCTCTCTCCAA
WI-6962	78 A G ---	---	AGTGATCTTGGGGAAAGGCTCCAGTGTTATCTGGACCAGTTCCTTCATTTTCAGGTGGGACTCTT GATCCAGAGA[G/G]ACAAAGCTCCTCAGTGAGCTGGTGATAATCCAAGACAGAACCCCAAGTCTCC TGACTCCTGGCCTTCTATGCCCTCTATCCTCTATCATAGATAACATCTCCACAGCCTCACTTTCATCCAC CTATTCTGAAATATTCCCTGAGAGAGAACAGAGATTAGATAAGA
WI-7059	43 C G GCCATC	AAGGCACCCA GGTCA	GCAGAGAAGAGAACCCATGCCAGGGAGAGGCCACCCAGCCATC[G/G]TGACCCAGCGAGAGCCAA CTATCCCAATATACCTGGGTGAATATACCAAATCTGCATCTCCAGAGGAAAATAAGAAATAAA GATGAATTGTTGCAACTCTTAAAAAA
WI-9063	53 A C TT	CACTTCACTGA AAGACACCAT	AGCAGCCATCAGATGCTGTTTTCACCACCTTCACTGAAAGACACCATTTAT[A/C]ACCCAAAGGG CAGAAAGTAGAAGCTTACTTATTAATGTTTGACACAAATTGGAATTGTC
WI-7079	293 T G ---	---	AAGGGCATTGAGACTATAAGCAGTAGACAATCCACACATACCATCTGTAGAGTTGGAAGTGCATT CTTTAAAGTTTATATGCATATATTTAGGGCTGTAGACTTACTTCTTCTTCTTCTTCTTCTTCTTCT TATCTTGAGCACAAATGATAATCAATTATACATTTATACATCACCTTTTGACTTTTCCAAAGCCC TTTTACAGCTCTGGCATTTCTCGCCTAGGCCTGTGAGGTAACTGGGAT
WI-9074	38 A G AAAAG	GGTAAAAGTT CTTTTGTCTT TT	TGGATGCCGAGTAAAAGTTCTTTTGTCTAAAAGAA[G/A]AAGGAACTAGGTCAAAAATCTGTCC GTGACCTATCAGTTATTAATTTTAAGGATGTTGCCACTGGCAATGTAACIGT
WI-7104b	249 C T ---	---	GGAGTTGCCCTTCTTAAGGAAGGAGATCTTATCTTCTGGTTGGCTTGACCAGTCACGTGGGA GAAAGAGAGAGTGCAGGAGACCTGAGGGCAGCCGTTCTTCTTGGACTGAGAGAGGAGGCC CCAGGCTGGAGCAGCATGAGGCCAGCAAGAGGGCTTGGTTCTGAGGAAGCAGATGTTTCATGCT GTGAGGCTTGACACAGGTGGGGCCACAGCACAGCATCTTTG[C/T]
WI-7104	157 C A ---	---	GGAGTTGCCCTTCTTAAGGAAGGAGATCTTATCTTCTGGTTGGCTTGACCAGTCACGTGGGA GAAAGAGAGAGTGCAGGAGACCTGAGGGCAGCCGTTCTTCTTGGACTGAGAGAGGAGGCC CCAGGCTGGAGCAGCATGAGGC[C/A]CAGCAAGAAAGGCTTGGTTCTGAGGAAGCAGATGTTTCAT GCTGTGAGGCTTGACACAGGTGGGGCCACAGCACAGCATCTTTGCT
WI-8974	34 C T AAGAACTCA	CCTGAGCCTC GCTGGC	CATACAATGAGAGCCCTGAGCCCTCAAGAACTCA[C/T]GCCAGCTAGCCCTACACCAGTTTCCACC TGGAGTTCATGCAAGGGCAAGGAGTGCCATGCAAGCTGTTAA
WI-9161	61 C T CTTGGC	GCTTACAGGAG AGACTAGACA GGAA	CTGTGAGGGTGACGTTAGCATTACCCCAACCTCATTTTAGTTGCCTAAGCATTGCCTGGC[C/T]TTC CTGTCTAGTCTCTCTGTAAAGCCCAAGAAATGAACATTCCA
WI-9014c	93 T C ---	---	CCCTGTTCCCATGTGACCTGTTTCTCTCCCATCATCTTCTCTGTTCCAGAGGTTGGGGCTGGAT GTCTCCATCTCTGTCTCAACTTTAT[C/G]TGCACTGAGCTGCAACTCT

WI-9014b	44 C T ---	---	COCTGTTCCCATGCTGACCTGTGTTTCCTCCCCAGTCATCTTTC/TGTTCAGAGAGGTGGGGCTG GATGCTCCATCTCTGTCTCAACTTTATGTGCACTGAGTGCACCTTCT
WI-7023b	206 C A ---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAGACCCCTGGTGCT CAGTGCCCTTTAAGTGCAATCCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGTCTACGGTCCCC TCCTTTTGGCCCCAGTATTATGCGCAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTTCAACAC A/C/AJACACACATTCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7023a	56 A C ---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAG/A/CJCCCTGGGT GCTCAGTGCCCTTTAAGTGCAATCCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGTCTACGGGTC CCCTCTTTTGGCCCCAGTATTATGCGCAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTTCAA CACACACACATTCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54 C T ---	---	CTGAAATCCCTCTCTGCTGCTGGCTGGATCCGGGACCCCTTGCCTTCCCTTC/TGGCTCCAGCC CTACAGACTTGTGTGTAACCTCAGGCCAGTGTCCGACCTCTCTGGCCCTCAGTTTCCAGCTATG AAACAGCTATCTCACAAAGTTGTGTGAAGCAGAGAGAAAGCTGGAGGAGCGGTGGGCCAAT GGGAGAGCTCTTGTTATTATTAATATTGTTGCCGCTGTGTTGTTGTTA
WI-9171	62 G A ---	---	ACATATCTGAAAAATGTTGAAAGCTAAGCCAGGAATAAAGAGAGAGATAATAATCA/G/A TTCTTTACACCGATGGTAATTAAAGCTTGTATTACAAAGACTTCAIGC
WI-9174	47 T C T	TCTAGAGGGTA TATAGGACAGG ACTG	GTGTGAGACCATCATGGTGCCAGCTAGGACCCCATCTCTCTATTAT/C/CJAGTCCCTGTCTATATA CCCTCTAGAAACAGAAAGCAATTTTAGGCAGCTATGGTCAATTTGAG
WI-7753	52 A G	CAGAGGTCTTG AAATACAGGG A	AAGGCCAGATGCACATCCCTGGAGGACATCCATGTTCCGAGAGAACAGAT/GJATCCCTGTATT TCAAGACCTCTGTGCATTTATTTATGAACCTGCCCTGCTCCACAGAACACAGCAATTCTCAGGCTA AGCTGCCGGTTCTTAATCCATCCTGCTAAGTTAATGTTGGGTAGAA
WI-9186	76 G A CGCA	AAAGGGAAG TCTGACCTAGG T	AAAGAACTACAGAGGACGATGTCCAAACAAAAATGGCATCACCTGTCAAAAATGGAGTTCACCT TCTCCCGCA/G/AJACCTAGGTGACACTTTCCCTTTCACTT
WI-9193	94 G A CA	AGAAATTGT CTGCCTTAAAG CA	TTGGACAAACCTAGAAATTTCTCCCTTTATGTATCTCTATCGATTGTGAGCAATTGACAGAGATAA CTCAGAAATATTGCTGCCCTTAAAGCA/G/ATACCCCTTACACACACACCCCTGTCCTC
WI-9015	48 C T ---	---	TTTGATTGATATCGTGAATCTCAGCCGAGAAATTCATTCCAGGTAGCTCGGACCACTAAGAA CTTTCCCTAAAGAGATAAACACAAAATCCATTCCAGGTAGCTCGGACCACTAAGAA
WI-7254	37 A G AGGAGCAC	GGTCTGAGAG CATTAGGGA	GGAGCCAGGAGACAGCAGGGTCTGAGAGAGGAGCCAC/GJGTCCCTAATGACACCCACTCTAGCC CTGAGGCTCGTCCCTCAGACTGGGGAAGAGTCCAAAGGAGGGGAGGAGCAGCCACTCTCAATGC TCAATGGCTCCCTGAAATCAAGACAGG

WI-9231	32 G	C	CAGTCCCCCA GATTGA	CAC TTGCCAC ACTCAGAC	GTGACCCCTGTGAGGTCCAGTCCAGATTGA[G/C]GTCTGAGTGGGCAAGTGTGTCAAAAGGGG TGCCCCCAGGAGATGAGGCTGAGAGCAGGGAGTTGAGGCCGAAGATCA
WI-7836	120 T	C	CAAATAACA ATGCAACGTT C	GCTCTCAGAAC CAAGATTAGA AATC	TTGTTTGGGAAATAGAGAGTTGAGATAAACCTCTCATTCAGTAGTTACTGAAAGAAAACCTCTGCTA GAATGATAAATGTGATGGTGTCTATAACTCCAAATAAACAATGAACGTTCC[C/G]GATTCTTAAT CTTGGTTCTGAGAGCCATTGGTTTCAGTTGAGCAATCCCATACCAAGCT
WI-7286	65 T	C	CAGCTTCAGCT TAAC TGACAG A	AAACAATCTA ACCAGAAAGCT TTAA	TCCATTCTTTTGGCCCTGCAGCATGTCTCCAGAAATTCAGCTTCAGCTTAAC TGACAGATTC GTTAAAGCTTTCTGGTTAGATTGTTTTCATCTGGTGATCATGTCTTTCCATGTGTACCTGTATAATT TTCCATCATATCTCAAAGTAAAGTCA
WI-7858	91 T	G	CTAAGCATGT ACGTGAATTTT TAAAT	CCCAATTTTA TTAAAGTTTA CATCTAT	CAAAATCTTGGAAATATCTCAAATGTTAATAACAATATGAATTTTCTCATGCATCTACTACT AAGCATGTACGTGAATTTTAAATTT[G/T]ATAGATGTAAACCTTTAATAAAATTTGGGTGTGG
WI-7860	50 C	G	A C		GAAAGATTAAAGGAGGGTGTCTGTGTCTCTCCCTGCCCTCTCCCCA[C/A]GTTGGGAGAGACC TGTAATTTGCCAAGTCCCTGGACCTGGACCACTAGTGGCCCTTATGGTTGGGGTGTAGGCAGG TGAGCGTAAGTGGGAGGGAAATGGGTAAGAAGTCTACTCCAAACCTAGGTCTCTATGTGCAGACCAG ACCTAGGTGCTTCTCTAGGAGGAAACAGGGAGACCTGGGGTCTGTGGAT
WI-9064	29 A	G	CGTACCTCCAA ACATAATTGA TTC	GCTTGAGTGTA AGTCTGCAGA	CAAGGCGTACCTCCAAACATAATTGATT[C/G]ATCTGGAGACTACACTCAAGCAATCCTGAGG AATACTGAGGAGGGCCTGGCTACTGTCTCTGCACCTGCTGCTTG
WI-7307	128 G	T			CACACTTGCTGTTCTTCAAGTCTGGAGGTCTGGCAGGGTCAAGGTGGGTAAGCCGGGTCCACA GGGCCAGCCCTGGCAGGGTCTGGCCCCCAGGTAGGCGGAGAGCAGTCCCTCCCTCAG[G/T]AAT GGAGGAGGGACTCCAGGAATGGGAAATGTGACACCACCATCTGAAGCCAGCTTGCAOCTCCAGT TTGCACAGGGATTGTCTGGGGCTGAGGGCCCTGTCCACCACCCGCC
WI-9274	25 C	T	GAAATGTGAC TTCACTTTGGT G	CAGGTAGAATT TTCTGTCCATT G	GAGGAAATGTGACTTCACTTTGGTG[C/T]CAATGGACAGAAAATTCACCTGTGTCTACATAGGAGAA GTTTGGAAATGCACCTTAATAGCTGGTTTACACCTTGATTTCGAGGTGAAA
WI-7313e	266 T	C			AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGTGTGTGATTAGTTCTTAAAT TGTTTGCAGTCTTTTATGTTTATTATCATAGGTATAGTGGACCTAAATCCCTTATCATATCTTTAT AATTCAGCCAGTGTATCCACCAGTTTGTGTTTATGTTTAAAGTAACCTATTATCTCTGGATTTCATG AAGGTGTAATATCGTTTGTGTTAACTGAATAGAAATGTATAGCGATGA
WI-7313c	256 C	T			AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGTGTGTGATTAGTTCTTAAAT TGTTTGCAGTCTTTTATGTTTATTATCATAGGTATAGTGGACCTAAATCCCTTATCATATCTTTAT AATTCAGCCAGTGTATCCACCAGTTTGTGTTTATGTTTAAAGTAACCTATTATCTCTGGATTTCATG AAGGTGTAATATGTTTGTGTTAACTGAATAGAAATGTATAGCGATGA

WI-7424	131 T A	CAAGAGAGAG AGAGGAAAGA A A A A A	TGCAAAAGAAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGGAGGGGAGAGCAGAGAAGTTAGAGAAAAAGCCACCGGAGGAAAGG AAAAAATCGGCCAACCTAGAAACGTTTTCATTCGTCAATCCAGAGAGAGAGGAAAGAAAAA TTA)ACAACTTTCATCTTCTTTCACAGCTTCATAAACATTCACATA
X86400	118 A C			TCCTGCAAGAAGTCTCAAGCCTTTTGATTTTGTGCAATAAAGTACAGCTTTGCATAAGAGTGA TTGGGCTAGCTTAAATGGATCCATAAACCTTCTCTAATTTTAAAGTGAGA)C)TCTTTTAAACACCT GTTAAATTTAATGTAGCAGTGTGAGAATCTAAATATATGTACCACTCGTTTATTTGTTTCATTCATCCA TCCCTTTCCCATGAATATTTCA
WI-8053	242 T A			GTGGCCACTACATGTTATAGAAACCATCATCTTGTACACAGCAGCTATGAATAAAGGCTGAG TTATCACTAAGCAGGAGAAAGCATTAAAGGTGCCATTAAAGGGACITTTTATCAACCTAA TAACTCTAATCTGCTGACTTTTAAAGATCTAAGGTCAITTTATACATGCTGAAAGGGTCCACA ATTAATCTTTGATCTTTTACTCACTGTTAACTTATATAA)T)TTCAGAAC
WI-6190	165 G A			TACAAATGAATTGCTTTTATTTGGGTATGCATCCACATTCAGCATTTAGTGTCTGAAACAGCAAG TGAAAGACGCAGCAATTTGCCAGGAGTCAAGCCACCAATTTCCGGGATCTGCTGTGCACACCGG GTCTCTTAATCCCTGCTGAGGATCTTG)G)A)GAAAGCAGCAGCACCACCAAGGATGCA COGGATTCAAGGTTCTTTTGTCCAGTTGTCAGATTCCAAACTAGACCCCA
WI-6275	148 G C			AACAGTCACCACCAACACATGACAACCTGCCAGGCAAGGCTTGTCTCCCTCCCTTTCGCTCCC ATGTGCTAGTCAGCAAGGTGGGGAGGCACCGATGTTAGCTTGCCTCAAGGGAGTATTACAGAGA GAGGCTTGGGAA)G)G)GAAAGGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAAACTG ATTTGCTTTTCAGTAACTGGTATGTCGAA
WI-6421	41 G T			ACCAAGAGATCAGCTGTCTAAACAGCAGCTTTTGTGATTGT)G)TGGGCTTCTGAAAGAAACCTTGC TGACAGCTTCTCACTGACCTGCAGGACGGAACCGTACCTGAGAGGGGATGGGGCTCTCTCACA GAATATTTGGGCGAGAACCTTGAACCTGGCCACAGGACATCCCAATATCCCTCCTCCTCAGGG CTCACCCCGACATCCTCAGCCAAATGAAGGCTCTGAA
WI-6905	215 T A			GGGTGAGACGGGTTTATTGTGCACATTTACACAGGTACAGCGTCTGGGCTGGCAGCGGCCATGCTC CTGTGGTGGGCTGCTCTACAAGGGCGTTCACTTTCTTCCACCACTATGTACAGTCAAGTGTCCAA GGTGATGGGCTACAGTGTCTGCATCAGTGAGTGTGTACACACATTTTACATAAATACACACGACTC ATACATGAAAAA)T)A)GAGCCCTAAGGGCTGTATTTTAAATGAGAAAAA
WI-9420	202 G A			AACCTGTTTACAAAAATAGGCTTTCACAACTTCATTACTGAATTTGTAAGTCAATGACTGTGTTGTTT TAAAAATGTACCAAGGAAATACAAATGGATATGATCATTTTTCATGCTCAGGAGAGAACAGCAC AGAAATAAGGATACTGCACAAGGTGCAAGGAAACCGGAACCCATTGTGTACACTGTCTTCACACAG G)A)GCATTTCTTCACCTTAACCTGACAGCTGTGCAAGATGCCTCAGTGTG

WI-9448	184	G A ---	---	TGGGGCTGCTTTTAGACTTCATTTCTAGAGCAGACACCTAGTGAGAGGAATACCTGGGAGAGAGAC TGCTTGCCCATGGTGGTTAAACCTACATAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCC TTTTAAGAAAAATGGCTTGGTTCCAAAGGCTGAGAGCTGGCACCAC[G/A]CACTGGTTTCTAAA TCTCTGGCTTGGATTTTATCCAAAGGCATGTTCTTAACGTGCCCCGTGAGCAG
WI-9470	204	G A ---	---	ATGTCAGAAGAGACACAGACAAGGAGTTTTCCTTTTAAATGCTAAACAAGTGCCACTAATCCACA GATCTGAAAAAGTACAGCTCTCCAGGTTGATAAATCAGATTCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCACGAATATGATCTCCCTAAAGCCCCAGATTCTACTAGAGCGCTGGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCCTCAAGCTCACAGGGCTCACCTTCCCAG
WI-1245b	201	G T ---	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATCTAAGCCTCATAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTCCTGATGCAGATCTGCTGTGAGCCATGTGCTGGCATCACAGGGTGGT TTATTAATTCATTATCATCTGACAGCCCTTCTTATAACGTACATCCTTGCCTCTCTGAGGCG/G TCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85	T C ---	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATCTAAGCCTCATAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTT/GCCTGATGCAGATCTGCTGTGAGCCATGTGCTGGCATCACAGGGGT GGTTTATTAATTCATTATCATCTGACAGCCCTTCTTATAACGTACATCCTTGCCTCTCTGAGGC GCTAAGATCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149	G A ---	---	TTCAAGTAAAGGACAGGCTAGAACAAAGCGTCCCAACCCTGGCACCATAACAGTGGAGCCAAA TAACITTTGTTTCAGGGGACTGCTCCTACACATTTGGGATGTTAGCAGCCTCCGTGGCTTCTACCCA CTAGATGCCAGCA[G/A]CACAAACACCCCTCCCAACAATCATGACAATGAAAATGCTTTAGACATT GCCAAATATACCTTGTGGACAAAATGGCCCTGATTGAGAACCACTGGTT
WI-5385	110	G A ---	---	AATGAGTCATTGTGGAGTTAGAGGAGTTACTGAAAATGGTGACTCCAATGGTGGGATTTGAAGAGG GAAAGTCGATAAATTTAACATATGTTTCTTCCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TTCITTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCCCTGAC CCCTGCTACGGGAAACATTGAATGCA
WI-5403	199	T G ---	---	ACCAAACCGTTGGCAAAGGCTCCCCAAGACTCACCAACCTTTGGTGCTTACCCTATGCCGGGTG GGATTGAAGAAATAACCATAAATATAATTGCTACAATTTTCCAGTAGTTACCAGGCACACAGCCTAT TGGAGAAATCATAAATGTAAACCTACAATGATTGCTCTGCTGGCTTGGTGCCAGGCATAGAGTT/G JGGCCTACAACCCATTTTATCATTTGAACCCCTCAGAAGCATCCAGTTGGGGCT
WI-5801b	157	G A ---	---	TGGTATTTTTCCTTTCCCTAAATGTTATGATTAAATAGTGCTTTGTAGAAATTTGAAAAAATGTAAA TCAGAGAACAGAAAAATAAGTATAGTTGAAACCTCTAACAAATTTTAGATTTTAAAGGCCTAG GGAAGAAAGAGAGCCCTGGGA[G/A]AGGGAATGAGAAAAAGCACACCAGAAAAAAGTGTGT GGCTTAAGGGGAAGCCCAAGGAAAGTTAAGT

WI-5801a	48 A G ---	---		TGGTATTTTCCCTTTCTCTAAATGTTATGATTAAATTAGTGTCTTTGT[AG]GAAATTTGAAAAAATGT AAATCAGAGAACAGAAAGAAATAAAGTATAGTTGAAACCTCTACAATTTTAGATTTTAAAGGCC TAGGGAAGAAAGAGAGCTGGGAAGAGGGAATGAGAAAGACACACCAACAGAAAAAAGTGTGT GGCTTAAGGGAAGCCAAAGGAAAGTTAAGT
WI-5696	61 C A ---	---		TTCTATTTAAATCTGTGCCCAATGCAAGACTGCATTAGTCTGCATGAGCCTTAGTTTCTC[CA]ATAA AAGCCCCCTCACACCGAGGACAATGTTCAAGACTAAATGACTGCAGGTGAGCAATTTCTCTGTATTA TACAACTGGACCAAAAGATGACTTTATAATAGTGGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAATAGATTATAAGGCTGTGGTGAGTTTATTTAACTT
WI-7461	153 C T ---	---		TATTACTAGGTTTCATAGAGCCCCGTTGTAATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATTCTAAGCTCTCACTTCCCTTCGAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCOCCTG TGGCAGGGACTGTGCTC[CT]GTTCCCTGTTGGTCCCGGAACCCAGTGTGGTGCCTGGCACAGAG GAGCCCTGAGTAGCATGTGCTGCA
WI-9716	221 G A ---	---		AGAAGACAGGAGCACTGGGATCAAGGACTGATAAAGTCTGAGGCTTTAATGGTCCCTTGCTCTAAC GCTTTGGTATACTTCTCTTTCTGAAGACCAACCTTTCAAACCTCTCAGAACACAGGCAAGATGCAT ATTCTGATGTTTCAGATGTGTAATCTCTACATCTGGAACACTAGATGAGTTAGGCTCTCTTCATCT CAATTGAAATTTCTAGA[AG]A/AAACACCTAATTGGCTCATCTTGGATCA
WI-9760	49 C T ---	---		TTTTGGTTAAGTCTTGTGAAGCCACACAGAGTGTACTCTCTTTAC[CT]AAGTGTACTTTTGCA TATATTTATGGGATGATCTATCCCTACTTAAGATTCTCTCTCAGGTTAAATATTCATTTCTCT TTGTCAGGAGTTTCTTATTTGGCTTCTTTCTAAACCTTAACCATCTGCTTATCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31 A C ---	---		GAAAACTCGTTGGCTCAAAGGAAACTGTAG[CA]AAATCTTTTTTTTATTTTGTTTTTAACTC AAAGAGTGGAGTTTGCAATTGACCTTGATGGCAGCTGCTCTTTTGTGTTGGTAAATCCTCTAGT GGGCACCTTGCAAAAGCAATTTAGAGCAAGGTGGTGGCATGGAGTTGTGTGAGGTTGCTGAAAAG TAGCAATGGAAGAAAGGTTAATGGA
WI-10312	41 A G ---	---		AAGCCCCAGTGGGAAAAGCAGACAAACACTCCAAGAATAC[CA]GAGATATAAACATCATCATCA GTAGAGATGGGATGACCTAGGAGTCTATGCTGATGAGGATGTCAGACCAAAAGACATTTGGGTCT TGAGGGTTGAATAGGAGTTTGTCTGTGAGTCTTGCCAGTCCCATAGTAGGTTGCCATAAATAAAC AGTGAATAAAGTGAAGTACAGTACAGAAAGAAATTTCA
WI-11152	179 C T ---	---		GATCTTTGGCAGATGCAGAGCAGATACGGCAAGGCATCTTGGGCATTTGGAAGGAAACAGCCCTA ATTCTAGAAACAGACTCTACAAGGACCAAGTTAAAGGTCGACCCAGGGGACTGGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGGACAAGTGGGACAAAAGGCTTGTC[CA]CTGTCTCAGAAACATTGAA AACAGCCAGTACATGCCACTGATAGA

WI-1968	167 A G ---	---	TGGTGAGGAGCTGTAAAGGCTGAAAGAATAGTCTCTGCTGGTCTTTGGTTGGAATGGATGAGTCCT TTTACAAAATTTTCTCTTGCCATGGGTGTTATGTTAGAAATCATGGAGTTGGAAGACCTTAGATTCA ATTTGGGGCTGTACAGTTTACTGGAAGTTGT[A/G]TGAACCTTGAGCAAGTGCTCTTAATGTCCTCA GCCTCAATGCCCTTCCCTGTAA
WI-4701	198 G A ---	---	GGGTTCATTTAACAGCCTCCCACTGGGTCTCAGATTGCACGGAGATGTAAAAATAGGAAGATAG AAAAATGGTGCCCACTATTGACTTGATAACACCTACAAAACACACATTAAACTCCTCCCACTCTA CCGCCAAAGTCTACCTTTGGTCTTTTATTCTGCTAATGACCATACTATTCCCAATTAGA[G/A] CCATGTCATTTTCAGAAAAGCAGTATA
WI-4823	164 C A ---	---	TTTATCTTCCAAACCATGTGTGTTTCTTCACATAGTTTACGTAATTTTAAATCATGTCATTTAATTA TGCACTTACTTGTGGCTACAGACATTGCTTCCAAATTTCCCTAACACAGCAAGCATAACT GATGTCCATCTTGTATTCCTAAA[C/A]AAAGAAAAGTGCTTTTGTGCATCTGCCCTCTCTGT CTTCTCTGTTTCACTCTCTGTTTCCCTATTCAGCATTCATGATTA
WI-4860	72 A G ---	---	AAAAAACAACTTCATTTGACATTTAAGAAGATAAGAAAAAACAGATCCACTGTGTGTTGCTT GATTT[A/G]GGAGATAAACCTGATCTCTAAGAAAAATTAACCAAGCAGTACACTAAAATAGCCT TTGTGTGGTTTTCAGGAAAGAAAGCCAAATCCAACTAAGTTGCTAAGAAAAATATGTTTCATATCA CTCTAATCTCCACATAGAGCATTAATATAGCA
WI-9705	111 C A ---	---	TGAAGGACCAGTTTCAATGCCTACCAAGTAAAGTAAATCGGAGGGGAGGAGTAGGAGTTGCTT CCGGATGTTGCATAAATTCAGGTTCTTTAAGGAGTTCGGCTGCC[C/A]AAAAATTTTAACTGATGC TGCTCAAAACGCACATAGAAATCGGTGGTAGATTGCGGTTCTTAGTAAGTAGCTAATGTTTAGATA TGATTGTTGAATATTGTTGCTGTGTTCTGGTG
TIGR- A004Z48	177 A G ---	---	CAAATAATCTCTGCTTAGAAGTTGCTTAGGGCCATGGATTTCATGTAAGGTGGGCGAGGTGGACTG AAGATCTGTTGGCAGGGCTCACAGACGGGGGTGAGGGGAGAGATCGTGGGTTTCATGAGATCCCAT CTTGGGCAATACGGTTATCCCGTGTCTTCATACGCCACAG[A/G]TCTCCAATTTTCAGGGGCTCCC GTGGGATGGTGGAGCCAAATGAAGACCAGGTAGATGATGCCACCTAGAGATG
U17579	34 T G ---	---	GGGATTCAATGTGTCTGTCTCATCCAATAAGCAC[T/G]CATGACCTCAGCCCCATACTCTTCTCCC TATGTTCCAGAGACAGAATAGACCTGGCCCTTCCTTCTAGGGGATCACAATAATTGGAAGGATGAG GACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTGTGGGATCAATTTCTATGGGAGCC TGGGAGAGGGATCCCTTCTAGTTGA
WI-7747b	88 T G ---	---	GTGAGAGCGAGGCTGAGCCTACAGATGAACCTTTCTGGCCTGCTTTCGTTAACTGTGTATGTACATA TATATAATTTTAAATTTGAT[T/G]AAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAGTT ATTCCTTTGTTGTTGTTGGGTATCCTGCCAGTGTTGTTTGTAAATAAGAGATTTGGAGCACTCTGA GTTTACCATTGTATAAAGTATATAATTTTTTATGTTTGTCTGA

WI-7747a	44 T C ---	---	GTGAGAGCGAGGCTGAGCCTACAGATGAACCTCTTTCTGGCCTGCT/CJTTCGTTAACTGTGTATGTAC ATATATATATTTTAAATTTGATTAAAGCTGATTACTGTCAATAAAGAGCTTCATGCCCTTTGTAAAGTT ATTCTTGTGTTGTTGGGTATCCTGCCAGTGTGTTTGTAAATAAGAGATTTGGAGCACTCTGA GTTTACCAATTTGTAATAAGTATATAATTTTTTATGTTTGTCTGA
WI-7189	197 T C ---	---	TCAGAAATTTCTCTTCAGCTCATTTTGTCTCTCTCACAAATTAAGGAGTAGGTTAAGTGAAAGGT CACATACCAATTTATTTCCCTTCAAAACAATAATATTTTACAGAAGCAGGAGCAAAATATAGGCCTTT CTTCTAAGAGATATAATGTTCACTAAATGTGGTTATTTTATATTAAAGCCTACAACATTTT/CJAG TTTGCAAATAGAACTAATACTGGTGAAATTTACCTAAACCTTGGTTATT
WI-7850	57 G A ---	---	AGCCCCAGCTGGACTCATGGATGTGCACCTTTGCTCCCTGCTCTTCTGCCCTCTGG[G/A]CTCATGTA TCTGGCAGCTCTGGTACCCTCTGTGGTGCCATCTCTACCTCTGACACAGACTGCCCTTGCCCTTGAAGCT GAGAAGCACAGGGCAAGGAGCCAAAGGACACAGAGCCTCAGCCAGGATCCGCTCCTCATTTT ATTGGTATGATGAATGGGAATGAAATCAGGGGGCTGCTACTAGAGCC
WI-7907	69 G C ---	---	CTCTCTCTCATCCCATCACCCCTAAATAGGTCAGGTGAGGGAGGCTGGGAAGAGGTGGGAGGAGG G[G/C]JAGAAAGTGAAGGAAGATAGGAAGGATATTACCTCTCTGTATTTTAAAGAAACATTTGTTT GGTGGCAGCAATCTCCCTGTCCCTATCACTGTTAGAGGCCAATTTTATATCTATAAATATATTAAAA AGCAAGTCAAACTTGGATGTATCAAGGTAATAATTATTGCAAGTTTAAAT
WI-7919	242 T C ---	---	GAAGGCAGCTGGATCACTTCCGCGAGTCTTGGGCGCGCTTGTCTGGAACACGAGAGCTCCTCCT CAGGGCCTGGCACTCACCTTCTATTCTGTATGATGATGATTTGGTTAAACACTGTCAAAATAATAGAGAT GTGCCAGATTTAGATTTTCTACCTTAATCTGTTTAAATTTGTAACCTTTATCCCATTTGAAAGTGCA AGCCCATTCAGATAAGCTATAATCTGGICTTTAAGGAAAT/CJACAACCTT
WI-7928	101 T G ---	---	CTCCCTTCTATGTCTCAGCAGCACGTTGGGCGACACTTGTTCATCTTCTGACCCGTTTGTGGGCTA TTCCCTGCGAGTGCAGACATCGTCAAAATTCAT/GJACAAGAGGAAATTTTCATGGAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTGCACCTTTAAACTGAAATTCAACTCTTTATATAGGATTTTCTTTT CTATCTCCATCTCCTCATTAAAAATACGTACATTTGAGGTAATGGTA
WI-7936	131 T A ---	---	TTTTGAGTCAAAAGACTTAAAGGGCCCCAATGAATTTATATACATACTGCATCTTGGTTATTTCTGAA GGTAGCATCTTTGGAGTTAAATGCACATATAGACACATACCCCAACACATTACACCAAACT[A] ACTGAATGAAGAAGTATTTTGGTAACCGGCCATTTTGGTGGGAATCCCAAGATTGGTCTCCCATATG CAGAAATAGACAAAAAGTATATTAAACAAAGTTTCAGAGTATATTGTTGAA
WI-7944	99 T C ---	---	TACAGTTCCAGCCCGTTGGCCCACTCATCTGCGCGCTTGTCTTGGTTGGGGGCGAGATTGGGTGG AATGCTTTCCATCTCCAGGAGACTTTTCATGT/CJAGCCCAAGTACAGCCTGGACCACCCCTGGTGTG TGAGCTAGTAAGATTACCCCTGAGCTGCAGCTGAGCCTGAGCCATGGCAATGGGACAGTTACACTTGACAGA CAAAGATGGTGGAGATTGGCATGCCATTGAAACTAAGAGCTCTCAAGTCA

WI-7805	101 A G ---			TTTCTAGGCTGTACAGTCTGATGCATGATTTTATATAATATTTTCATACTCTTGGAATTTGGATCTTT TTTACTTTGAGCATATATTTAGAAATATGTGT/GTGTAAAGGATCTCCACAATGTCTGCAGTGTG AAGGAGGTTTATTGTGGAATAGTTTAAACAGTCAGGAAGGCTAAACTGGTCAGTATTAATGTGTAGC CCTACCAAAAATAGCCAGTAGTATCTGAAAAATGAAAAATAAATGAAGTAT
WI-7416	137 G T ---			GGCCAGGAGATTAGCAACAAGGATTCACTTCTGTACTTACTTGGCCCTTTTATCTTTCCCTCTTGCCC CAGTCCCTTCTCTCCAGCTTCATGTGAAGCTCTGCAGACAAGACACTCAGTGTCTTGGCAGTGTCT [GT]CTACTCTCTCAGGTGCAGCATACATAACCAAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACACTCAAAAATTGGCAATGTCAATCAG
WI-140	252 C T ---			ATTTGAAGATTGGAGGGCTTGCAGAGGAAATAGATTTCAATTGGATCCCAAACTATAATGACA AGTTTTTAATTAGGTGTGATCAAGGCTTCTAAAAGTGAAATGCAAGTTGTACCAGTAAAGTTTATA TCTCCATTCAGCCAGCTCATTGGCCAGAAAATTCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG GATGAAAAATTTAGTTAAAAATGTGTCTGCTGATTTGGCATTTCCCTTC/
WI-198	218 C T ---			GAGGTCTTTCAGCAACATGGAAGCCCTACTGCTTCAACCCCGAGTCCCGGATCAAGTGTGGCAAC CATGATGGAACCTCTTGCCATGGTTTGTAGTACCCCTGGACCAAGTAGTCAATCCATCTGACTTTAAAA TTCTAACAGCCCTTGTGATGGACAATCTCTGTAAAGACTAACCACTTCCCTATCTTATCTTCAGCTA CCTGCTTCCCTTC/CTGTGTTTAAACAAGCATAGAAATATCTGAACAAC
WI-205c	146 T C ---			TTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAAATAGCCCTCATCTCTTAACATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTTCAT GCATGAGTTTGTC/CCAAAGGCTTGATGGGAAAAATCTCAACATTTGTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAACTGCATATGCCTTTATTTTGTAGTTCCC
WI-205b	146 T C ---			TTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAAATAGCCCTCATCTCTTAACATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTTCAT GCATGAGTTTGTC/CCAAAGGCTTGATGGGAAAAATCTCAACATTTGTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAACTGCATATGCCTTTATTTTGTAGTTCCC
WI-234	165 G C ---			GAAGACTGAGTTTCCAGGAGGTTGCAGCCGTTTCTCTCGGCCATATGGCTAATAAGGAGCTTGAGCA GGGATTCAACCTGTTTGAACCCCAAGTNCCTTCCAAGAGGTCTCAGACTACCTCCTCCATCTCCCT CTCCCCCAACACACAAATACAGAGATTG/CJAATTGAGGAGCCAGTTTCTAGGTGGGCTTTGAGC AATCATACACAGTAATCTCTTGGTGTCTTGTAGTTTCTCAAAATGGAAATGG
WI-276b	25 A G ---			AGCTTTTGAATCCAAAAACACAT/GCTTGACTCTCTTATCCTCCTCTTGTGTAACTATCTCC CTGAGGCAGAAAATACAGAACCCCTGTGGCTGCCTGAACGGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAGCATCTCTGCTGCTGAAAGACCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGTCTTATCCTCCTTGTCTATCCCTGATGACTGGGCAAA

WI-276	25 A G ---	---	---	AGCTTTGAAATCCAAAACCACAT/G/GCTTGACTCTCTTATCCTCCTCTGTTGTAACTATCTATCC CTGAGGCAGAAAATACAGAACCCCTGTGGCTGCCTGAACGGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAAAGCATCTCTGCCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGTCTTATCCTCTCTGCTATCCCTGATGACTGGGCAAA
WI-427	59 G A ---	---	---	TTTTCCCAATCCACAGGTAAAACTAATAATGGATGTATAGAATTTAGAACTACTTCG/GA/GTTTT TTTCCCTGGGGAATAATTCACAAAACATTTGTGCTGCAATCAGGTTAAAGACATAGTGTGCCA TTTGTCAATCAGACAGGTAGAGGCTGACTCTGGCAGGATTAGCTACCACTAGCTGTGAGACTTTATGT ATTCATTTAATAGAGCCAGGGTCTTGCTCTGTCAACCCAGCTTTCAGTGCAGT
WI-562c	106 T C ---	---	---	CTCTCACTCCCAACACTATATTGCTTACTTAATGGTTACAGATTAGCCCAAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562b	106 T C ---	---	---	CTCTCACTCCCAACACTATATTGCTTACTTAATGGTTACAGATTAGCCCAAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562	103 T C ---	---	---	CTCTCACTCCCAACACTATATTGCTTACTTAATGGTTACAGATTAGCCCAAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-597c	141 A G ---	---	---	GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAGTATCCTTAGGATATTCT GATACATG/GJTAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATAAC TTGATCTAATATTCTTCACAACATAATACCTGAGAGAAATAAGTCTATTAAAT
WI-597b	141 A G ---	---	---	GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAGTATCCTTAGGATATTCT GATACATG/GJTAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATAAC TTGATCTAATATTCTTCACAACATAATACCTGAGAGAAATAAGTCTATTAAAT
WI-597	136 A G ---	---	---	GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAGTATCCTTAGGATATTCT GAT/GJCATGATAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATAAC TTGATCTAATATTCTTCACAACATAATACCTGAGAGAAATAAGTCTATTAAAT

WI-611	66 G C ---			TTCAAAATTTAACACCATTTGGGTATATTATAATTTTNGCTCTATCCATAGTTCTAACCCCTCTTCTCT[G/ CJACAGTGAGACACCTGCTCTATTGTCTTGACGTATTACGTATTTCGATCAGTCACCCATCTGGA ACCAAGGTTTCATTCTGCTGACCCCTCCCTCCTCACCCCTACTTGGGCTCTGACTTCCTTCTCTGGGCT GAACCTTCTGCTGGGCTGTCCGCTTCTCTGCTTGGGCTCCAATAC
WI-681b	156 A G ---			TGAAGCCCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTGCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTCATACAGGGGAAGCACCTTGTNCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATT[GJTTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTTAAGATAIGCAGCAAGCACAAATCTGTCATGGTTT
WI-681	156 A G ---			TGAAGCCCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTGCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTCATACAGGGGAAGCACCTTGTNCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATT[GJTTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTTAAGATAIGCAGCAAGCACAAATCTGTCATGGTTT
WI-867b	119 G A ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCC[GJATTTGTGTTTGGC CAATAATATCTCCCCCAGGACGCTCTCTTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTGTATGTTTGAATGTGTCTCCCCCACAAGCACACATTAGAAACTTA
WI-867	113 A G ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCC[GJATTTGTGTTTGGC CAATAATATCTCCCCCAGGACGCTCTCTTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTGTATGTTTGAATGTGTCTCCCCCACAAGCACACATTAGAAACTTA
WI-867	119 G A ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCC[GJATTTGTGTTTGGC CAATAATATCTCCCCCAGGACGCTCTCTTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTGTATGTTTGAATGTGTCTCCCCCACAAGCACACATTAGAAACTTA
WI-871b	123 C G ---			TCATCAGACCTGAGATTCAGGATGAAATCTACCAAGGTACCACAAATGTAACCTTGTCCTCAACCGA ATCTCAGTTTCTGCATATGTAATGGGAATGATAAGAGCACCACCTACCTCATG[CJGJAACGTGT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGAATGCACGTATTGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGCTGATTTGTACATAA
WI-871	123 C G ---			TCATCAGACCTGAGATTCAGGATGAAATCTACCAAGGTACCACAAATGTAACCTTGTCCTCAACCGA ATCTCAGTTTCTGCATATGTAATGGGAATGATAAGAGCACCACCTACCTCATG[CJGJAACGTGT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGAATGCACGTATTGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGCTGATTTGTACATAA

WI-884	198 T C ---	---	---	AGGTTCTGGACCTGATGCTGGGAAACAATTGGGTCNCTGGGAAATTCCTATTTTGGTNTTTCACAGAT CAGTAGAGCCAAATGGGAAAGGTATCCTAGTCCATCCCTTTATTAGGAACCTTCTCTGATCTATTGGGA ACTTCTCTCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAGGAATA[T/C]G ATCCGCGATGCAACATTTATTCAGTGAAACATGATGAAAATGAACATAAT
WI-921b	205 G A ---	---	---	CACCTOCCAAGGCTCTGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGACAGTTACTGG CAGTGATGCTCTCAGCCTGGCCCCCAAGAAAGTCTTNGCCAGGAAAGACGATCCATCTAG TCT[G/A]GGGAGAGATCTGACAAATTTAATCAGGAGGAAGAAATCTTCCGAG
WI-921	205 G A ---	---	---	CACCTCCCAAGGCTCTGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGACAGTTACTGG CAGTGATGCTCTCAGCCTGGCCCCCAAGAAAGTCTTNGCCAGGAAAGACGATCCATCTAG TCT[G/A]GGGAGAGATCTGACAAATTTAATCAGGAGGAAGAAATCTTCCGAG
WI-945c	90 G C ---	---	---	GGCTGGGATGAGAGGTCTACTTGTGGTACTGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAGNA GAAAGACACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGCCCCCAAGCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAGTTCAAACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAAATCTTTAAAGGGAATCATGACAGATTTCTTGGCTTTA
WI-945b	90 G C ---	---	---	GGCTGGGATGAGAGGTCTACTTGTGGTACTGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAGNA GAAAGACACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGCCCCCAAGCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAGTTCAAACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAAATCTTTAAAGGGAATCATGACAGATTTCTTGGCTTTA
WI-960b	167 C T ---	---	---	TTGCTTCAAAGAAAGTTCTGCTCAGGAAGTTATTTCATTGAGCAACCTAAAATGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTCTACC CTGAGGAAATTTATCAAAGATGTTAAGTTAICTTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155 G A ---	---	---	TTGCTTCAAAGAAAGTTCTGCTCAGGAAGTTATTTCATTGAGCAACCTAAAATGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTCTACC CTGAGGAAATTTATCAAAGAT[G/A]TTAAGTTATCTCCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181 T C ---	---	---	TCCACTGAGTATGGCTTTCAGTAGTTTTTATTATGATGGCTAGGTACATTTGTTTTTATTGTTCTG CGAATTGTTGATTACTTTGGGAGAAATGCTCAACTATAAATATTGCTTCTGACCCCTTTCTGTGTTCTC CTTCTTAAGATACAAAATAAATGTAACATTAGACCTCTCAGTAT[G/C]GCTGTTTTTACTCTCCTCTG ATTTTTTTCATTATTTTATGCTCTGGCTTCATTTGTAAATNG

WI-1147b	204	G A	---			TTTGCCATTATTTGAAGATAACCCACACCTTGGTGTCAGGGTTTTACAGGTTATTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATATCCAGCCACCGCAAACTTCTCCTCCTCCTGCTGGCTC CTGAGCCAAAACAGGCATTTACCATAAATCACCTTTGTTAGGATGAACCTTATCTGGCCAAACTGATA C/GA/GCATGACCCACAGCCTCAGGTATATAAAACACTCTCATCAGGCAGA
WI-1158b	147	C T	---			GCATTGAGAGGGTTCGTTTAAATGACATTCACTGAGGCCCTGTCTATGTGAGGCCCTTGGTTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG/C/GGCCAGGTGGC TAAGTGCTGGGG/C/TTCTGGGGTCAGGCTGCCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1158a	124	C G	---			GCATTGAGAGGGTTCGTTTAAATGACATTCACTGAGGCCCTGTCTATGTGAGGCCCTTGGTTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG/C/GGCCAGGT GGCTAAGTGCTGGGGCTCTGGGGTCAGGCTGCCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1304	124	T C	---			AAGTTTACAGAAAAAATACCGAAAAAGTGACTTCAAGANTCAGCTGAGATAGAAAAATATGCCCCA TCATCTCAANGTNCACAGACACTTATCCCTAGACAGCCATTCTTTTGAATGN/C/GNCANT AAAATGATTTGAAATTTGGGAATAAGCCCTCCCTCTAATGATTTGACAGTGTAGACCTTGCCTAG GCC
WI-1305d	202	C T	---			TTCTCAATCCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNATATG/C /TAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305c	46	C T	---			TTCTCAATCCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTC ACATCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNINATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305b	153	T C	---			TTCTCAATCCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAA/C/JNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNINATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305	202	C T	---			TTCTCAATCCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNINATATG/C /TAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA

WI-1306b	248 A G ---	---	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNGCAATAATAATGGACAATCTTGNGNNNTNG GGCTGGGTGACTGTGCCTGGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGGNGAGAAGTGGCCCTNNTTCTGTAGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCTCTA/GJGC
WI-1306	240 A G ---	---	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNGCAATAATAATGGACAATCTTGNGNNNTNG GGCTGGGTGACTGTGCCTGGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGGNGAGAAGTGGCCCTNNTTCTGTAGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTA/GJCTTCTAGC
WI-1307b	118 T C ---	---	GACAAGGCTGGTACTAGTTCCAAATTCCAAATCTATGTACACTTTCTCTCACATTTCTCAAGTGGACA GATTTTCTGCATTACTGCTTGGGGTTGGGGAGCAGTGGTGTAGGCAAT/CJGTGAGATTGTCTTT CCTACCCCTTAAATGTATCTTNCATTAATATNATGCTAAACCGGTACTGTGATCTATCACTGGTT TCITTTGGGTGTTGTTGTTGCTGTGTTTCTCTCTGTAAGNTGTTT
WI-1307	118 T C ---	---	GACAAGGCTGGTACTAGTTCCAAATTCCAAATCTATGTACACTTTCTCTCACATTTCTCAAGTGGACA GATTTTCTGCATTACTGCTTGGGGTTGGGGAGCAGTGGTGTAGGCAAT/CJGTGAGATTGTCTTT CCTACCCCTTAAATGTATCTTNCATTAATATNATGCTAAACCGGTACTGTGATCTATCACTGGTT TCITTTGGGTGTTGTTGTTGCTGTGTTTCTCTCTGTAAGNTGTTT
WI-1325b	169 T C ---	---	GAGAGATGGCCAAAGACAAGCAGAGGGGAGAGAGAGCAACCNCTGTGGTTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCCCTTGTCTCTCTT/CJACCCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1325	165 C T ---	---	GAGAGATGGCCAAAGACAAGCAGAGGGGAGAGAGAGCAACCNCTGTGGTTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCCCTTGTCTCTCTT/CJACCCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1327b	162 T C ---	---	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAGCTGTGTAGTGCAAGAAGTCTGTTATTTGTAAA ACACCAAGTGCGGTTTAAATGGAATCGGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTG/CJGAAGTTGGGTAGTACCAGGCTCCCCAAATGTAGT TCITGNGCTGAAAGTCTCTCTACTGAAAGGCAATGGTTCCATCTCTAAG
WI-1327	175 C G ---	---	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAGCTGTGTAGTGCAAGAAGTCTGTTATTTGTAAA ACACCAAGTGCGGTTTAAATGGAATCGGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGAAGTTGGGTAG/CJGTACCAGGCTCCCCAAATGTAGT TCITGNGCTGAAAGTCTCTCTACTGAAAGGCAATGGTTCCATCTCTAAG

WI-1341b	136 GA ---			TATCAGCATGATTGGCTGTTGGACACAAAGTCAATTTGTACTTTTGNNGNNNTCCTTTCTNITT ACCTGATCCACTATCTTCTCAAGATCANGTTCAAATTTGGCTTCTGTTNAAATATACCCCAAGC [GA]GGATTGTGATGGATCTGTTTATTTTCCTGTCTTGGAAACAGAGAGTGTCTCTGNGAGTNTG GTTTCAGGATTGTCTCTGTTTCCACAGCCCACTTGCACCTAGCAAGTGT
WI-1349e	192 GC ---			CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGAGGCGAGGTGGTAGGTCTGGCTGTGAGTTGATATATATG GCAGGTCTCAACAAATGATGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAAAATA
WI-1349d	264 CA ---			CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGAGGCGAGGTGGTAGGTCTGGCTGTGAGTTGATATATATG GCAGGTCTCAACAAATGATGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAAAATATGAT
WI-1349c	192 GC ---			CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGAGGCGAGGTGGTAGGTCTGGCTGTGAGTTGATATATATG GCAGGTCTCAACAAATGATGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAAAATA
WI-1349b	264 CA ---			CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGAGGCGAGGTGGTAGGTCTGGCTGTGAGTTGATATATATG GCAGGTCTCAACAAATGATGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAAAATATGAT
WI-1349	264 CA ---			CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGAGGCGAGGTGGTAGGTCTGGCTGTGAGTTGATATATATG GCAGGTCTCAACAAATGATGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAAAATATGAT
WI-1403b	57 CT ---			TGGTATTTGGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/TTTCCGAAT GCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACGT AAAGTTTACATCAACATAAATCTTGGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCTCA TAATCCCAAAAGTGCCAAAAGGGTTGTATCTGATTGT
WI-1403	58 T C ---			TGGTATTTGGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTGCTTCTCCGAA TGCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACG TAAAGTTTACATCAACATAAATCTTGGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCTC ATAATCCCAAAAGTGCCAAAAGGGTTGTATCTGATTGT

WI-1417c	31 C T ---			CAGCCGGAAGAGATTACGTGGAGAGATGTCJTJTTGGCCAGGGGGGAGATGTGAGCCACGGG GGTGACAGCATGCCTGCTGGCATTGGAGGGCCCAAGAGGAATCCAGTGGCCCTCTCAATGACTTG GGGTCTCGACTTCGGAAGTTTAAGGGCTCGGCTTCAAAAGCTGGTCCGGTTTGAGGCGGTTGC AGGCGAGGCCCTTAGGTCGGTATTAAATGTTTCTTTGTAGAAAAAGTCGC
WI-1417b	31 C T ---			CAGCCGGAAGAGATTACGTGGAGAGATGTCJTJTTGGCCAGGGGGGAGATGTGAGCCACGGG GGTGACAGCATGCCTGCTGGCATTGGAGGGCCCAAGAGGAATCCAGTGGCCCTCTCAATGACTTG GGGTCTCGACTTCGGAAGTTTAAGGGCTCGGCTTCAAAAGCTGGTCCGGTTTGAGGCGGTTGC AGGCGAGGCCCTTAGGTCGGTATTAAATGTTTCTTTGTAGAAAAAGTCGC
WI-1729	172 A ---			CCATGAGCAACAGCATGTTTCTACTCTGTGATGTATGTAGGGGGCATGTATCTGTATTTCTT TTTTATTCTCTCCAAAGAAATTTCAATATGCAAAACATTATCAGGCAATGCAGCTCGTAATAAAGA TGTTGGAGAACTGAAAAAGAGAGCTTACATGACCCCAATAGCAAACTCTCCACACATTTCCAGCA GATGTATGTCTCTCGGTGGTNACCTTCTCTCCACCACATCACCTGTGTTTT
WI-1732b	122 T C ---			TGCCCTACTTCTTTGTTCAATCCACCATTACATTTGTAAATGGAACTTCTAGGAGGTAGAAGGA TATGCTGATCAAAAAAGGGGACATATCAAGGAGTNTCCCTGGTCAACCCCTTTC/JATTGAGTCT CTGCCACATGTCTAGTAAGTGTGATGGTGCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTTCACACTACTATCATATTTGGCTAAGGTATTCATCATATTTGGCTAAG
WI-1732	114 C T ---			TGCCCTACTTCTTTGTTCAATCCACCATTACATTTGTAAATGGAACTTCTAGGAGGTAGAAGGA TATGCTGATCAAAAAAGGGGACATATCAAGGAGTNTCCCTGGTCAACCCCTTTC/JATTGAGTCT CTGCCACATGTCTAGTAAGTGTGATGGTGCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTTCACACTACTATCATATTTGGCTAAGGTATTCATCATATTTGGCTAAG
WI-1750	97 A G ---			GCGAATTTAATGACTCCAAAGGTAGTAATTCCTTCCCCCAAAAAAGGTTTAAAAATCTGTGTGGA CATAATGTTTGAATTTGCAGTTCACCTTGG/JGJTAAAGGTGTGCTGTTTTCTGGCAAGAGTCAG TGGGAGTGTCCGGGAAAGGGCTAAAGTCTTTGTAGTCAGACAAACCGGCTTGACGTCCTGACTGAG CTACATTCACTTTATGATCTCCAGCAGGTTCTTCCA
WI-1780	31 A G ---			GGTACACAAAGAAATGCTTCTGGAAATCTAC/JGTAGCGCCTTAACAATTTGGCTGAGTATTAATC TGTACATGTGTAAATGTGAACCAACCATGAAGCTGGGCAAGAACAAATCCTAGGAAAGTACAATTAC TGGGAACTGTAGAACAAATAATCTCATAGTTTACACATAGCTGGGAATCACTCATGTGCCCATCA ACTGGAGAGACCTTGTGTAGTACAGAGGACATTCAGGAATAATCATAAAAAT
WI-1803c	77 A G ---			CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTTTTCAGGCAGAA CCATTATGAT/JAGTAGGGTAGAGCATCACACTTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGCTAATTTCAAAATATATCTACTAAAGCATGACTTCTAGAAAAATCTTATTACTCTTGTCCTCAA GGAATGGGAATACCTATAATACAGTCTTATTGAGGAAAAATACTGGAATCA

WI-1803b	77 A G ---			CCACTCAGTAATAATAGTGTGGAGATAAGTATATGTTAGGCACATAATAATTATTTTCAGGCAGAA CCATTATGATAGTAGGTAGGTAGGCATCACACTTGGGAGGACATATTCTGGAGNAGATATCCTG GGTGCTAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAATTACTTATTACTCTTGTCTCAA GGAAATGGGAATACCTATAATACAGTCTATTGAGGAAAATAACTGGAATCA
WI-1837b	112 C T ---			TTTACTGGGATTTTCATAGCTGATCATAAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGATAGACCCGTTTATACGCTTCTGTCCCCAGTTTATTTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAACAAACCTCAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACCTGGGAAGTCTGGGAACGTTTAGCTTTCTGTGTGGCT
WI-1837	112 C T ---			TTTACTGGGATTTTCATAGCTGATCATAAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGATAGACCCGTTTATACGCTTCTGTCCCCAGTTTATTTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAACAAACCTCAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACCTGGGAAGTCTGGGAACGTTTAGCTTTCTGTGTGGCT
WI-1840b	79 G T ---			TCACCTAGGGAGGTCGCTAAATGTAGCTTCATTAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGTGGTGGAGAACTGTAATTCAGCACATACAAGTGTGACAACTGTTTGTAGTAT ATTTATCTCCAGAGTGTGTTGAAATTTACTAAAAGTTCTTAAAGAGCCATGAAGAAATTAAGACT ATCGCA
WI-1840	79 G T ---			TCACCTAGGGAGGTCGCTAAATGTAGCTTCATTAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGTGGTGGAGAACTGTAATTCAGCACATACAAGTGTGACAACTGTTTGTAGTAT ATTTATCTCCAGAGTGTGTTGAAATTTACTAAAAGTTCTTAAAGAGCCATGAAGAAATTAAGACT ATCGCA
WI-1879b	110 C T ---			GGGCTCACTTTCATCAGAGCACATATCAGTGATAGTCTGTTTCTTTTCATAACTTACTCCCCCG CACTGTAGGNTTCTTTGAGGTNAAGGACCTGCCNTTTTATGCTGTGCNAAATAAACTCCCAAAA AAGTGGTTAGTCCACAGGGTTTAAATAGTCTTGTGTAATGAATTTCTGTGTGCGACCCCTGTGCCTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTACCCACT
WI-1879	110 C T ---			GGGCTCACTTTCATCAGAGCACATATCAGTGATAGTCTGTTTCTTTTCATAACTTACTCCCCCG CACTGTAGGNTTCTTTGAGGTNAAGGACCTGCCNTTTTATGCTGTGCNAAATAAACTCCCAAAA AAGTGGTTAGTCCACAGGGTTTAAATAGTCTTGTGTAATGAATTTCTGTGTGCGACCCCTGTGCCTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTACCCACT
WI-1900b	119 C T ---			TGTTCTCTGGTCCAGGACCGGGCTAAGTCTTGTCTGCATAATGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGGCTGTGCTCTGAGAGGT AAAGTGCCCTGCCCCAACGGGCACAACTAGAGAGCAGCAACAGGTGTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTGCTTAAGTGCATGAGAAACCACTTTCTTGTCTCC

WI-1900	119 C T	---	---	TGTTCTGGTCCAGGCACCGGGCTAAGTCTTGTCTGCATAATGGAATAATCAACTGGACAACCCNG CTNAGGTAGNTACCTNGGCAATTAGCCCATCTTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGT AAAGTGCCTGCCCAACGGCACAACTAGAGAGCAGCCAAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTCTTAAGTCCCATGAGAAACCACTTTTCTTGCTCC
WI-1943c	165 C T	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAAATGGGTAGGGAAGACCAGCC[C/T]CTCTGAANCTGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCACAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943b	165 C T	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAAATGGGTAGGGAAGACCAGCC[C/T]CTCTGAANCTGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCACAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943	164 C T	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAAATGGGTAGGGAAGACCAGCC[C/T]CTCTGAANCTGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCACAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1960c	270 A T	---	---	CCAGGTGAGGCTGAAAGAGGAGGAGGCAATTGCTGTTGGAGTGAGGGATCTGGAGAAGCACCCCT GCAGAGCTTCATCTGTTTCAAAGTGTGCCATGCANGGCTGCTGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCCAATTT
WI-1960b	270 A T	---	---	CCAGGTGAGGCTGAAAGAGGAGGAGGCAATTGCTGTTGGAGTGAGGGATCTGGAGAAGCACCCCT GCAGAGCTTCATCTGTTTCAAAGTGTGCCATGCANGGCTGCTGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCCAATTT
WI-1977	203 T C	---	---	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTTGGATCTGGTAAGTAGGAGTCA TTCTGGGCATTTCTCATAGAGNTGTTTTTAGTCTCGTAATAATACTGTGCCCTAGGAAGGTTGTT TTTCTACTGCGTCTGTGAAAGCCCTTCCCCATCGAGTGATACAGTACTTTCCAGTTATGGAGATTIT /C/TAAACAATCAACACTGGCTGAGGCTGTTGG
WI-2012	102 T C	---	---	AAATTTAGAGGCCAGAGTCAAGTCAAGTAAATGATTATAAAGTTGAAGTAAATGCAATTGTAGTTTCATGT TTTCTCTTAATCTGCACAAAAGTACTGTAATAATCTGTTTAAATCAGTTACCAGAGGGCAATACCT GGGTTAATGTAGCACTCAAAAGTTATGTAGAGTAGCTGTCTGAGTCACTTTTTTCTACTCTCATTT GGCTTACCAATGCTTCCACTGGATC

WI-2573d	129 T C ---	---	TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTACAAAGGTGTTCCGTGCTTT/CJTG TATCATCTGATCTTCCCAACAGGGCTATTATGCCTAGGTAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573c	165 A C ---	---	TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTACAAAGGTGTTCCGTGCTTTTGATAT CATCTGATCTTCCCAACAGGGCTATTATGCCTAGGTAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573b	165 A C ---	---	TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTACAAAGGTGTTCCGTGCTTTTGATAT CATCTGATCTTCCCAACAGGGCTATTATGCCTAGGTAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573a	129 T C ---	---	TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTACAAAGGTGTTCCGTGCTTT/CJTG TATCATCTGATCTTCCCAACAGGGCTATTATGCCTAGGTAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2868b	60 A G ---	---	GACTTCATGCTCATGAACAAGCATTTGCTTAAATTTACAGACATTAAAGAACAAGCTTTC[C]/GJCTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTAAACGCTTCCCAATGATGCAGCCCAAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACAGCTGAAAAATGAAATATCGATATAC
WI-2868	60 A G ---	---	GACTTCATGCTCATGAACAAGCATTTGCTTAAATTTACAGACATTAAAGAACAAGCTTTC[C]/GJCTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTAAACGCTTCCCAATGATGCAGCCCAAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACAGCTGAAAAATGAAATATCGATATAC
WI-2870b	131 T C ---	---	CATGCTGTGTAACCTCTGTGCTGCTTGTCTGTCGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCCATTTAAATTATATCACAGCTTTATGTCCACTTCTCTGTTCCCTGCCATCAC TGGGCTTTTACAAAGGAGGCTTT
WI-2870	131 T C ---	---	CATGCTGTGTAACCTCTGTGCTGCTTGTCTGTCGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCCATTTAAATTATATCACAGCTTTATGTCCACTTCTCTGTTCCCTGCCATCAC TGGGCTTTTACAAAGGAGGCTTT

WI-2954c	49 T A ---	---	TTAGCACACATATCTGTGTGGGACTTAACTGAGACAAGGCATAAAAAA/T/A/CAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAAATAAGTCCA GAG
WI-2954b	41 A G ---	---	TTAGCACACATATCTGTGTGGGACTTAACTGAGACAAGGC/A/GT/AAAAAATCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAAATAAGTCCA GAG
WI-2954a	38 G T ---	---	TTAGCACACATATCTGTGTGGGACTTAACTGAGACAAG/GT/GCATAAAAAATCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAAATAAGTCCA GAG
WI-2971b	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGA/T/C/G CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTGTAACCTCCTCCTCTTAAATAAACCTAAC ATTTCCTTTGTTCCTGACATTTCTGAAGGCCACGCTGGTCTAGATGTATGTCCTCAGATTGCAATCCT AGTTCCTTAATGTTATTCTGAAAGAAAACCTTTTACTTAGGGATTGCT
WI-2971	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGA/T/C/G CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTGTAACCTCCTCCTCTTAAATAAACCTAAC ATTTCCTTTGTTCCTGACATTTCTGAAGGCCACGCTGGTCTAGATGTATGTCCTCAGATTGCAATCCT AGTTCCTTAATGTTATTCTGAAAGAAAACCTTTTACTTAGGGATTGCT
WI-2995d	133 A T ---	---	TTCTGGGAAAGAAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTTNATCAAGATAAGACCTGGAAGACCCGAGCCAAAAGGAGGCTGGANTTTTTTTA /TAAATCTTTCTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT
WI-2995c	151 G C ---	---	TTCTGGGAAAGAAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTTNATCAAGATAAGACCTGGAAGACCCGAGCCAAAAGGAGGCTGGANTTTTTTTNA AATCTTTCTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995d	133 A T ---	---	TTCTGGGAAAGAAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTTNATCAAGATAAGACCTGGAAGACCCGAGCCAAAAGGAGGCTGGANTTTTTTTA /TAAATCTTTCTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT

WI-2995c	151	G C	---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133	A T	---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA /TJAAATCTTTCTTTCTGGTGTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995c	151	G C	---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995b	151	G C	---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995a	133	A T	---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA /TJAAATCTTTCTTTCTGGTGTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGTT
WI-3147	85	C T	---			GTGGTGCAGTTATCCTCTGGAGTCCCTGTGAGATCAGACTGGAGCCAGTCTCCAGCTTGAGACCCAC ATCTCACTTAGCTCCTT[C/T]CCTGCCATATCCTGTCTTCTTACTCCTATCTCCTGAGACTCTTCTCT GAATGAATTACATGCACCTCAATCCCTGCCTCAGTCTCTGCTTTNAGGGAAGTGGACCTAAGACAGAA ATCTTAGTACCAATACTTTGCAAGG
WI-3234b	68	T C	---			ATTCTGTAATGTTTTCACTGCTCCAGTAAAATCTTTATTGAGGTCCATGCTCCATTACCTCTACTTA T/CJGACAAGCAAGAAACAACAACAGAAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATACCTTCTG TATAATTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATAATCAAAAATTTTAC TCAGTAATTCAGAAGAAAGGACAATGGAATGTACTTATTTTATATCTTTAT
WI-3234	68	T C	---			ATTCTGTAATGTTTTCACTGCTCCAGTAAAATCTTTATTGAGGTCCATGCTCCATTACCTCTACTTA T/CJGACAAGCAAGAAACAACAACAGAAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATACCTTCTG TATAATTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATAATCAAAAATTTTAC TCAGTAATTCAGAAGAAAGGACAATGGAATGTACTTATTTTATATCTTTAT

WI-3292b	106	G A ---	---	GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACTCATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCTG/AJGGTATGGATGGATGGATTACTT GCCATGAATATTTCCATTGTTTCTCATTAATGTATTAATTAATTAAGTAAATATTATTNCCATGA GACACAATGGAAAAATGGAAAAACATTCATGGAAAAACCCATTTCATC
WI-3292	106	G A ---	---	GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACTCATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCTG/AJGGTATGGATGGATGGATTACTT GCCATGAATATTTCCATTGTTTCTCATTAATGTATTAATTAATTAAGTAAATATTATTNCCATGA GACACAATGGAAAAATGGAAAAACATTCATGGAAAAACCCATTTCATC
WI-3355	19	G C ---	---	CCATGAACCATGGGCTACA/GCJATATTCTTAACTTCAGAGTCCCTCCTTACTGGAGAGGATCCA CTTTTAAATATGATTTCTTGAAGTGGCTGCATACTATTCTTCCAAGCACTTAAAACTCATCAGAA AAAAAATCATCAAAAAGTCGAAAGTTAGTTTNNATTACCTTCACCTTTTCAATGGAAAACTTTATAA ACTGTGGATCAATTTATATTACTTTTGGATCAGTTTAGATGACTTTNAGTTG
WI-3408	194	G A ---	---	CCATGAAGAATGAGTTCCCTCCCTCCCTGGGTACGCTAAGATAGCACACCCCTTGAGAAATTTNACT TAGCACGTGGCATTGTAATGGCTGGATTTCTCCGCTCTAAGACACACCTTATGCTTTCAAGCTTT CTGGAATGGGATGAATCTNACATTCATGTCACCCCTGCTGGGATCAGTCTCC/G/AJTGCCCC ATCTCTGNAGAAGCCACTGGGAAGTCGAAGGAGTGACTTCAAAATCAGG
WI-3505b	131	G A ---	---	TAACCTATGCCTCATCTGGCTTACTGCTTAGTCCCATTTGTCATCAGTGCACCTTAAAAAATTTT GAAAAATTGCCATTTTAAATATCTTTGGAACCTTCTTAACACATTACCTATTTTNAACCAAC[G/A] AGGTGATTCCTTATGGGAAAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTGCATAT
WI-3505	131	G A ---	---	TAACCTATGCCTCATCTGGCTTACTGCTTAGTCCCATTTGTCATCAGTGCACCTTAAAAAATTTT GAAAAATTGCCATTTTAAATATCTTTGGAACCTTCTTAACACATTACCTATTTTNAACCAAC[G/A] AGGTGATTCCTTATGGGAAAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTGCATAT
WI-3564b	177	C T ---	---	GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGATCACTAAATGTTTGGAAAAATAAAGT GAAATCAATGTGCTTCCAGTGATTCACATGGCAGCAGTGCACAGAGGGCTTGAGCGCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGCTGTTT/AACAAGTGTGTTGTTGTTGTCATC AGTGCACACATGCTACCTTCCCTCACAAAAA
WI-3564	177	C T ---	---	GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGATCACTAAATGTTTGGAAAAATAAAGT GAAATCAATGTGCTTCCAGTGATTCACATGGCAGCAGTGCACAGAGGGCTTGAGCGCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGCTGTTT/AACAAGTGTGTTGTTGTTGTCATC AGTGCACACATGCTACCTTCCCTCACAAAAA

WI-3649	64	A G ---			AATGTCCATGCTGTGACTGACCTGTCTAACACCCCTTCCCTAGTATCCCTTAGTGGAAGATTCCAC[A/G] AGACCAGTTTGCCTTCACCTTAGTAGGGCCAATGATAGACTTTTAGGTGCTACCAACAGGGTACCTGC ACAGCCACATCATATGTCACAGTATGGTTGCAAGGACCTGTCTAGACTCTTTCTGCCTGGCTTGGTC TTCTGTTTACCATAITTAATGATGACATGCAAAACCTCAGAGCCTTTTA
WI-3674b	133	G C ---			ACAGTACATGCGCCCAITATGGAACAATCATCTGACTTATGTTACCTGAGAAGTCCCTCTCTAA ATTTAACTACCAGGGGAGTGTCTTTATAGTAATTTAAATATGTTTATTTAGAAAATAACAAAAT[G /C/JAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAATTTGTAACCTGGTCAAAATGATTGTT AATCTTAATTAATTGTGTTTATGTTTNAATTAATGCTCAATCAGCCCAAG
WI-3674	133	G C ---			ACAGTACATGCGCCCAITATGGAACAATCATCTGACTTATGTTACCTGAGAAGTCCCTCTCTAA ATTTAACTACCAGGGGAGTGTCTTTATAGTAATTTAAATATGTTTATTTAGAAAATAACAAAAT[G /C/JAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAATTTGTAACCTGGTCAAAATGATTGTT AATCTTAATTAATTGTGTTTATGTTTNAATTAATGCTCAATCAGCCCAAG
WI-3682	137	G A ---			CAATATAGACCAATGACTGCCACAAGAGAAATAGTGGATCTACATTTAGAAACCAATGTTTTT ATTGGCTCTCTCTCTCTCTCTTTTAAATGCTCTCTCAACACCAATTCACCTTATCTTTTCAA T[G/AJAGCATTTGTCCTCAATTTAAAGTCAATGAAAAATAATGTACATTTTCAACAAGTATACATTAA GCCTGCAAAAGTCTTATATGCTAT
WI-3854b	194	G A ---			GGTATGTTGAGGTCAGCTAATGGTCACTGTGGTTTGGAGTGAATCTAATGGATTTTGGCCCTTGGA CAAAGACCAAGGACAACCTGTAGGACITTCGCTGCTACCTGCTACCTGCTTCTTGATTAATAACTC TGTTTCAGGAAGGCAAGGCGAGTTATGACCACTTTACAACCTGAGGAAATCAAAGCAAC[G/AJAGAA GTTAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
WI-3854	194	G A ---			GGTATGTTGAGGTCAGCTAATGGTCACTGTGGTTTGGAGTGAATCTAATGGATTTTGGCCCTTGGA CAAAGACCAAGGACAACCTGTAGGACITTCGCTGCTACCTGCTACCTGCTTCTTGATTAATAACTC TGTTTCAGGAAGGCAAGGCGAGTTATGACCACTTTACAACCTGAGGAAATCAAAGCAAC[G/AJAGAA GTTAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
WI-4039	210	G A ---			AGCCAGCCACATCATGTTGAGTCTGCTCATCTTCCATCTCTTATTTCTCTACTGCCTTCACCTT CCATTAAACAAGAACTCTTGATTAATGATGTTGTGGTTACACTACAGAATCCAAGATGACCTC CCCATCTCAAGGTCAACTAATTAACACCTTAATCTATTTGCAATCTTTGTCATTACCATAACATATT CATGG[G/A]TTCTGGGATAAGGGGTAGACATTTTATGGGAGGCATTA
WI-4110b	130	T C ---			GAAAAATGATGTTTTTGTATTTCCCTTCCCTATCTCAGATTATTGGAGTGTCAATTAGAAAACTGATAGT AACCCTTTATTTGATGAAACTCTGTCTATAATTAACCTTCCCTCTCTCTGCTTTATTTGCCIT/CJACA GTTTAGGTAATAAAGATGCCCAAGAAATTCAGTATTCAGTACAGTAAAAAGTAGCAACCATGGG GTAGGGACAAGTNCAGAAAAAGGGAGGAGGTNGGGGGTTTTCTGGGAAGA

WI-4110	130 T C ---	---	GAAAAATGATGTTTGGATTTCCCTCCTATCTCAGATTATTGGAGTGTGATTAAGAAAACTGATAGT AACCTTTTATTTGATGAAACTCTGCTATAATTAACCTTCCTCTCCTGCTTATTTGCTT/CJACA GTTAGGTAATAAAGATGCCAAGAAATTCAGTATTCAGTACAGTAAAAAGTAGCAACCATGGG GTAGGACAAGTNCAGAAAAAGGAGGAGTNGGGGGTTTCTGGGAAGA
WI-4119b	168 G A ---	---	ACCTCTCTATGCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGGTGGGAAAAAGTAATAATAG AATGGAAGGATAAATAAAGGTAACACGGGGAAGAACAGGACAGAACAGACAGAAAGGGGT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTTCA TGAGACCGTCTGCATTCTTTTGTGTTTTTAAAGGGCTCTGTGATCATCATCTTCA
WI-4119	168 G A ---	---	ACCTCTCTATGCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGGTGGGAAAAAGTAATAATAG AATGGAAGGATAAATAAAGGTAACACGGGGAAGAACAGGACAGAACAGACAGAAAGGGGT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTTCA TGAGACCGTCTGCATTCTTTTGTGTTTTTAAAGGGCTCTGTGATCATCATCTTCA
WI-4123b	51 T G ---	---	CAAGTCAGATTTTGAATTCAGGATAACAAATTTGAAAAATAGAAAAGTG[G/J]TTAAACTATTT CAAAATAACAATAAAGAAAAACATGATGAAATTTCTCGTTACATAATTTGTATAGAAATTTAGTGGG TTCTCCATGACATTGGCTTGTCTTCTCAACAGTGGGTGTTGGATGTTTCTATGCTTTCTC AGGCACAAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4123	51 T G ---	---	CAAGTCAGATTTTGAATTCAGGATAACAAATTTGAAAAATAGAAAAGTG[G/J]TTAAACTATTT CAAAATAACAATAAAGAAAAACATGATGAAATTTCTCGTTACATAATTTGTATAGAAATTTAGTGGG TTCTCCATGACATTGGCTTGTCTTCTCAACAGTGGGTGTTGGATGTTTCTATGCTTTCTC AGGCACAAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4149b	145 G C ---	---	TTGTACATGTTTCAATTCATCCCTCCCATTTCTTTCTGCTTATAAAGAACCTCGCTTCTTCCAAAGT CTTACTTCCACCTGAGCCACAGATCTTTTATTTCCATCAAAGCTTTCTCAGCATCTTCTATATACT GTGCTG[G/C]CCTTGTGAAGAACCCAGAGCCGAGCATACCAACATGATCTTTTGTGTTGAAGTGTAGT AGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
WI-4149a	137 T C ---	---	TTGTACATGTTTCAATTCATCCCTCCCATTTCTTTCTGCTTATAAAGAACCTCGCTTCTTCCAAAGT CTTACTTCCACCTGAGCCACAGATCTTTTATTTCCATCAAAGCTTTCTCAGCATCTTCTATATACT T/CJGTGCTGTGCTTGTGAAGAACCCAGAGCCGAGCATACCAACATGATCTTTTGTGTTGAAGTGTAG TAGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
WI-4182	188 G A ---	---	TAACACACTTTTCAATTTGGTTTCCATTAAGTGCAGTTAAAGGACCATCCATTATATTACAATTCCTC AGTTCTATGCTTTAGAGTNCATTAATAGGACTACTGTAATAATTTAGAGGGGAATTTACTCCTGGAGTA GGGGAATGAGTTAAATAATCTACCACATGCCAATTCAGGGACTGTGGTTAA[G/A]ATGTCCTCTCT TGCCCCCTTCCCAAGTCTTAATTCCTAG

WI-4230	93 T	---	---	AGAGACGTTGAATGGGGACATCTTTCTATTTTCGATTTTAGTTTAAACATTTTGATAAGAAATTGATGAAA GTTTGTCACATTCAGATTTATCTTTATAGCAGCAGAAGTCTGGCAAAATAAAGACGACACACTGACT TTTCCATGGTAAAAAAGATTAGAGAAAAACAGCCTATTTTCTTAATGTTAAATGTAATTTCTGAAT ACATTTTAAATGGAGGAGAATGAATAGTGACCTTTTGAATTTTGAATTTATGG
WI-4241	118 C T	---	---	GAAATTCATTGAAGTTTGGACCTTGAACGTGATCTCATTAATACCTTTTNCCTGTAGTGGTTGTATTT CATTTTGTACAAACAGACAGCAAAATTTCCACTTAAATTAATCTC[CT/TAAGTATCTATGAT TTAGCACTGTTAGCACCAGAACTGTGAAATTTATCTCTAGATATCTTTCAGAACTCTAGGATGGAAG AA
WI-4271b	151 A	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAAGCAGANCTGGACCTAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCTGGAGGATTAAGAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAACGGGGAATATTAGAGTNTCTACAGGGAGCCCCCAACCCTTCTGCTCAGG CTCTAGAAGGTCCAGTCAGGGGC
WI-4271	151 A	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAAGCAGANCTGGACCTAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCTGGAGGATTAAGAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAACGGGGAATATTAGAGTNTCTACAGGGAGCCCCCAACCCTTCTGCTCAGG CTCTAGAAGGTCCAGTCAGGGGC
WI-4389b	156 G A	---	---	AATCGAAACATTGATTTTGTAAAGGAACACCATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAAGAAAGGATATTATGATAACCTTTTGA AGGTAAGATGTGAACCTATACA[G/A]JNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4389	156 G A	---	---	AATCGAAACATTGATTTTGTAAAGGAACACCATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAAGAAAGGATATTATGATAACCTTTTGA AGGTAAGATGTGAACCTATACA[G/A]JNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4488	31 A G	---	---	GATGACAAATTATTGTGATTTGGCATTTTAA[G/G]GTACCATTCCATTTTCTTCTGGCTTTCGIGIT TGTTGTTGAGAAGTCAGGGTTAGTCGATTGCTCTTTTCTAGTCTTCTCAGTAGGAAGACTGATC CTAAACAACCTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTTAAAGAACATAAATCAAAATTG TATTATCCTATGCTTAAATGCTCAG
WI-4491	145 G C	---	---	ACCATCAATGTATCACCCTCTAAAATTTATTAGATGATTAACTGGCTCTGTTAAAAAATAAAAAACCT GTCCTGGACATTGAAAAATAAACATTACTATTGGTCATTTCTGCTACTTACAAAGGACTGCACTA AACAAGTTAAG[G/C]GTTTTTGGAGGGGAAAAATCATAAAAATGCATAAAAAATTTCTACCACCTGCA TTTCTGTCCCATAAATAAAATTTTACATGCT

WI-4584	144	A G ---			TTGGTTGGCATTAGCCTCATAACAACATTTACAAATCAATTTGTTACTCTTATTTTACAAACAAG AAAAATGAGGCTTAACATCAGACTCTGCTTAGTCGAGAGCCAGATTTGAAGCCAGGAATCCATT CACCAGTACAGTGTCTACCTGGTAAAAAATGTTTAAATTAATCTATGGCATTAGATTTCAAAGA GTCTAATGTGGTTTGAATAAGGTGCTTTAATTTGTTATCAGTATGC
WI-4639	185	CT ---			TTTTCGATTTGAATGTGTATGGTCAGACTTCAGAGGAACCCAGGAATCTCATTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTTCCAAATCCACCATTAC TGACCATAATGACTTGGGAACATTATCTCAGCTATCTGAGTCTGATCCGCTCATCTTTAAATTTGTA AATTTAAGGACACCTATCATAGTAATATTGTGAGGATAAAATGAAATAA
WI-5327	63	A ---			AAATGAATCCGCTTTAGAGCAAAATACCAGTAAGGGCTGGTGCAGGATGGTGGCTGAGAGA/- JGATTACTCATAAAAGCATATTAAATTTTATAAATATGGAATAATTAACCTAGATAATTAATGTGAAT TGAGTTGAAGGTTGCATGAGAGTAGGAGGAGGTAGTTCTACTTATAGGGTTTATATAAGTNTGCT TCAATAGAATGGCTCTTTGGATGACAATGATGAACCTGTTCTAAGCAGACAG
WI-5390	87	CT ---			GCTTTGAGAAATGAAAAGGGAGCCCTGGACCATTCAGGGCTCTTCATCTCTGATTATTTGTGTAT TTATTGTCACATTATTTATCTGCTGTCTCCCTCTGCTGATGCTTGTGTCATGAACAATGAATTC CCAGTGCCTGGCCGATTGCTGGCTCCTAGAGGTGTCAGAAAAAAGTTTGGTGAATAGAAATTG ACGAATGGTTTCAGAAATGAAACCTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87	G A ---			CCTTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCTGTCAGAAATCAATTTAAGCAGT GCAACATTATTTAATTTG/AJAAAGAACTTTGTTCTGAAACTTTGTACTCTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTGTGAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTAGAGTTTCATAACAA
WI-5404	87	G A ---			CCTTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCTGTCAGAAATCAATTTAAGCAGT GCAACATTATTTAATTTG/AJAAAGAACTTTGTTCTGAACTTTGTACTCTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTGTGAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTAGAGTTTCATAACAA
WI-5455b	77	A C ---			TAGGAAAGGGGATGGTATGGCTCTGAGACATTTAAATCTATCTTTCACCACCTCACACTGCCGCCA TATCTCTCAG/CJCCAACACCTCTGTTTCTGACAGCCAGTTCCATCAGTTGATGGGACTATTT GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCATTCA
WI-5545	77	A C ---			TAGGAAAGGGGATGGTATGGCTCTGAGACATTTAAATCTATCTTTCACCACCTCACACTGCCGCCA TATCTCTCAG/CJCCAACACCTCTGTTTCTGACAGCCAGTTTCCATCAGTTGATGGGACTATTT GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCATTCA

WI-5860b	134 A G ---	---	---	ACTCAAGTTGGGGATAAAATCAGAAGTTTCTATGTACAACCTAAATTTTCTAAGATTTTATTGT TTCTTTTATATAAAATATGGAATTTGTTTACCTCCCTAACCAACCTTCTAAGTGAAGAACTAC(AV GJTATAGTGAATCATGTGAAGACATCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-5860	134 A G ---	---	---	ACTCAAGTTGGGGATAAAATCAGAAGTTTCTATGTACAACCTAAATTTTCTAAGATTTTATTGT TTCTTTTATATAAAATATGGAATTTGTTTACCTCCCTAACCAACCTTCTAAGTGAAGAACTAC(AV GJTATAGTGAATCATGTGAAGACATCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-6106	208 C G ---	---	---	GCAACAACCTATTATACCTGATCCAACCCAGGTCTACTAACATTAAATCAACCCCTAACCAATAC TATATTTGTCCTGTTCTGAATTTATTTTCAATTTAGAATCTGATGAGATTTAGCATGGGATAAGTGCAG TGCAGAGATAGTAACACTGCTCTTTTGTCTCCAGGAGTCTCAATGTGAAGTATAATTCTTACAGAG TAATTIC/GJATAGTAGGTCACCACAAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129 T C ---	---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATATTCTGAGAGAAATGTAC ATTGAGTCTTCCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAGGAAAAAACCTAA AAACCTATATTNCTGTCCTTGTGCATCTTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATGT GNAAAATTATCCCTGAAAAATTTTATACCA
WI-6109c	147 T C ---	---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATATTCTGAGAGAAATGTAC ATTGAGTCTTCCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAGGAAAAAACCTAA ACCTATATTNCTGTCCTTGTGCATCTTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATG TGNAAAATTATCCCTGAAAAATTTTATACCA
WI-6109b	147 T C ---	---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATATTCTGAGAGAAATGTAC ATTGAGTCTTCCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAGGAAAAAACCTAA ACCTATATTNCTGTCCTTGTGCATCTTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATG TGNAAAATTATCCCTGAAAAATTTTATACCA
WI-6109a	129 T C ---	---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATATTCTGAGAGAAATGTAC ATTGAGTCTTCCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAGGAAAAAACCTAA AAACCTATATTNCTGTCCTTGTGCATCTTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATGT GNAAAATTATCCCTGAAAAATTTTATACCA
WI-6112	96 T C ---	---	---	AATGCCATACACCTTCCATCATGCTGCATAACTGATTGATTCATATGCTTATTGTTAGCACCTGTC TTCCAACACATGCTGTTTGTCAATGAT/CJGCATATCCCAAGTGCCTTAGACAATGCCCTCCCATAC AGTGAACAGTATTGACTAAACATACCTGTTAAATCAATAAAATTAATCAACTTGGCATAATGCAGG GAAC

WI-6244	103	T C	---	---	TAATTGCACAACCTTACATATCAGGGTTTCTGATTGAAAGGAAGAGAATATTCCTTTCTTTAGTGATT GCTTAATATTAATTCATAATAAGTGCACCATCTCTTCGCTCCTTATAAATGTGTTTAGAAGAAGG AAATTGAGTGTGGGAATTAGCAACAGGAGACATTTTATATACTCCTACAGTGGGGGAAGACTT CCTATTTCTTTCCCAAGGATGGATACATTTCTAC
WI-6268	124	C T	---	---	CTGGCCTTATAATCCCAAGTTTAGGATTAATCTTACCCCAACTTAATAGACTTCCAGACAGTTGCAGTT GTCTACAAGATTTCCTCCTAGTAGGGCTTTGGGTGTGGCACCGTTTGGCTCATTC/C/TACTCTCCCT GGGTCTTATTGACTTTCAGGGAGCCTAGAAAGAGCTGGACAAAACCTGCTTCTTTGCAGAAAGAGTCG GGTTCCAAAGATTTCGTACGATTTTATA
WI-6336b	234	C T	---	---	AGGTGCCATTTAATCCATTCAAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTACATGTTTCTTATAAGACATACAGTTTAACTAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTATAGATCACATGAAATGGACCATGTG GTACCCCGAGTGCATTATGCTTGGTAGAGCC/C/TTGAGGACACTGACAGT
WI-6336	234	C T	---	---	AGGTGCCATTTAATCCATTCAAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTACATGTTTCTTATAAGACATACAGTTTAACTAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAAATAGATCACATGAAATGGACCATGTG GTACCCCGAGTGCATTATGCTTGGTAGAGCC/C/TTGAGGACACTGACAGT
WI-6381	92	C A	---	---	TTGGATACAAAAATTCAGTTACACAATCAGTAGCATTCACAAATTAGTTATGAGTATTTATACAATTA CAAAAATGNTTCATGTTTAAACAA/C/A/GTATTTTAAAGCTCAAAACATTTTAAACAGGCACAAT ATTCTAANGGCATATGCATTCACCATGGGCTTTTGAATGTCCTCACTCCCACTTCCACAATCAAAATC TACAGANGCGGCAAAAGATCAGAGTTCAG
WI-6436	198	C G	---	---	GGTTGAGGCATTGGGAAAGGCAGAAATTTAGGCAGTAGAAAATGGACATTTTAGGAAAAGAGAAGT TCAGAGGCAAGTCATGACAGACAGGAAATACAAAGCTTAGGAAGACAGTAGTCTGTGGTTGAA ATTTGGTGTCAATAAAGAAGTTTAGACTTTGGTGGTTGTAGTAGTTGTAGTAGGAGCGTT/C/ G/ATTGGGTGATTCCACAGACAAGGTGATGTTCTAAGATTTGATATTTATTGT
WI-6449	186	C T	---	---	GAGGCCTCTTTGCTTTTCCCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGCTGATTGGTGGTGTCTACACTGCCAGATTGTTAAATATTTTGAATAATC GTATCTGGTTCTATTTCATCTGCATTCTCTGATCTTATGCTGGCTCTATT/C/ATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCCCTAAATTTTCTGTGGTGTATTATA
WI-6449	186	C T	---	---	GAGGCCTCTTTGCTTTTCCCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGCTGATTGGTGGTGTCTACACTGCCAGATTGTTAAATATTTTGAATAATC GTATCTGGTTCTATTTCATCTGCATTCTCTGATCTTATGCTGGCTCTATT/C/ATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCCCTAAATTTTCTGTGGTGTATTATA

WI-6463	72	T C	---			GCTGGAGAGAAAGACCTCCAAAGAAAGAACTAAATCAGAGTCTCTTGAGCAAGAGGAAATTGAAA AGAACAT/CTGTAAGAAATTAAGTAGAACTCAAGAGAGCCAAAGTCCCAATTTGTGTCATTA TAAGAAATATTTGAATGGAAATCTTAAGAAATGATTTTATTGATCAGTTAAATGTTCTTCTCTCCTC CAGTCCCATTTATATGACATTCGGATGCTG
WI-6474b	76	C T	---			AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAATGTTATAGAACTTCAGAGGANAC AGAGGCAAA/C/TGTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTGAAAGGCACAGAGAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACATAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6474	76	C T	---			AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAATGTTATAGAACTTCAGAGGANAC AGAGGCAAA/C/TGTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTGAAAGGCACAGAGAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACATAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6478b	175	T A	---			GAACTCAATTAACTTGCACACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGAATGCCACGCTTCGAGGCCGTGCTATATGCTTTATTTTGTA CACTGTCTATTTACCTCCCTCCCAATAGTGGAGAAATCAGAGT/A/GCTCCTTGTGAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6478	175	T A	---			GAACTCAATTAACTTGCACACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGAATGCCACGCTTCGAGGCCGTGCTATATGCTTTATTTTGTA CACTGTCTATTTACCTCCCTCCCAATAGTGGAGAAATCAGAGT/A/GCTCCTTGTGAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6559	149	G A	---			CACATTTTGAATGCAACTGAGAAANTGGTTTNTAGGCCCTACCTTTATTTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAAGGCAACAATCTGATCATTTTATAGGNTCCCAAGCCCA TTAGCAATATCTTA/G/A/TTCAAAATTTTAAAAAGAGAACAGGAAATAAGGAAGGCCCTAACAGAGGAG TTAAATAATTGTGCAAAACTTATCAGTTCTTC
WI-6564b	54	G A	---			TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCTCTATGC/G/A/CACTGGCTTTG TAGGCATTCACATCATATGCTGTGCTCTGAAATCTCAATTAATTTCTCTNCCTATTCCTTTTCCAT GCTCTGCCTCATTTNCTCAGAAATGAAAGGCAATGATTATNAATTTTGTGTTGGGCTGTGTAAAG GTTCTTGGCAGGAGAACATGCATATGACTTTAAAAATAAGACCAACA
WI-6564	54	G A	---			TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCTCTATGC/G/A/CACTGGCTTTG TAGGCATTCACATCATATGCTGTGCTCTGAAATCTCAATTAATTTCTCTNCCTATTCCTTTTCCAT GCTCTGCCTCATTTNCTCAGAAATGAAAGGCAATGATTATNAATTTTGTGTTGGGCTGTGTAAAG GTTCTTGGCAGGAGAACATGCATATGACTTTAAAAATAAGACCAACA

WI-6608b	46 C	---	---	CTAATCACAGTAGCACTGAACATGGCTCTAGTAGTGAGTGGCCCTCAGT[C/- JAGTTACGGCAGCTAAAGGGAGGGGATTTCTCTAGTCTCTCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTGAACCTCCAGCACTAG GTAAACTGCAAAAAAGAAAAACACCTGTGCCCAGGCACTAGCTACAAGGCCACACCAAGAAAAAGGAA AGC
WI-6608	46 C	---	---	CTAATCACAGTAGCACTGAACATGGCTCTAGTAGTGAGTGGCCCTCAGT[C/- JAGTTACGGCAGCTAAAGGGAGGGGATTTCTCTAGTCTCTCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTGAACCTCCAGCACTAG GTAAACTGCAAAAAAGAAAAACACCTGTGCCCAGGCACTAGCTACAAGGCCACACCAAGAAAAAGGAA AGC
WI-6666	68 C A	---	---	GTTAGACAGTATCCAGCAAAAAAGGTTATTTTATACCTCTACTTTTCCAAAACGAGGAAACCTCCCC A[C/A]AAATCCCATCAACACACAGTCATGCTGGAAGGCATCTGTCTTACTCTGTGGTTTCATGTAA ATGTTGGGGTGACTCATTCGGCTCTCTTCTCAAGTCCAGGCTCTTGGGTAGACCAAAAACTA ATACAAATGTTAGGACACACAAGAGA
WI-6670b	120 A G	---	---	AGATTAACATAATTATCTAGGGCCATTGTAGGGTNGGAGGAGTGTCTTCTATCTGCAGCCAAA CAGAAATCTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTAGCCA GCATTGCCATTGAGGCGGAGTCAGGGTTGTGGGCCAGAACTTAGACAATTTGGGGAATTCGA AAAAAAAAGAAATACAGAAATTGTAAACACAGACACAGAAATCTTAGAAGGGAT AGATTAACATAATTATCTAGGGCCATTGTAGGGTNGGAGGAGTGTCTTCTATCTGCAGCCAAA CAGAAATCTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTAGCCA GCATTGCCATTGAGGCGGAGTCAGGGTTGTGGGCCAGAACTTAGACAATTTGGGGAATTCGA AAAAAAAAGAAATACAGAAATTGTAAACACAGACACAGAAATCTTAGAAGGGAT TTTGAAAAATAAATTCATGCACCAATGTTTAACT[C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATAAAACGTTTACAAATAAGTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCAATTAATCGATTGTTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6670	120 A G	---	---	TTTGAAAAATAAATTCATGCACCAATGTTTAACT[C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATAAAACGTTTACAAATAAGTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCAATTAATCGATTGTTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704c	33 T C	---	---	TTTGAAAAATAAATTCATGCACCAATGTTTAACT[C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATAAAACGTTTACAAATAAGTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCAATTAATCGATTGTTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704b	33 T C	---	---	TTTGAAAAATAAATTCATGCACCAATGTTTAACT[C]AACCTCACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATAAAACGTTTACAAATAAGTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCAATTAATCGATTGTTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28 T C	---	---	TTTGAAAAATAAATTCATGCACCAATGTTTAACT[C]AACCTCACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATAAAACGTTTACAAATAAGTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCAATTAATCGATTGTTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

WI-6710	106 G A ---	---	---	CCATGGACAGTTTAAITAGGAAGCTTCGACTTGTAGATAACAGAGGAAGTCCAGTTATCTACCT ATTCTTAAACACATTTTGTAGGCTGGAATGATCCCG[G/A]TAGTAAACCTCAACATCCACACCT GCATAACATCGCTCCCAAGTGACTATTTACTGAGTCGACACAGGATGTCACCAGTGAGCCTC ATCTCCAGTCCAATGGAGGAGTTGACTTAGACCTTCCTTGGACAGGAAGGGTC
WI-6766b	148 G C ---	---	---	AAACAAATGGTGCAATGCATAATTTTGTGGTCACAGTATAAACAATACAAATAGTTCATATAAC ATTGGATATGGACAAAAATACACANGATCCTTTCTTTGTCTACGGAAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACAGTGGAGNGAACTTACCCAAATCCAGTTCCTTCTTC
WI-6766	148 G C ---	---	---	AAACAAATGGTGCAATGCATAATTTTGTGGTCACAGTATAAACAATACAAATAGTTCATATAAC ATTGGATATGGACAAAAATACACANGATCCTTTCTTTGTCTACGGAAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACAGTGGAGNGAACTTACCCAAATCCAGTTCCTTCTTC
WI-6787b	97 A G ---	---	---	ACAGATAAAAGTCTTTATCCCTGTATGTTTACATAAGAAAGTCTTTACAGACTTTTTTTTATACA ATACTTGTGCAGCAATGTTCAAATTTTAC[G/A]GTTTTACTGCATAAGATATCTTCATGTACAACTGT ATGCTTTGTCTCTTGGAGGACGCGTTAAAGACCTATGATAACACACATCCACATGACAAAGGA GAGTGCAATAGGGCAGAGTAGANTACTCACAGGAAAGAGTAAATTCAGGT
WI-6793	105 C G ---	---	---	GAACCCACAGGTCCTGTTATTTTAAAGGAGCATTTACATTATGATAGCAAGTTTCAACACATTCA TCAACAAGGCGGCTTCAAATCAATCAGTCAACCCCG[G/G]GAGTTAGAAAGTAGAGTCATGAGGAA GAGCTGCTTGGCTGAGGAAGTAGGGTTAATGCCCTCTAATCCCGGAAAGGGGAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACCAGTTTCTCATCACAGGTAAAAAGGCAAC
WI-6810b	37 T C ---	---	---	CACAATAATAAATCACTCCCTACCTTGAAACCTTTAT[C/J]AGAAGCAATTTTAAITTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTAGTCTGTTACGNGCCAAAGGATAAGGCTGAACAATA AATTAAACCTTTAAATGTCTATGNACAAGTACAATTTCTTTTGTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6810	37 T C ---	---	---	CACAATAATAAATCACTCCCTACCTTGAAACCTTTAT[C/J]AGAAGCAATTTTAAITTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTAGTCTGTTACGNGCCAAAGGATAAGGCTGAACAATA AATTAAACCTTTAAATGTCTATGNACAAGTACAATTTCTTTTGTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6817b	145 C A ---	---	---	GCATGATTAAACAGTGCAGAAAAATACCAAGTACATTTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACACATCATCACTAACTCAACAATGTAGCT GCAGGGTAAAC[C/A]TTGTGGATACCTGTGTGCTCTACTNGCCTCCAAAGGCATTCAGGGGATCA AAGATGTTGGACACCTTGTGTTCAAATCTTGTTTCAGGTGCGGCTGTGCAG

WI-6817	145	C A ---	---		GCATGATTAAACCAAGTCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACACATCATCACTAACTCAACAATGTAGCT GCAGGTAAC[C/A]TGTGGATACCCCTGTGTGCTCTACTNGCCCTCCAAAGGCATTGAGGGGATCATCA AAGATGTTGGACACCTTGTTCAAATCTTGTTTCAGGTGCGGCTGIGCAG
WI-6819b	221	C -- ---	---		GATGAAAGCCATTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAACACATTTAGTAC CATCATGTCAACCCTGAATGCCAGCAATACCTCGACTTTTACACAGCAGGAAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTT[G/T]CATATACAAAATTTCTGCTATTTTG CTTTAGCAACACAGCAATAACTTTTGTTTCTCTATATGACACCTAATATCCAG
WI-6819a	175	G T ---	---		GATGAAAGCCATTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAACACATTTAGTAC CATCATGTCAACCCTGAATGCCAGCAATACCTCGACTTTTACACAGCAGGAAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTT[G/T]CATATACAAAATTTCTGCTATT TTGCTTTAGCAACACAGCAATAACTTTTGTTTCTCTATATGACACCTAATAT
WI-6826b	154	A G ---	---		GCAAAAGCTTTATTGGCTCCCAACAAATTATCCCTTTTAAAACTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTTAAGAACCATATAAATAC ATGCAAAACCTTGTACAT[A/G]GAGCTTAAATAATATCAAAATGCAAAATATAGATTGGGTGCACGT TAAGCTGAATTGCAAAATTATGGCAACACACACTGGACTGGGTATACGTTG
WI-6826	154	A G ---	---		GCAAAAGCTTTATTGGCTCCCAACAAATTATCCCTTTTAAAACTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTTAAGAACCATATAAATAC ATGCAAAACCTTGTACAT[A/G]GAGCTTAAATAATATCAAAATGCAAAATATAGATTGGGTGCACGT TAAGCTGAATTGCAAAATTATGGCAACACACACTGGACTGGGTATACGTTG
WI-6857a	122	T C ---	---		AGTGCAAACTATTTTGAACAAAAGTAACTATGAGTCACAGCATTCAGCAAGACATCAGACACGGA AGAGTGAACAATATTCACTAAGTAAATACAGCAGATGAGATGCTCTCACATGAT[C/A]TTAAT TATTCATGCTTTTCAATAGTCTCTTAGTCAACTTTCAGTGAATTTCCACAAATATAGCAGCTCA AACACAAATGCAGGAGCAATGGCAAGTTTGGCAACTGTTTGGGCTAAT
WI-6865	153	G A ---	---		TTATAGAATACTTATGGGGCATACNGTAAATGAAGTCAACCTTAAATCTAAACAACAGCTTG TTTGTTGTTCTGCTGAAATCTCCCTGCTCACAACACAGCCAGCTACTNGGTTTCTTAAAGACGTA ATTTGCAGGCAAACTT[C/G/A]TAGAGCCATTCTGTGCAAGAAGGGAAGGAGGAGCTGTTTGTT TTACCTGTAGTATGAAGATATCTTTGCGGTGTAGAACTGAGCTCAATTA
WI-6909	73	C T ---	---		ATTGAAAACCTGGTTAGCAACAGATAAAATACAATAGAGCCTGGATATAAAAAATGAGAGAAGAATGC AGACTT[C/T]AAGCTTATAGAGAAAGTCAAAAGGAGCAAGTTTGAATCAGATTTTATGATAC GGAAAAAAATTTCCCTTTTTCGCAACAGGATTATTTGGAATAATAAAATCTGCCAGTGCCAAATCAG AAACACCAATTTCCACAATATTGTCATGCCCTAGTTGCCCTATTTTATACATATC

WI-6910b	163 G T ---	---	---	CACTCAAAACCTTTATTCAATTGATTACAAACTGTACAATATTTACAAAGTTTAGGCATTAATCCCA TATTGACATGAATGCTGTGGAGAGTCTAAAAATAAATATGTGGCAGATAGCTTAAATATACACATCAT GGCTCTTTACACTTAAGCCATTACCAATA[G/TTTGAGATGTAATGGAGAAATTTAAATGTGGTAGAAAA GTCAGAGTGGCTGACCAGTCCGGACCTTCCATGTGAATGACTCTTCCTTGGC GCTGTTTTTTTTTTGTTTTTAAAGTGACACCTTGGCCCTGTGGGCATTCTTCACATTATCTTACCC AAAGTGCCCTTTGGGCCAGCCACTGACTGATTTAAACCCAGAAATGTGGTTTTTAAACAATGTGGT CGTGGTGAAATTCAGGTGATTTTNNATTTCTATTTGGTAGTATTTTCAGATTTTCCACAAAGAACATG TATTGCTTTTGTAAATTTGAAAAAAAATCAACACAGGATAGTAAAGATAT
WI-6915	144 A ---	---	---	CAATCAAAAGTTCCAAGTTTCAAGCTGGGATGAAAGCCAGGCTCTCTGACTTGCACCTGTGCAC ACTGGATTTNCCTCTGATCCAGCTGCAGCCTCCCATAGAAGTTCACCTTAAATTCATGTCCCATG CTTTGCTTGGTCCCTGTGAGGAAAGGGTCAAGTAAAGGTT[C/AACCTGTTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTTCCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928b	175 T C ---	---	---	CAATCAAAAGTTCCAAGTTTCAAGCTGGGATGAAAGCCAGGCTCTCTGACTTGCACCTGTGCAC ACTGGATTTNCCTCTGATCCAGCTGCAGCCTCCCATAGAAGTTCACCTTAAATTCATGTCCCATG CTTTGCTTGGTCCCTGTGAGGAAAGGGTCAAGTAAAGGTT[C/AACCTGTTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTTCCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928	175 T C ---	---	---	TTTTATGAACATTTTCAGATTCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAAATTCCTCAATCCTAGGTAGATATCAAGTTACAAANTAC AAGTGCCGNTAATTAACATATAGGTAGTATATTAAACAAAATGNGTTTTTNGCAAATTTATGTGAAAT AAGGCTTTAACCAAAGC
WI-6955b	79 G A ---	---	---	TTTTATGAACATTTTCAGATTCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAAATTCCTCAATCCTAGGTAGATATCAAGTTACAAANTAC AAGTGCCGNTAATTAACATATAGGTAGTATATTAAACAAAATGNGTTTTTNGCAAATTTATGTGAAAT AAGGCTTTAACCAAAGC
WI-6955	79 G A ---	---	---	AAACTAAAAACCCCTTATTGTCTCCAAGTGTGGGCAAAATAGAAAAAT[C/G]TTTCAATTACATTAGG AAATCGGGTGGATAACGGAGTATAGTTATTCACATTAAGAAGCATTCCAGTCAAAATAATCACAATA ACAAATTCAGATTGCTTGGATCTGGTCATTTATGGCTTGAAGAAGTGGATTTGAAACCCACTTTAGG CTAAATAAATGTATATGAATAATGCATAGACTGTGTATCTAGAAAATCATGC
WI-6957	47 C G ---	---	---	ACTTCTAGTGCCTCTGTACCACCACTCTAATGCCCTGTGGTGGCCGACCTCTCTGATGTCCGTAGGCCT TAAATCTGCCTGGCGTCCCTCCCTCTGTCTTCAGCACCCAGAGGAGAGAGCGGCGAGTTCCCTG CAGGAGAGAGGAGGGGCTGTGGACCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCTGACT CTCTCCTGATGGTGGGCCCTCTGTGCTCTCTCTCTTCG[G/TTGCGGATC
WI-6996c	242 G T ---	---	---	

WI-6996b	242	G T	---		ACTTTAGTGCCTCTGTTACCAACACCTCTAATGCCTCTGGTGGCGCACTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGGTCCCTCCCTCTGCTTTCAGACCCAGAGGAGGAGAGCCGGCAGTTCCTTG CAGGAGAGAGGGGCTGCTGGACCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGCTCCTGACT CTCTCCTGATGGTGGCCCTCTGCTCTTCTCTTCCGCTGCTGGGATC
WI-6996	228	T G	---		ACTTTAGTGCCTCTGTTACCAACACCTCTAATGCCTCTGGTGGCGCACTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGGTCCCTCCCTCTGCTTTCAGACCCAGAGGAGGAGAGCCGGCAGTTCCTTG CAGGAGAGAGGGGCTGCTGGACCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGCTCCTGACT CTCTCCTGATGGTGGCCCTCTGCTGCTCTTCTCTTCCGGTGGATC
WI-7021b	112	G A	---		TGGGAGGACAGGGAGATGCTGCAGTTCCTCAAAAGAGAGGTTTCTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGTCTGAAAGCCACAGACAATATGGTCCCAATG/AJCCCGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTTCCGTTCCACATCCACACAGCAATCCAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7021	108	A G	---		TGGGAGGACAGGGAGATGCTGCAGTTCCTCAAAAGAGAGGTTTCTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGTCTGAAAGCCACAGACAATATGGTCCCAATG/AJCCCGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTTCCGTTCCACATCCACACAGCAATCCAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7056c	118	C T	---		GGCAGTAGGACCAACAGTGTGGGTTCTGCTGGGACCTTGGAGAGCCTGCATCCAGGATCGGGTGG CCCTGCAGCTCTCCACCTCACCCTCCTCATGACAGCGCTAAACGTTGGTGA/C/TGGTTGGAGCCTCT GGGCTGTTGAAGTCACCTTGTGTGTTCCAAAGTTCCAAACACAGAAAGTCATTCCTCTTTTAA ATGGTCTTAAGTTCAGCAGATGCCACATAAGGGGTTTGGCATTGATA
WI-7056b	118	C T	---		GGCAGTAGGACCAACAGTGTGGGTTCTGCTGGGACCTTGGAGAGCCTGCATCCAGGATCGGGTGG CCCTGCAGCTCTCCACCTCACCCTCCTCATGACAGCGCTAAACGTTGGTGA/C/TGGTTGGAGCCTCT GGGCTGTTGAAGTCACCTTGTGTGTTCCAAAGTTCCAAACACAGAAAGTCATTCCTCTTTTAA ATGGTCTTAAGTTCAGCAGATGCCACATAAGGGGTTTGGCATTGATA
WI-7091b	153	A C	---		AATTCGCTGAAAAGGAACCTACCTATCCCTACATTTACCTTACTAATGTCTCTTCTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTATAGTCTCTATAAATAGTATTCCTCAATCACTGTG CTTAATTTAAATAGCATT/AJCTCTTATCATTTATCAGCCTTTTATGTATTTCCAAAGTAAATATTA ACATATTATTCATTGGTCTCTTTTATCTGTTCTATATGAATGCTAT
WI-7091	153	A C	---		AATTCGCTGAAAAGGAACCTACCTATCCCTACATTTACCTTACTAATGTCTCTTCTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTATAGTCTCTATAAATAGTATTCCTCAATCACTGTG CTTAATTTAAATAGCATT/AJCTCTTATCATTTATCAGCCTTTTATGTATTTCCAAAGTAAATATTA ACATATTATTCATTGGTCTCTTTTATCTGTTCTATATGAATGCTAT

WI-7136	58 TC ---	---	TGTGAAGCCACATTTTCCAACATGAGCCTCATGAAGCCAACTAAGTGTATTGAAGCTGT/CJAATTC TCTCAATAACTCAGTGTAGCACTTTAAGTCTGAAGGACGACCAACATGAAAAAGAGCATATCAATGTG GTGAGAAAGGGAAGGGTGGCTTTTAATTTATTTCTTCATCTTTATAACAAGAAAGNNNNIN NNNGTAGCTTCTATATAIG
WI-7146c	210 AG ---	---	GGGACGCCCTGTTGTTTGGCTCAAATTTGGGTTGTTGGTCACATGGAGCTCTCCATTTCGTTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGTCTCTCTGTTGCCCCCAAGCCCCATGCCCTGCCG TGGTGGCAGCTGGGGCTGTGGATGGAGGGTCCCAACATGGATGTGTGGCCCTCTCCGGCATGOC AACGC[AG]GTTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAAATTA
WI-7146b	210 AG ---	---	GGGACGCCCTGTTGTTTGGCTCAAATTTGGGTTGTTGGTCACATGGAGCTCTCCATTTCGTTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGTCTCTCTGTTGCCCCCAAGCCCCATGCCCTGCCG TGGTGGCAGCTGGGGCTGTGGATGGAGGGTCCCAACATGGATGTGTGGCCCTCTCCGGCATGOC AACGC[AG]GTTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAAATTA
WI-7146	202 GA ---	---	GGGACGCCCTGTTGTTTGGCTCAAATTTGGGTTGTTGGTCACATGGAGCTCTCCATTTCGTTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGTCTCTCTGTTGCCCCCAAGCCCCATGCCCTGCCG TGGTGGCAGCTGGGGCTGTGGATGGAGGGTCCCAACATGGATGTGTGGCCCTCTCCGGCAT[GA]]CCAACGCAGTTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAAATTA
WI-7153	161 AT ---	---	ATATTACAACTGCTTTTAGCTGATCTTCCATCCTCAAATGACTCTTTTTTCTTTATATGTTAACATA TATAAATGGCAACTGATAGTCAATTTGATTTTATTCAGGAACATCTGAAATCTGCTCAGAGCCT ATGTGCATAGATGAAACNNNNNNIN[AT]AAAAAAGTTATTTAACAGTAATCTATTTACTAATTAT AGTACCTATCTTTAAAGTATAGTACATTTTACATATGTAATGGTATGTTT
WI-7155	156 TG ---	---	TAGAATAGATCGGGTCATATCTCTTTGGCTCTGGTCTCCAGCCCTCAIGTTGGCATCACATAT GCGTGCATGCCATTAAACACCAGCTGGCCCTACCCCTATATGATCCTGTGCTCTAAATTAATACAC CAGTGGTCTCTCCCTCCCTGT/GTAAAGACTAAATGCTCAGATGCTGTTACGGATATTTATATTCTAG TCTCACTCTCTGGCCACCCTTCTCTCTCCCATCCCACTCCAG
WI-7169b	161 AG ---	---	AGCTCCACCAGATGCAGATTTGTGTTTGTGTTTCTGTTATCTGTCACACAGCTTAAACATGTAT GCTTTTTCAGATAACAGTTGCTAGCCAAAGCCCATCAAGTGTCTGAAATTCATATTTGGTTATGCAAA ACAGCAAACTTTTATTAAGTAGAT[AT]G/GGAGAAATATGTTTAAAAATATTAGGAATCCTAGACCATA TTTTCAAGTCATCTTAGCAGCTAGGATTTCTCAAAATGGAAAGTGTATATATA
WI-7175b	194 CT ---	---	CTCCTAGACTAGTGCCTTACCCTTTATTAATGAAGTGTGACAGGAAGCCCAAGGCAGTGTCTCCACCA ATAACTTCAGAGAGTCAAGTTGGAGAAAAATGAAGAAAAAGGCTGGCTGAAATCACTATAAACCATC AGTTACTGGTTTCAGTTGACAAAAATATATATGTTTACTGCTGTCTATGTCCTATGCCTA[CT]AGAT AATTTATTTGATTTTGAATAAAAAACATTTGTACATTCCTGATACIGGG

WI-7175	194	C T	---		CTCCTAGACTAGTGCTTACCTTTATTAACTGTGACAGGAAGCCCAAGGAGTGTCTCCTACCA ATAACTTCAGAGAAAGTGGAGAAATGAAGAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAATATAATGGTTTACTGCTGTCATTTGCCATGCCTA/C/TJAGAT AATTTATTTGATTTTGAATAAAACATTTGTACATTCCTGATACTGGG
WI-7178b	273	G A	---		TGATCAGGTCAGGGACTTGGACAGGAGTCAGTCTGGCTTTTCTCTGAGCCAGCTGCCTGGAG AGGGTCTCGCTGTCAGTGGCTCCTAGGGGAACAGACCAGTGACCCAGAGAAAGCATAACACCA ATCCAGGGCTGGCTCTGCACCTAAGAGAAATTTGCACTAATGAATCTCGTTCCCAAGAACTACCC CCTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7178	273	G A	---		TGATCAGGTCAGGGACTTGGACAGGAGTCAGTCTGGCTTTTCTCTGAGCCAGCTGCCTGGAG AGGGTCTCGCTGTCAGTGGCTCCTAGGGGAACAGACCAGTGACCCAGAGAAAGCATAACACCA ATCCAGGGCTGGCTCTGCACCTAAGAGAAATTTGCACTAATGAATCTCGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7182b	116	A C	---		GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAG AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCCACTCTGAGCCTA/C/TCTCTCCTCTATTT TACTTGAGGCTGCCAATTACCAGCCCAAGTTTCAGCTCAAGAGATGCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGATGGCAGCTATTCTGAGCCTAGTACCCCAATT
WI-7182	106	C A	---		GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAG AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCCCA/C/ATCTGAGCCTATCTCTCCTCTATTT TACTTGAGGCTGCCAATTACCAGCCCAAGTTTCAGCTCAAGAGATGCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGATGGCAGCTATTCTGAGCCTAGTACCCCAATT
WI-7191b	273	T A	---		ATAATTGCTGTTTCTAGCCTGGCAAGATATTTTCAATAAAGAGGGATAACAATGCTGATTACTAC CTTTTAAATAATTTAGATAAATGCACAGCACACAGACCACATCTAAGCATTAGTGATGGTAGC TGATGTCAGCTTCATGTGGATTTTAAAGCACCTAGAAACAATGAAGCTTCTTGGCATATTTAAGGAG CTCCCAAAATGTGTACCTATTAAATTGTAACCTCAGCAAGTAGAAGACCATT
WI-7199c	112	T C	---		CCAGTGGTGAACAGAACCTCCCAAAATTTGAGTTGCACCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTGAGCTCCTGACCTATGAGCT/CJGGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATAGCATTCCTTAATGTTTGGTGGTCTGAAATTCCTCTTATTAT AGTCTATAGTTTACTCCTCAGTTCCTCACCATCATCATCTGTCTAA
WI-7199b	112	T C	---		CCAGTGGTGAACAGAACCTCCCAAAATTTGAGTTGCACCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTGAGCTCCTGACCTATGAGCT/CJGGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATAGCATTCCTTAATGTTTGGTGGTCTGAAATTCCTCTTATTAT AGTCTATAGTTTACTCCTCAGTTCCTCACCATCATCATCTGTCTAA

WI-7216c	237	T C ---				TGACACTAACACTCTTAATTCAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGCTCTTCTCCCC AAGGACAAAATGTAGAAAGATGTGAGATAACTTACTAAGATCCCTCCAGAAAAATACGTATGT TTAAAAACCCCTTCTGCTATACATAGGAAAAAGACACACATCCACCTAAATTTGACTGACTGTTTAA CTGTCAATTCCTCTGAGGCTAACACAGTTTGTTTTC/CJCTTGTAATCACTT
WI-7216b	237	T C ---				TGACACTAACACTCTTAATTCAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGCTCTTCTCCCC AAGGACAAAATGTAGAAAGATGTGAGATAACTTACTAAGATCCCTCCAGAAAAATACGTATGT TTAAAAACCCCTTCTGCTATACATAGGAAAAAGACACACATCCACCTAAATTTGACTGACTGTTTAA CTGTCAATTCCTCTGAGGCTAACACAGTTTGTTTTC/CJCTTGTAATCACTT
WI-7220b	147	A T ---				AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCACCATTAATTTGCTCTTTAAGCTGGCAACCCCA TCATTAATAGCACATAAAATAGCAATCATATGGGTAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAATTAATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTTAGTGTTT
WI-7220	140	A T ---				AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCACCATTAATTTGCTCTTTAAGCTGGCAACCCCA TCATTAATAGCACATAAAATAGCAATCATATGGGTAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAATTAATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTTAGTGTTT
WI-7226	232	C ---				GATCGAATTTTTCAGATGATTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATGTATA TACATATCACCTCCTATTCTTTAAATTTTGTAAATGTTAACTGGCAGTAAGCTCTTTTGTGATCAT CCCTTTCCATATAGGAAACATAATTTGAAGTGGCCAGATGAGTTTATCATGTGAGTGAAAAATAA TTACCCACAAATGCCACCAGTAACCTTAACGATTCCTTCTTGGGGTTT
WI-7228b	254	G A ---				ATAGCTCCAGATTACAAAGGCCAAGGTAATAGAAATGCATACCAGTAATTTGGCTCCAATCATAA TATGTTCCACCAGGAGATTACAAATTTTGTCTCTTGTCTTTGTAATCTATTTAGTTGATTTAATTA CTTCTGAATAACGGAAGGATCAGAAGATATCTTTTGTGCTAGATTGCAAAATCTCCAATCCACA CATATTGTTTTAAATAGAAATGTTATCCAATATTAAGATATCTCAATGTT
WI-7228a	163	G A ---				ATAGCTCCAGATTACAAAGGCCAAGGTAATAGAAATGCATACCAGTAATTTGGCTCCAATCATAA TATGTTCCACCAGGAGATTACAAATTTTGTCTCTTGTCTTTGTAATCTATTTAGTTGATTTAATTA CTTCTGAATAACGGAAGGATCAGAAAG/AJATATCTTTTGTGCTAGATTGCAAAATCTCCAATCC ACACATATTGTTTTAAATAGAAATGTTATCCAATATTAAGATATCTCAA
WI-7233c	213	C T ---				CGATCGTACTGCCAGTAGCATTTGCTGTCTGCCGGCTTTGTTGTACATTCATTTTCAATTTGTACA GATGTGAATTTTATCCTTGTCACTAATTAATTTAAATTTATTTCTAGGAAGTCAAAAAATAA TAAAGGTTGAGCCCTCTACTTTCTTCTGCCACCCTTTTGTGGCAATATTAAGTGAACCTGCTAATA GTGTAAGTATCTGTGCACAAAACCACTGCCAGATAACCCAGAGGGGCTG

WI-7233b	213	C T	---			CGATCGTACTGCCAGTAGCATTTGTCTGTCTGTCGGTCTTTGTACATTCATTTTCAATTGTTACA GATGTGAACITTTATTCCTTGTCACATAATTATTTAAATTTATTTAGGAAGTCAAAAAATATAA TAAAGGTTGAGCCCTCTACTTTCTTCTTGCCACCTTTTGTGCAATATTAAGTGAAGTGTAAATA GTGTAAGTAC/TGTGCACAAAACCACTGCCAGATAACAGAGGGGCTG
WI-7233	211	T C	---			CGATCGTACTGCCAGTAGCATTTGTCTGTCTGTCGGTCTTTGTACATTCATTTTCAATTGTTACA GATGTGAACITTTATTCCTTGTCACATAATTATTTAAATTTATTTAGGAAGTCAAAAAATATAA TAAAGGTTGAGCCCTCTACTTTCTTCTTGCCACCTTTTGTGCAATATTAAGTGAAGTGTAAATA GTGTAAGT/CIACGTGCACAAAACCACTGCCAGATAACAGAGGGGCTG
WI-7238	128	T C	---			GCGTCTACAGACAGCTCACCATTTTGTCTGTATCTGTAAACACITTTTGTCTTGTAGTCTTTTCTTG TAAATTTGATGTTCTTTAAATCGTTAATGTATAACAGGCTTATGTTTCTGTTTGTTC/CJCGT CTGTTTAAACAGAAATAAAGGAGTGAAGTCTCTTTTCTCATTTCAAAGTTGCTACCAGTGTAT GCAGTAATTAGAACAAGAAACAATTCAGTAGAACAATTTATTGCTTA
WI-7252f	520	T C	---			CCACAGGATCCAGCCAAAGCGGCCCTCCGGCCCTTCCACTCGCAGCAGCGCGGGGACAGAG GCCTGCCCCGGGCGCCAGCCCCGGCCCTGGGCTGGAGGCTGCCCCGGCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCTCTCCA
WI-7252e	552	T C	---			CCACAGGATCCAGCCAAAGCGGCCCTCCGGCCCTTCCACTCGCAGCAGCGCGGGGACAGAG GCCTGCCCCGGGCGCCAGCCCCGGCCCTGGGCTGGAGGCTGCCCCGGCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCTCTCCA
WI-7252d	540	T C	---			CCACAGGATCCAGCCAAAGCGGCCCTCCGGCCCTTCCACTCGCAGCAGCGCGGGGACAGAG GCCTGCCCCGGGCGCCAGCCCCGGCCCTGGGCTGGAGGCTGCCCCGGCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCTCTCCA
WI-7252c	552	T C	---			CCACAGGATCCAGCCAAAGCGGCCCTCCGGCCCTTCCACTCGCAGCAGCGCGGGGACAGAG GCCTGCCCCGGGCGCCAGCCCCGGCCCTGGGCTGGAGGCTGCCCCGGCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCTCTCCA
WI-7252b	540	T C	---			CCACAGGATCCAGCCAAAGCGGCCCTCCGGCCCTTCCACTCGCAGCAGCGCGGGGACAGAG GCCTGCCCCGGGCGCCAGCCCCGGCCCTGGGCTGGAGGCTGCCCCGGCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCTCTCCA

WI-7252a	520 T C ---			CCACGAGATCCAGGCCAAGCGGCCCTCCGCCCTTCCACTCGCAGCAGCCGCGGACAGAG GCCTGCCCGGGCGCGCCAGCCCGGCCCTGGCTCGAGGCTGCCCGGCCCTCTGTCTCTGTCCG GACACTCTAGAGAACGCGCCCTAGAGCTGCCCTGGAGCTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCCTCCA
WI-7265m	252 T A ---			AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATATATGTAATAATAACGATCTCTT AAAATACCAACAGTTGTATTTTCTTTAAGGAGTAAAGATTGGCTTT/
WI-7265l	231 T A ---			AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATATGTAATAATAACGATCTCTT AAAATACCAACAGTTGTATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265k	121 T G ---			AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTA GTTTAAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATATGTAATAATAACGATCT CTTAAAAATACCAACAGTTGTATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265j	174 T A ---			AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATATGTAATAATAACGATCT CTTAAAAATACCAACAGTTGTATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265i	227 T C ---			AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATATGTAATAATAACGATCTCTT AAAATACCAACAGTTGTATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265h	80 T A ---			AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTA GTTTAAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATATGTAATAATAACGATCT CTTAAAAATACCAACAGTTGTATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265g	170 T G ---			AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATATGTAATAATAACGATCT CTTAAAAATACCAACAGTTGTATTTTCTTTAAGGAGTAAAGATTGGCT

WI-7265f	231	T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATTATGTAAATATAACCGATCTCT AAAAATACCACAGTTTGATTTTCTTTT/AJ/AAGGAGTAAAGATTGCCT
WI-7265e	227	T C ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATTATGTAAATATAACCGATCTCT AAAAATACCACAGTTTGATTTTTCJTAAAGGAGTAAAGATTGCCT
WI-7265d	174	T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTT/AJ/TATATTATGTAAATATAACCGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCCT
WI-7265c	170	T G ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATTATGTAAATATAACCGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCCT
WI-7265b	121	T G ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATTATGTAAATATAACCGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCCT
WI-7265a	80	T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTT/AJ/TATTTGCCACAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATTATGTAAATATAACCGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCCT
WI-7281b	183	C ---	---	GATCACCCCAGCCACAGCCCTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGGCCAAGC ATCTCCCTGGGAAGTCTTCTGGCCAAAGTCTGGCCAGCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGCATGAAGCATCTCAGACTCTTGGCAAAAACGGAGTCCGAGGCCGCGAG GTGTTGTGAAGACCCTGTTCTGTGGTTGGGGTCTGCAAGAAGGCCTCCTC
WI-7281	171	C A ---	---	GATCACCCCAGCCACAGCCCTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGGCCAAGC ATCTCCCTGGGAAGTCTTCTGGCCAAAGTCTGGCCAGCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGCATGAAGCATCTCAGACTC/AJ/TTGGCAAAAACGGAGTCCGAGGCCGCGG CAGGTGTTGTGAAGACCCTGTTCTGTGGTTGGGGTCTGCAAGAAGGCCT

WI-7282b	159	G C	---			TGTCACCTGGACATTCATTTCTCAGTTGAAGAAGAAAAATTTGAAAAATGTCCTTATGCTTTTAGA GTTGCAACTTAAGTATATTTGGTAGGGTGAAGTGTTCCTCACTCAAAATATGTCAACTNNNNNNNT AGGCCCTTTCATAAAACCAAACT[G/C]TAGCAAGATGCAAATGCATGGCAAATCTGTGCGTCTCCA GTTGGTATCTGAATAGTGTCAACAAATCCACCAAGACAGTGTGAGATTGG
WI-7292	92	T C	---			CTTGATTACTTCCACTGAGGTGGGAGCATCTCCAGTGTCCCAATATATCTCCCCCACTCCACTAC TCTCTCCCTCCACTTCATTTTC[C]/C]TTGTCTCTCTCTAATTCAGTGTTCGAGGCTGACCTTG GGGACAACGTATTATTGATATTATGCTGTTTCTCTCTCCCAATAGAAGAAATAAGTCATGGAGCC TGAAAGGTGCCTAGTTGACTTACTGACAAAAGGCTCTAGTTGGGCTGA
WI-7301f	133	A G	---			AACTATGGCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGGGACCGAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTG[A/G]CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCA ATCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301e	94	T G	---			AACTATGGCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGGGACCGAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGT[A/G]TAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301d	138	A G	---			AACTATGGCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGGGACCGAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAATCA AATTATGGAC[A/C]CATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301c	211	A C	---			AACTATGGCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGGGACCGAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATT[A/C]TAGTGGACAACAGCAA TCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301b	182	C T	---			AACTATGGCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGGGACCGAGGATATGGAA ACCAAGGTGGTGGATATGGTGGTGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA TGACCGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301	88	G T	---			AACTATGGCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGGGACCGAGGATATGGAA ACCAAGGTGGTGGATATGGTGGTGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA TGACCGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG

WI-7301	205 A C ---			AACTATGGCAGTGGTCTGTTATAGTAGTAGAGCGGGTATGGTGGTGGACCCAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGGAGGATATGATGTTACAAATGAAGAGGAATTTTGA CGGTAGTAACATATGGTGGTGGGAACATAATGATTTTGGAAATTACAGTGGACAACAGCAATCA AATTACITGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7314c	49 GA ---			CTCTCCTTTTCTTCAGATCTGCTCTGGGTTTAAITGGGAGGTCA[AG]ATTGTTCTACCTCACTG AGAGGGAACAGAAAGGATATTGCTTCCTTTTCAGCAGTGAATAAAGTCAATTAATAAATTTCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGTCTTCTGTGCACATGAACGCTTCTTTCCAGGA CAGAAATGTAGTCTACCTTTATTTTATTAACAAAACCTGTTTTT
WI-7314b	49 GA ---			CTCTCCTTTTCTTCAGATCTGCTCTGGGTTTAAITGGGAGGTCA[AG]ATTGTTCTACCTCACTG AGAGGGAACAGAAAGGATATTGCTTCCTTTTCAGCAGTGAATAAAGTCAATTAATAAATTTCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGTCTTCTGTGCACATGAACGCTTCTTTCCAGGA CAGAAATGTAGTCTACCTTTATTTTATTAACAAAACCTGTTTTT
WI-7314	36 A G ---			CTCTCCTTTTCTTCAGATCTGCTCTGGGTTTAA[AG]TTGGGAGGTCACTGTTCTACCTCACTG AGAGGGAACAGAAAGGATATTGCTTCCTTTTCAGCAGTGAATAAAGTCAATTAATAAATTTCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGTCTTCTGTGCACATGAACGCTTCTTTCCAGGA CAGAAATGTAGTCTACCTTTATTTTATTAACAAAACCTGTTTTT
WI-7321b	199 C T ---			ACTCAGGGAAGGGATCCCCATTAAAGTGACAAAAGGGTGGGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGACTGCTTTGGCATCCAGGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAAATCAAGNNNNNNNAGGGTGGCACACCCATC[C /T]GTTTGTGGGTGTGGCAGCCACATCCAAGACTGGAGCAGCAGGCTGGCCA
WI-7321	199 C T ---			ACTCAGGGAAGGGATCCCCATTAAAGTGACAAAAGGGTGGGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGACTGCTTTGGCATCCAGGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAAATCAAGNNNNNNNAGGGTGGCACACCCATC[C /T]GTTTGTGGGTGTGGCAGCCACATCCAAGACTGGAGCAGCAGGCTGGCCA
WI-7336b	248 A C ---			AGACATTCTGCTTCCCTGAAAGACTGAAGAAAGTGTAGTGCATGGGACCCACGAAACTGCCCTGGC TCCAGTGAACCTTGGGCACATGCTCAGGCTACTATAGTCCAGAAAGTCTTATGTTAAGCCCTGGCAG GCAGGTGTTTATAAATCTGAATTTGGGATTTTCAAAGATAATATTTACATACACTGTATGT TATAGAACCTTCATGATCAGATCTGGGCAGCAACCTATAAATCA[AC]CA
WI-7338c	221 A G ---			CTCTTTCTCAGCACATTGATGGCAACTAGAAATACAGCAGTTTCAAACCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTCAGAGAAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTTTCTTCTTACACAC[AG]TATACACACAGACATCAGAAAAATTCGT

WI-7338b	125 A C ---	---	CTCTTTCTCAGCACATTGATGGCAACTAGAAATTACAGCAGTTTCAAACCTCACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTTGGCAAAAGGTGCTTTA/C/CCTTG AGCCATTATTTGTGTGAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTTTCTCTTTACACACATATACACACAGACATCAGAAAATTCGTGTT
WI-7338	125 A C ---	---	CTCTTTCTCAGCACATTGATGGCAACTAGAAATTACAGCAGTTTCAAACCTCACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTGAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTTCTCTTTACACACATATACACACAGACATCAGAAAATTCGTGTT
WI-7338	221 A G ---	---	CTCTTTCTCAGCACATTGATGGCAACTAGAAATTACAGCAGTTTCAAACCTCACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTGAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTTCTCTTTACACACATATACACACAGACATCAGAAAATTCGTGTT
WI-7384c	146 T A ---	---	CTCTTTCTCAGCACATTGATGGCAACTAGAAATTACAGCAGTTTCAAACCTCACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTGAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTTCTCTTTACACACATATACACACAGACATCAGAAAATTCGTGTT
WI-7384b	146 T A ---	---	CTCTTTCTCAGCACATTGATGGCAACTAGAAATTACAGCAGTTTCAAACCTCACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTGAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTTCTCTTTACACACATATACACACAGACATCAGAAAATTCGTGTT
WI-7384	145 T A ---	---	CTCTTTCTCAGCACATTGATGGCAACTAGAAATTACAGCAGTTTCAAACCTCACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTGAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTTCTCTTTACACACATATACACACAGACATCAGAAAATTCGTGTT
WI-7388c	106 A T ---	---	CTCTTTCTCAGCACATTGATGGCAACTAGAAATTACAGCAGTTTCAAACCTCACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTGAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTTCTCTTTACACACATATACACACAGACATCAGAAAATTCGTGTT
WI-7388b	106 A T ---	---	CTCTTTCTCAGCACATTGATGGCAACTAGAAATTACAGCAGTTTCAAACCTCACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTGAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTTCTCTTTACACACATATACACACAGACATCAGAAAATTCGTGTT

WI-7388	94 T A ---	---		TGAAATCCTGGGCTCTGGCCTGCTCTGCTAGCTGGTTATTTTACTTTGGCCCCCTCCCACTTTT TGAGATCCATCCCTTTATCAAGAAGT/AJCTGAAGCGACTATAAAGGTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTTGA CTTGCTGCTGCTCCAGAACCTTTCCCCCAAGATGTGTATAGTTATGG
WI-7438	64 A G ---	---		TTAGATTTTAATTGGCAACCAGCAACTCACTGCCACCATCCACTGCAGATCTNCTATTCTCGG/A/GJ GTTGATATGACAAGGAAACCCATTGGAAACCAAGTCTTCAGATTGNCATGTGCAGACAGGCTCCT TGCTGTAGGTGTAGTAGCATGTACACTGTACTGTCTACTGTAAACATAGTTTGTCGTTATTTGTTA TTGGAATGAATATCGCTCCACTGACTTTTACCA
WI-7454b	152 T C ---	---		CCATGATCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCCAAACC CAGTACAACTGAGAAATGAGAGAACCTGATAGCACTGTCTGAATGGCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTTCTT/CJTGTTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTTGTCTACTTCTCAAAATGTTTTGACA
WI-7454	152 T C ---	---		CCATGATCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCCAAACC CAGTACAACTGAGAAATGAGAGAACCTGATAGCACTGTCTGAATGGCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTTCTT/CJTGTTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTTGTCTACTTCTCAAAATGTTTTGACA
WI-7464c	177 G C ---	---		AATTTGAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAATGCATAAATTAATTTTCTATGTA CAACAGAGCCACAGCACAAGAGGGTGGGCATAAGCAGTTGCCAIG/CJCCAGAAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAAAGCAACGTTCCACCAACAATTAT
WI-7464b	168 C A ---	---		AATTTGAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAATGCATAAATTAATTTTCTATGTA CAACAGAGCCACAGCACAAGAGGGTGGGCATAAGCAGTTGCCAIG/CJCCAGAAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAAAGCAACGTTCCACCAACAATTAT
WI-7464a	103 C A ---	---		AATTTGAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAATGCATAAATTAATTTTCTATGTA GTACAACAGAGCCACAGCACAAGAGGGTGGGCATAAGCAGTTGCCAIG/CJCCAGAAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAAAGCAACGTTCCACCAACAATTAT
WI-7499b	134 T G ---	---		CAATTCTCAATCCAACCTAGTCTGTNTGCCTAAACCATCCAGACAAACTCCACTTCGAAGGTTTTA AATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGACATCAGCTTCTTTGAATGCTTCAT /GJTATAGTCTCTTCAATTTAGCAATCAGTGAGGGAATACACTGGCATCATGCCCTTTTTTTAGGA ACTCTGTACAAAAATCCCTTTGAAAAATATAAATTTGGAAATGAGTGATGA

WI-7576b	168 A T ---				AATGATGATGATAATGATGATGACGACGACACGATGATGCTTGTAACAAGAAAAACATAAGAGAGC CTTGGTTCATCAGTGTTAAAAATTTTGAAGGGGCTACTAGTTCAGACACTTTGGAAAGTTTGTGT TCTGTTTGTAAACTGGCATCTGACACAAAAAATGTTGTAAGGCCCTTATCTACATTTCCACCTAC TTTGTAAAGTGAGAGAGACAAAGAAANNNNNNNNNNAAGAAAAATAAAC
WI-7577g	77 T C ---				AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTTGCCTTCCCTTAA AAATATGCAATGCAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACAGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTC
WI-7577p	50 GC ---				AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTTGCCTTCCCTTAA TAAATATGCAATCAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACAGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTC
WI-7577o	157 GA ---				AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTTGCCTTCCCTTAA AAATATGCAATCAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTTACACGATAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGTAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTC
WI-7577n	48 A G ---				AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTTGCCTTCCCTTAA TAAATATGCAATCAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACAGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTC
WI-7577m	84 GA ---				AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTTGCCTTCCCTTAA AAATATGCAATCAATCGATGATGCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACAGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTC
WI-7577l	93 T C ---				AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTTGCCTTCCCTTAA AAATATGCAATCAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACAGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTC
WI-7577k	154 CA ---				AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTTGCCTTCCCTTAA AAATATGCAATCAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTTACACGATAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGTAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTC

WI-7577j	117 A G ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577l	77 T C ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577h	50 G C ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAACCCCAACATAAGTGTTCCTTTAA TAAATAATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577g	157 G A ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTTACAC/GA/JTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACT ATTGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577f	48 A G ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAACCCCAACATAAGTGTTCCTTTAA TAAATAATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577e	84 G A ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGA/JTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577d	93 T C ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATT/JACTTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577c	154 C A ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTTAC/JACGTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACT ATTGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577b	117 A G ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTCAATCTCTGAGGGTTTAGTA[G]ACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGATTTTC
WI-7577	107 G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTCAATCTCTGAG[G]A/GTTTTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGATTTTC
WI-7619q	106 C G ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACT[G]TCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGATGGGGCCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCT CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGGAAACCTATTTC
WI-7619p	150 T C ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTT/CJCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGGAAACCTATTTC
WI-7619o	228 A G ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCTCT CGCTTTCTTCTTACACAGAAACAT/A[G]CACATACCGGAAACCTATTTC
WI-7619n	237 G C ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCTCT CGCTTTCTTCTTACACAGAAACATACACATACCGGAAACCTATTTC
WI-7619m	99 C T ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG TGCCAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGGAAACCTATTTC
WI-7619l	189 T A ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGGAAACCTATTTC

WI-7619k	90 C G ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCC/C/GJCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619j	206 T G ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGCT/GJTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619i	106 C G ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619h	150 T C ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCT TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619g	228 A G ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619f	237 G C ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619e	99 C T ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG TGGCAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCT TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619d	189 T A ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619c	90 C ---	---	ACAAGGCGACTTGAAGAGGACGCGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCC[C/G]CTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	206 T G ---	---	ACAAGGCGACTTGAAGAGGACGCGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTCTCT CGC[T/G]TTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189 T A ---	---	ACAAGGCGACTTGAAGAGGACGCGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCCCTTTTCCAT[T/A]CTTTTCCCTC TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105 A G ---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAAAACAACCAACAGTAA TCTATGTGTTCTGTAACAAATGGGATCTGTCTGGC[A/G]TTAAACCACATCATGGACCAATGTG CCATACTAATGATGAGCAATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTTCCCTTGGACTGTTC
WI-7626c	155 C T ---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAAAACAACCAACAGTAA TCTATGTGTTCTGTAACAAATGGGATCTGTCTGGCATTAAACCACATCATGGACCAATGTGCCA TACTAATGATGAGCATTTAG[C/T]ACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTTCCCTTGGACTGTTC
WI-7626b	28 T A ---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAAAACAACCAACAGCAG TAATCTATGTGTTCTGTAACAAATGGGATCTGTCTGGCATTAAACCACATCATGGACCAATGTG CCATACTAATGATGAGCAATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTTCCCTTGGACTGTTC
WI-7626	144 T C ---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAAAACAACCAACAGTAA TCTATGTGTTCTGTAACAAATGGGATCTGTCTGGCATTAAACCACATCATGGACCAATGTGCCA TACTAATGAT[C/G]GAGCATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTTCCCTTGGACTGTTC
WI-7689c	134 A G ---	---	TCCATAACCGCTGATTCTCAGGGTCTCTGCTGCCGCCCAACCCAGATGGGGAAAGCAGGTGGGC TTCCAGTGGTGTGCTGCCAGGCCAGACCTTCTAGACGCCACCCAGCAAAAGGTTGTTCTCTAA[A/ G]TAAGGGCAGAGTCACACTGGGCAGCTGATACAAATTCAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGTGGTGCCCAAAATAAATGGATTATTAGAAATTCATATGAC

WI-7689b	134	A G ---	---		TCCATAACCGCTGATTCACAGGCTCTGCTGCCGCCACCCACCCAGATGGGGAAGCAGAGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTCCTAAAJA /GJTAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGGTGGCCACAAATAAAATGGATTATTAGAAATTCATATGAC
WI-7689	121	G A ---	---		TCCATAACCGCTGATTCACAGGCTCTGCTGCCGCCACCCAGATGGGGAAGCAGAGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTCCTAA AATAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGGTGGCCACAAATAAAATGGATTATTAGAAATTCATATGAC
WI-7690	45	G A ---	---		TGGAGAACATTCATCTTCCGTCACATTTTCATCAATGAAGATTAGJAJACTGAGATCCAGAGAGG CTGGATGACTTGCTCAAGTTACACGACATGGTAGTGGCAAGAGAGTCCAGAGTCTGGCCCTTGAT GCCAGCTCAGTGCCACAAAGCTCAGTAGGAGGATGTTCCAGTGATGAGGCCACCCAGGAAGCAC AGGTCCAAAGGCTGGTCCACACTTATCAGCAGCAACAACTGTCAAGTTCATCC
WI-7703b	164	T C ---	---		ACAGAAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTAACAGTTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGTTTTCACATTTGGAACAAGTCAGTCAATTCAGATATGATCAAA TGCTATAAACCAAACTGATGTAAGTAAATTCJGGTCTCCTCACTGTTTTTAACTCTAAATTCCT TTCAATTTAGGGTAGCATTTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7703	156	T C ---	---		ACAGAAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTAACAGTTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGTTTTCACATTTGGAACAAGTCAGTCAATTCAGATATGATCAAA TGCTATAAACCAAACTGATGTTJJAAGTAAATGGTCTCTCACTGTTTTTAACTCTAAATTCCT TTCAATTTAGGGTAGCATTTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7743e	106	C A ---	---		TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCCTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCAGGAGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGOCAGCCAGCAGCCAGCTCTCAGCC
WI-7743d	275	C T ---	---		TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCCTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACT TACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCAGGAGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743e	106	C A ---	---		TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCCTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCAGGAGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGOCAGCCAGCAGCCAGCTCTCAGCC

WI-7743d	275	C T ---	---	TTAAATGAGTGTGTTGTACACCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAGCCCCAGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTCTACCTCACTGGGGTCTCTGGGCCCTCGAGCCTCATCCGAGGAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743e	106	C A ---	---	TTAAATGAGTGTGTTGTACACCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAGCCCCAGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATTCGTCTACCTCACTGGGGTCTCTGGGCCCTCGAGCCTCATCCGAGGAGGGTTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743d	275	C T ---	---	TTAAATGAGTGTGTTGTACACCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAGCCCCAGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTCTACCTCACTGGGGTCTCTGGGCCCTCGAGCCTCATCCGAGGAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743c	106	C A ---	---	TTAAATGAGTGTGTTGTACACCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAGCCCCAGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATTCGTCTACCTCACTGGGGTCTCTGGGCCCTCGAGCCTCATCCGAGGAGGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743b	275	C T ---	---	TTAAATGAGTGTGTTGTACACCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAGCCCCAGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTCTACCTCACTGGGGTCTCTGGGCCCTCGAGCCTCATCCGAGGAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743	106	C A ---	---	TTAAATGAGTGTGTTGTACACCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAGCCCCAGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATTCGTCTACCTCACTGGGGTCTCTGGGCCCTCGAGCCTCATCCGAGGAGGGTTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743	275	C T ---	---	TTAAATGAGTGTGTTGTACACCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAGCCCCAGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTCTACCTCACTGGGGTCTCTGGGCCCTCGAGCCTCATCCGAGGAGGGTTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7758	144	A G ---	---	TGACATTTATTCAAAGTTAAAGCAACACTTACAGAAATTTAAAGAGGTTATCTGTTTAAACATTTCC TCAGTCAAGTTTCAGAGCTTTCAGAGACTTCGTAAATTAAGGAACAGAGTGAGAGACATCATCAAGTG GAGAGAAATC/A/GTGTAGTTTAAACTGCAATTAATAATTTTATAACAGAAATTAAGAGTAGATTTTAAAA GATAAAATGTGTAATTTTGTATATTTTCCCATTTTGGACTGTAACTGACTGCC

WI-7765b	126	GC	---	---	ACAGGGGCTTTGGCAGGTGCAGCCCCCACTGCGCTTTGACCTGCGCTCCCTTCATGCATGGAATTCCTCTCATCTGGAACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAGGGTCAAGTATGG[G/C]TAGGGGAAACATTCCTCCTTGAGTCAAAAATCTCAATCTCTCCCTATCTTGCCACCCCTCATGCTGTGTGACTCAAAACCAATCACTGAACCTTTGCTGAGCCTGTAAAATAAAAGTGCGGA
WI-7773b	237	CG	---	---	TTAATTTACTGATTCAGCAAGACCAATCATTTGATCAGATTATTTTAAAGTTTTATCCGTAGTTTTGATAAAGATTTTCTATTCCTTGGTTCTGTCAGAGAACCTAAATAGTCTACTTTTGCCATTAGGCCA GACTAGGGTTCAATGCTTTTACCCCTTNNNNNNNNNTGTAAGTCTAGTTACCTACTTTTCTTTGATTTTCGACGTTTACTAGCCATCTCAAGCAAC[G/TTTCGACGTTTGA
WI-7774b	170	TC	---	---	TGCAACCTCTTTTCGTGATGGGAGCCTGCTGTCAGACTCCAGTAGCGAGACGGACCCAGCAATCAGATCCAGCTTCGGCAITTTGATCAGACCAACAGTCTGTTCCCGGGGAGGAACACATTTTTTAA TTACCTTTTGCAGGCACCACTTAACTCTGTTT[C]ATACCTTGTATTAAATGAGCGACTTAAATGATTGAAAATAATGCTGCTCTTAGTAGCAAGTAAATGTGCTTGCT
WI-7785c	165	G	---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATACTGTAATGCAATGGAAATAAACTGTCTCCCATTTGCTCTATGAAACTGCA CATTTGGTCAITTTGTAATANNNNNNNNNGCCAGGCTAATCCAAATTATTATCACAATTTACCA TAAATTTATTGTGCTCAITTTGATGATTTATTTTGTAAATGTATCTTTGGTGCTGC
WI-7785b	165	G	---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATACTGTAATGCAATGGAAATAAACTGTCTCCCATTTGCTCTATGAAACTGCA CATTTGGTCAITTTGTAATANNNNNNNNNGCCAGGCTAATCCAAATTATTATCACAATTTACCA TAAATTTATTGTGCTCAITTTGATGATTTATTTTGTAAATGTATCTTTGGTGCTGC
WI-7785	156	T	---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATACTGTAATGCAATGGAAATAAACTGTCTCCCATTTGCTCTATGAAACTGCA CATTTGGTCAITTTGTAATANNN- /TJNNNNNNNGCCAGGCTAATCCAAATTATTATCACAATTTACCATAATTTATTTTGTCCATTGA TGTATTTATTTGTAAATGTATCTTTGGTG
WI-7789c	84	GA	---	---	TCTCCCCCTCATCCAACCTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCCTCTACAGAGACTCTCCC TGACGGTGGAAATTTAA[G/A]TTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTCAGGCCCGCTGCCCTAGGATAT GCGCTCTCTGCTGCTGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT
WI-7789b	84	GA	---	---	TCTCCCCCTCATCCAACCTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCCTCTACAGAGACTCTCCC TGACGGTGGAAATTTAA[G/A]TTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTCAGGCCCGCTGCCCTAGGATAT GCGCTCTCTGCTGCTGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT

WI-7789	73 GA ---	---	---	TCCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCAAAGGAGGGACCACATCTTACAGAGACTCTCCG TGACG[G/A]TGGAAATTTAAGTTAGGGTCCCTAAAGCAATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGGTGAAGTGGGGCTGCTCAGACGACTAGCCAGGACCCATCT
WI-7790b	190 CT ---	---	---	AATTGTCAGTCACTTCTTCAAACCTTACAGTCTTCTTAAAGTTACTTTCATGAGATTCATCCATT TACTAATACTGTATTTTGGTGGACTAGGCTTGCCCTATGTGCTTATGTAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAGTTGTGTTCTATTTTCTTGAAGTCTC/TTCTATACTTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7790	190 CT ---	---	---	AATTGTCAGTCACTTCTTCAAACCTTACAGTCTTCTTAAAGTTACTTTCATGAGATTCATCCATT TACTAATACTGTATTTTGGTGGACTAGGCTTGCCCTATGTGCTTATGTAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAGTTGTGTTCTATTTTCTTGAAGTCTC/TTCTATACTTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7795b	81 CA ---	---	---	CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTGGCTCATATTTCTTTCTCAT CTTGATGATGATC/AJGTCATCATCAAGAAATTTAATGATTAATAAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGTACTTTTCTCCAGAAAATCTCCTTGAGGAAAATGTCCAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAATATAATCTG
WI-7795	81 CA ---	---	---	CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTGGCTCATATTTCTTTCTCAT CTTGATGATGATC/AJGTCATCATCAAGAAATTTAATGATTAATAAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGTACTTTTCTCCAGAAAATCTCCTTGAGGAAAATGTCCAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAATATAATCTG
WI-7814c	41 GA ---	---	---	TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG[G/A]TTTCATTTAGTCATGTGACCCTC TGCTTGTTGTTTCCACAGCCTGCAAGTTCAAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAAATATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA
WI-7814b	41 GA ---	---	---	TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG[G/A]TTTCATTTAGTCATGTGACCCTC TGCTTGTTGTTTCCACAGCCTGCAAGTTCAAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAAATATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA
WI-7814	28 GA ---	---	---	TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCGTTTCAATTTAGTCATGTGACCCTC TGCTTGTTGTTTCCACAGCCTGCAAGTTCAAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAAATATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA

WI-7830d	150	C T	---			GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAACTCTTTTCCCTTTCTGTTAATAGTATCATCATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGT[C/T]TTAATGTACACATTGCATTTTGATAAAATAAATTTGTTGTTCCCTTTG AGGTTGATCGTTGTTGTTGTTGCTGCACITTTTACTTTTTTTCGGTGTGGA
WI-7830c	54	G A	---			GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGTTTAGTAAGAGAAGTCT[G/A]TCTGTCTGA TGATGATAGGGGGCAAACTCTTTTCCCTTTCTGTTAATAGTATCATCATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATAAATTTGTTGTTCCCTTTG AGGTTGATCGTTGTTGTTGTTGCTGCACITTTTACTTTTTTTCGGTGTGGA
WI-7830b	134	G A	---			GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAACTCTTTTCCCTTTCTGTTAATAGTATCATCATTTCTATGCCAAACAGGAAC[G/A]ATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATAAATTTGTTGTTCCCTTTG AGGTTGATCGTTGTTGTTGTTGCTGCACITTTTACTTTTTTTCGGTGTGGA
WI-7830	44	A G	---			GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGTTTAGTAAGAGAAGTCTGTCTGTCTGA TGATGATAGGGGGCAAACTCTTTTCCCTTTCTGTTAATAGTATCATCATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATAAATTTGTTGTTCCCTTTG AGGTTGATCGTTGTTGTTGTTGCTGCACITTTTACTTTTTTTCGGTGTGGA
WI-7865e	25	C T	---			CCACTTCTATCTGATTTTCCAG[C/T]AAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865d	191	C T	---			CCACTTCTATCTGATTTTCCAG[C/T]AAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTGGGT ATGCTACTCATAAGATTTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865c	25	C T	---			CCACTTCTATCTGATTTTCCAG[C/T]AAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865b	191	C T	---			CCACTTCTATCTGATTTTCCAGCAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTGGGT ATGCTACTCATAAGATTTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA

WI-7865	25 C T ---			CCACCTCCTATCTGATTTTCCAG[C]/JAAATGAGGCGAGGCAATCTAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAGATTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865	191 C T ---			CCACTTCTATCTGATTTTCCAGCAATGAGGCGAGGCAATCTAGTCTTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGGGT ATGCTACTCATAGATTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTA[C]/JGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7867c	92 A C ---			TTCAACACCTGTCTTCCACCTCCACCATCTGTGCAATCACTTCACCTTCAGCCTCACTAGTCCCC CTAACAAATTACCCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTAAATGTTGGTTTAAATGGC CTGTTGAGTTTAAATGTTTAAATGTTTCTTTAAGTAACCAATTTCTGTTCTTGTCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7867b	92 A C ---			TTCAACACCTGTCTTCCACCTCCACCATCTGTGCAATCACTTCACCTTCAGCCTCACTAGTCCCC CTAACAAATTACCCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTAAATGTTGGTTTAAATGGC CTGTTGAGTTTAAATGTTTAAATGTTTCTTTAAGTAACCAATTTCTGTTCTTGTCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7868c	173 C T ---			TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCGGGCTTT CACCCAACTGTCTCCCTGTATCTCCATCAGGGCCAGATCTTCCAGTCTCCATCTCAGTACACAAT CATTTAATTTCCCTGTCTTACCCCTATTCAAGCA[C]/JTAGAGGCCAGAAAAATGGGCAAAATTAT CACTAACAGGCTTTTGAAGTCAAGTCCAGTAGTTTCAATTCATGCTAGAT
WI-7868b	173 C T ---			TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCGGGCTTT CACCCAACTGTCTCCCTGTATCTCCATCAGGGCCAGATCTTCCAGTCTCCATCTCAGTACACAAT CATTTAATTTCCCTGTCTTACCCCTATTCAAGCA[C]/JTAGAGGCCAGAAAAATGGGCAAAATTAT CACTAACAGGCTTTTGAAGTCAAGTCCAGTAGTTTCAATTCATGCTAGAT
WI-7868	66 T C ---			TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCGGGCTTT /C/TCAACCAACTGTCTCCCTGTATCTCCATCAGGGCCAGATCTTCCAGTCTCCATCTCAGTACAC AATCATTTAATTTCCCTGTCTTACCCCTATTCAAGCAACTAGAGGCCAGAAAAATGGGCAAAATTAT CACTAACAGGCTTTTGAAGTCAAGTCCAGTAGTTTCAATTCATGCTAGAT
WI-7870b	85 T C ---			ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTGCAGTGATTAGAAGGG GTGGGGTGGCGGGAATCC/JCIATTTATCAGACTCTGTAATTTGAATATAAATGTTTACTCAGAGGA GCTGCAAAATTGCCTGCAAAATGAAATCCCAATGAGCACTAGAAATTTTAAACATCATTTACTGCCAT CTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTG

WI-7870	76 C T ---	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTACTCTGCAGTGATTAGAAGGG GTGGGGTGGC/TGGGAATCCTATTATCAGACTCTGTAATTGAATATAAATGTTTTACTCAGAGGAG CTGCAAAATTGCCTGCAAAAATGAAATCCAAATGAGCACTAGATAATTTAAACATCATTAATGCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACTAATATCAATTG
WI-7889c	54 C ---	---	---	TTAGGTCATGCCACTCCCGAGGAGCAGCTGGCACTGACAGCTGGGGGGGGCGCTCTCCOCTG CAGCCGTGAGGACTTAGCTCATGAGTGGAAGTCACTACAGGACTGGCCGGGGCGGCGCTCT GGCTCCCTGCCAATCCTCCCTGGAGAAAGGACATGGGAATGAATTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCAAGGCTGTCTCTCCAGAGCAAGAAG
WI-7889b	54 C ---	---	---	TTAGGTCATGCCACTCCCGAGGAGCAGCTGGCACTGACAGCTGGGGGGGGCGCTCTCCOCTG CAGCCGTGAGGACTTAGCTCATGAGTGGAAGTCACTACAGGACTGGCCGGGGCGGCGCTCT GGCTCCCTGCCAATCCTCCCTGGAGAAAGGACATGGGAATGAATTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCAAGGCTGTCTCTCCAGAGCAAGAAG
WI-7894c	142 A G ---	---	---	AGCCACCCCAATATACTGTTATCCAGAAGCTGTTATGCTCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTATGCTCTATTGTTTGGAATTTATTTGCGTATAC ATTATC/A/GJTATGTAATAATTGCAITTTTATTGAAATTAATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTAAATCGTTAATTTAACCGCTATAGAGTATCCATA
WI-7894b	142 A G ---	---	---	AGCCACCCCAATATACTGTTATCCAGAAGCTGTTATGCTCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTATGCTCTATTGTTTGGAATTTATTTGCGTATAC ATTATC/A/GJTATGTAATAATTGCAITTTTATTGAAATTAATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTAAATCGTTAATTTAACCGCTATAGAGTATCCATA
WI-7900e	84 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/C/TCCCTGCCATTGAACAGTGATTAAAGTTGATCAAGCCATGGTGA/C/TACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCAAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAGAAATC
WI-7900d	128 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/C/TCCCTGCCATTGAACAGTGATTAAAGTTGATCAAGCCATGGTGA/C/TACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCAAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAGAAATC
WI-7900e	84 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/C/TCCCTGCCATTGAACAGTGATTAAAGTTGATCAAGCCATGGTGA/C/TACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCAAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAGAAATC

WI-8021b	57 C T ---			ACAACTCTCAGAAGGACTGTGCAAGTCAATGAGTCGGCTGTGAATTCATCTGGAAC[C/T]GATCCC ACGTCCTTAGAACCTTCACCACAAGGAGTTTCTGTAGTATTCTCAAAGTCTTGGTAGGCATTCGA ACTGGTCTTTCACCTTTGAGATCTTTCTTTTGGCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTTGGGCTTGTAGGSGTGATTCGAATTCGGTGAATGGCA
WI-8021	57 C T ---			ACAACTCTCAGAAGGACTGTGCAAGTCAATGAGTCGGCTGTGAATTCATCTGGAAC[C/T]GATCCC ACGTCCTTAGAACCTTCACCACAAGGAGTTTCTGTAGTATTCTCAAAGTCTTGGTAGGCATTCGA ACTGGTCTTTCACCTTTGAGATCTTTCTTTTGGCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTTGGGCTTGTAGGSGTGATTCGAATTCGGTGAATGGCA
WI-8024c	206 A G ---			CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGGATCCCAAGTGGCCTCTCCCATGGGAAGACAGAAGAGT GGCCCCAGAGATGGAAGGACCCCAAGTGTATCACCACAACACCATTTCAAGCCGCTCTAGCCTCTAA TTCCC[A/G]CTCTAGAACAGCTGGCCCTGGTCGTGCTCAGTACACAAGGAAGAGC
WI-8024b	206 A G ---			CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGGATCCCAAGTGGCCTCTCCCATGGGAAGACAGAAGAGT GGCCCCAGAGATGGAAGGACCCCAAGTGTATCACCACAACACCATTTCAAGCCGCTCTAGCCTCTAA TTCCC[A/G]CTCTAGAACAGCTGGCCCTGGTCGTGCTCAGTACACAAGGAAGAGC
WI-8077	167 A G ---			GAATGAGCCTTCTAGCGCCGAGGACCTGCTGCTGTGTTGGCCTGCACATGCTATGGAATGC TTTTGGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNNATCTGCCCAACTCCTTTCT AAGGAGTCTGGGTGTCATGCCCTACAACCC[A/G]TAAATTCATCAGATGGAATTTTATTAAACGTT GTGATTGTGACTTACTTTCCAACTGACTCTGGCATAACAAGGGAAGAAA
WI-8118f	114 G C ---			TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGACCACCTCCCTTGTAAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGAATGAGCTGTGTTG[C/T]TTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCT AAAAATCAGACTCAATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40 A G ---			TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGACCACCTCCCTTGTAAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGAATGAGCTGTGTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCT AAAAATCAGACTCAATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118 T G ---			TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGACCACCTCCCTTGTAAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGAATGAGCTGTGTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCT AAAAATCAGACTCAATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

WI-8118c	44 C T ---			TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGATGA/C/TCACTCCCTTGCTAAGGAAGC TATGTACTTCTATGCTGTGGAACTGGCAATACAGAAATGAGCTTGTTGTTTCTTAGCCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTTGACCACTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118b	88 T C ---			TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAC/T/CJGGCAAAATACAGAAATGAGCTTGTTGTTTCTTAGCCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTTGACCACTAGTCTTGAGGACTCAAGCTGAATGA
WI-8171d	299 C T ---			TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGGCGCTCGGGAAG AGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGGAAAGAGACCCCTCTTGGCACACA TTTATGGAGGTTGTCCCTGAAGAGAGGCGAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGACAAATGAAGAGGATGATGATAAAAAACAATCACGGCA
WI-8171c	46 A G ---			TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAAC/AGTGGCAGCAGGCGCTCGGG AAGAGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGGAAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGTTGTCCCTGAAGAGAAAGGCGAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACCAGTGGGCAAGAGACAAATGAAGAGGATGATGATAAAAAACAATCAC
WI-8171a	46 A G ---			TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAAC/AGTGGCAGCAGGCGCTCGGG AAGAGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGGAAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGTTGTCCCTGAAGAGAAAGGCGAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACCAGTGGGCAAGAGACAAATGAAGAGGATGATGATAAAAAACAATCAC
WI-8171b	298 T C ---			TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCAGGCGCTCGGGAAG AGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGGAAAGGAGACCCCTCTTGGCACACA TTTATGGAGGTTGTCCCTGAAGAGAAAGGCGAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGACAAATGAAGAGGATGATGATAAAAAACAATCACGGCA
WI-8314b	85 G C ---			GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTGCAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTAAGGG/G/CJAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCAGCTGTCCAATAGAACTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAAACCCT
WI-8314	78 C G ---			GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTGCAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTAAGGG/G/CJAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCAGCTGTCCAATAGAACTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAAACCCT

WI-8321	178	G A	---			TTTTAAATATGCCCCGTTTAGAGCAGACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTTCAAGAGCTGCTGTATACTAGTCTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTCAGAA[GA]AGTATCTTAGTATTTCTTCTA TTTTGCTATGGTCTAGTTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-8321	178	G A	---			TTTTAAATATGCCCCGTTTAGAGCAGACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTTCAAGAGCTGCTGTATACTAGTCTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTCAGAA[GA]AGTATCTTAGTATTTCTTCTA TTTTGCTATGGTCTAGTTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-832b	123	A C	---			TATGTACTACCTTTCAGTTACCCCGTGCCTCCAGAAATCGCATGTTGCTCCACCTGGGGGGGATATA AATTAACCTCTAGATTGTCCAAAGCCAGTCTTCCCTTCCCTGTGCAGCCTTAGA[AC]ACTAAGTAG CAGTACTGTTGGTGTGTTTCTTCTCCAGCAATGCCTACTGCAGCTACTTAGTAACAACCTAG AGGTGGAGGNTTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114	A C	---			TATGTACTACCTTTCAGTTACCCCGTGCCTCCAGAAATCGCATGTTGCTCCACCTGGGGGGGATATA AATTAACCTCTAGATTGTCCAAAGCCAGTCTTCCCTTCCCTGTGCAGCCTTAGA[AC]ACTAAGTAG CAGTACTGTTGGTGTGTTTCTTCTCCAGCAATGCCTACTGCAGCTACTTAGTAACAACCTAG AGGTGGAGGNTTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311	T C	---			TGCGGGCTTAACAGGAAGCATGACTGGGAGGCCTCAGGAAGCTTATAATCATGGCAGAAGCGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAAGGAGAGAGTCTACACACTTTT AAACAACAGATCTCATGAGANTTCCATCGGGAGACAGCAGTGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACTNTCAACAGGCCCTCCTCCAACACGTTGGG
WI-8378	308	T C	---			TGCGGGCTTAACAGGAAGCATGACTGGGAGGCCTCAGGAAGCTTATAATCATGGCAGAAGCGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAAGGAGAGAGTCTACACACTTTT AAACAACAGATCTCATGAGANTTCCATCGGGAGACAGCAGTGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACTNTCAACAGGCCCTCCTCCAACACGTTGGG
WI-8426	184	T G	---			TTTAGCACATATTTAGCATTAGCCTCAACGATACAGCAATATGTTACATTCTCTTGTAACAAACAG TTGTTGTAGACTGTTAANNNNNNNAATGTAACTCCGACTTGTGCCTAATAGGATTTGACCNNTAA GAGGNTTCTTTGCTGTGGANGGGTGGCTTGTGTTGAACCTCCATTCTGT[GTG]GCTTGTAGCTGGTG AGGCTGGAGTATGGANGGNCNCGGGGGCCCTTGGCNATGNATTCAGTGAG
WI-8450h	61	C A	---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCCTTCTACATACACT[CA]CA TCTTCTATCTTAGTTCCAAGTTTATGTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTGAGAAACTATGATTTAGCTTACCCCTTCCACTACCCAGCAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTCTAT

WI-8450g	55 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCCAT CTTCTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450f	108 T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTCJTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450e	125 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTCJTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450d	125 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTCJTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450c	108 T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATTATTCJTTTAAAGTATTCATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450b	61 C A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTTCACJCA TCTTCTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450a	55 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCAT CTTCTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8458b	60 A G ---			CAAGGAAAGCTGTCAGTCTTCATAAACTTCAAGAGTTACAAAATACGTATTTTAAAGJCTA CAATTCAAGATTAGCATCCAAACCTACAAACATGATGATACCTCGTCACACACCATACAACTTCAG ACCTGGCTACAGCAATGTTGACTTACATCACCATTGTTTACTTGTGAAACCTTATTGTGACAGT GACATCCATTCCGCCAGACTTAATGTTATAAAGCAGCTGAGCAGAGTCTCTCA

WI-8461c	105 A T ---	---	---	CTTCCTCCTCCAAAATCTACATGAATAGTGAAGACAAATTAACATAACACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATATAATCAATTTTATJNNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAATTTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38 T C ---	---	---	CTTCCTCCTCCAAAATCTACATGAATAGTGAAGACAAATJGATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATATAATCAATTTTNNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAATTTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38 T C ---	---	---	CTTCCTCCTCCAAAATCTACATGAATAGTGAAGACAAATJGATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATATAATCAATTTTNNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAATTTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105 A T ---	---	---	CTTCCTCCTCCAAAATCTACATGAATAGTGAAGACAAATATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATATAATCAATTTTATJNNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAATTTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-9438	77 A G ---	---	---	AATAACATGTTATGAAACAAGCTGGTTACAAGTAGTAGGTAGTAAATTTTGTATAAAAAAAT TAAAAAGCATJGJAACATGCATATAAAAAATTAGATTATGTACAAAATACCAACAGTATTACTTC TGCTCAGTAATTAATATTCTCCCTTTGTTTGTCTTTTAAAAAACATTATTCTGAAAAAATAA ATCAGAAAAACATGATCGTGGAGAAATTATTA
WI-9439b	101 C T ---	---	---	ACAGAAATGACCTTTATTTGTTGTAATAAGCCTGTTTAACTTTGTACAAAAGTAACATTTTAGTA CAGAAAAATCCCAGTCTGCAGTCACTACCTGTGCTJGTGCACACTGTACCATCTCAGTCCCCTCT GCCTGTAACCTTAGAAAAACAGCCCTACCCCAAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTGTCTGAGCTAGAAAACTTGACCTGTAAAAACAAG
WI-9439a	76 C T ---	---	---	ACAGAAATGACCTTTATTTGTTGTAATAAGCCTGTTTAACTTTGTACAAAAGTAACATTTTAGTA CAGAAAAATJCCAGTCTGCAGTCACTACCTGTGCTGCACACTGTACCATCTCAGTCCCCTCT GCCTGTAACCTTAGAAAAACAGCCCTACCCCAAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTGTCTGAGCTAGAAAACTTGACCTGTAAAAACAAG
WI-9446b	75 T C ---	---	---	GAAAGCTTGATTAGGGAGGNTTTATTTGATGTNAACCTTACCATCCATAGACTATAAAGANCATTA TAAAAAAATJCCCTCTAAAGNGACACATGCCCCAAATGACCANGNCATAGCAAAACCTTTTAAAT TACTCATCTTCATATGTGTGTTGTNCCCTACTNTTATCACTGTGCTCTCTGCTTTTGTCTACCTA TGNGAACTGCACACTATCTGTGGCAATATGT

WI-9446	75	T C ---	---		GAAGCCTTGATTAAAGGAGGNNTTATTTGATGTAACCTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAAT/CJCCTCTAAAGNGACACATGCCCAAATGACCCANGNCATGAAGCAAACCTTTTAAAT TACTCATCTTTTCATATGTGTGTTGTCNCCCTACTNTTATCACTGTGTCTCTGTCTTTGTCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT
WI-9497b	185	A ---	---		ATTAAAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAAATGGTATATATACATTTTTT GAGATAATATTCTAGATCCAGGCTTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTTAATTAATCAAAAGTATGTTAATGTCACTT GGAATTTCTACATGGAAGGCCAACAAAATAACTAAAACCTTGACTAATGAAG
WI-9497	185	A ---	---		ATTAAAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAAATGGTATATATACATTTTTT GAGATAATATTCTAGATCCAGGCTTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTTAATTAATCAAAAGTATGTTAATGTCACTT GGAATTTCTACATGGAAGGCCAACAAAATAACTAAAACCTTGACTAATGAAG
WI-9523b	193	C A ---	---		GTGAAAAAGTTTCTATTCCATCATACAATAGATTGTGCTAAGGATCATTTTGGAAAGATGTG CAGCATTGAGAAGTTGTATCTCATGTCAGTCACTCAGCAGCATTTTATCTAAAAGTACGTGCACA GACTCAGACAAATTACAAACTATTTTCAGCCATGATCTATGGTGAATTTCCACACATTGTAC/C/AJAGTG AAAGCTCTTCAGCTTGGAAACAACCTTGTCAGGCAGACTGCATGCACATATAT
WI-9523a	47	G A ---	---		GTGAAAAAGTTTCTATTCCATCATACAATAGATTGTGCTAAG/C/AJATCATTTTGGAAAGAT GTGCAGCATTGAGAAGTTGTATCTCATGTCAGTCACTCAGCAGCATTTTATCTAAAAGTACGTGCA CAGACTCAGACAAATTACAAACTATTTTCAGCCATGATCTATGGTGAATTTCCACACATTGTACAGTGA AAGCTCTTCAGCTTGGAAACAACCTTGTCAGGCAGACTGCATGCACATATAT
WI-9554	202	T C ---	---		AAAAACACAAGTTTTCATACATCACAAAAAGCTTCCATTATAACACAGAGTGATTATTACCAGAC AAGCATCAGTGATGTATCTACTGCCCTTNTAGTTGTTTATTGTACAATGCTGTAGATAATGCGCCCATG CAATACACCCAAAGAACACTAGAGTCTCTACACCCCAAGTACAATAATGATAAAGCAGCCCTCTGCAAGTG GT/C/GCTGGATACCACTAAGAACTCTACTGCAGCCATGTTGGTTATGATTTT
WI-9555	97	G A ---	---		CCAAAAGCCAAACCACTTCATATGATGGATTTCATAAACAATTTATGATCCTTTTGGAGTAAGTAT AAATACCTTTTACATGGCTAACCTTCTAAC/C/AJCTTGAAAAATCAATTTCAAGGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAGGCCAACAAATGATCATACTTCAGATTAAATACAGGTAAGTATTCAG GGNTAAATGGTACAAAAAGGCTGTAACTCTTTTNCITTCACATTGATCACA
WI-9625b	172	A T ---	---		TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCCTGGGAAAAAATCTTGGAAAAAACAACACGCACA TAAGTATCAATAACTGAGGGTTGTGGACAAGTTACTTCTTA/TGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCATTTTAAAAAACAACACTGACAAATCTTTTC

WI-9625	172 A T ---			TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGGTACCATATATTGTATCTNCTCCTTGGAAAAACCTTGGAAAAACACGCACA TAAGTATCATAACTGAGGGTGTGGACAAGTTACTTCTTA/TGTGTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCAATTAATAAAACACACTGACAAATCTTTTC
WI-9647	144 C T ---			TTTTCTGAGATTCAAAAGAGCTACATTTTGGTAGTGATGTCTACTATACCTTTTTCATCCTTTCA ACATCTTTTGTACATTTTAGGTGATGCTCTGTAAACAGTGATGCTAGACCTAAAAATCCAAGCT TACAACTC/TGTGCTTTACCTGATACATTTATCCATTTACTTTCAATTTGGATTTTAAAAATGTTA ACTTAATACGTCTCTTCAGATGTCCTGCTTTTGTAGTTAATGTGTTT
WI-9676n	114 A G ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTTATAATGCAGAGCA/AG/GATGTGGCTTTCCTGCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676m	184 G T ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676l	84 A C ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676k	202 C T ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA C/T/CAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676j	92 C T ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676i	173 T C ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTTCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT

WI-9676h	134	C A	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCCCC C/AJATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTG AGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676g	202	C T	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCCCC ATTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGAGG C/TJAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676f	184	G T	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCCCC ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676e	173	T C	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCCCC ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTT/CJCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676d	134	C A	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCCCC C/AJATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTG AGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676c	114	A G	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676b	92	C T	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676a	84	A C	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT

WI-9738b	40 C A ---	---	---	TGGACCAACACAGACAGATGATTCTCGTGGTGCCTGTGTAC/AJATTACAACCTCAATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAAATGACTCCACATTTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTACCTTGCCTGGAGCGGGTGGTTTTCACATATGTGAGTATCTA TCTTTTATTCTGTCCCTTATGTTGGTGGGCACATGCTGTATTGCTGTCC
WI-9738	40 C A ---	---	---	TGGACCAACACAGACAGATGATTCTCGTGGTGCCTGTGTAC/AJATTACAACCTCAATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAAATGACTCCACATTTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTACCTTGCCTGGAGCGGGTGGTTTTCACATATGTGAGTATCTA TCTTTTATTCTGTCCCTTATGTTGGTGGGCACATGCTGTATTGCTGTCC
WI-9756	47 A ---	---	---	ACTGAAATGTAATGGCCAAAGGCCACCCAGGACCTTAAATCATAGAAGTTAATCTGTGGGAAAA GAGTAACTACAAAAGATCTAAACAGAGCAGGATGTGATGTAAATGTGCCCTTATCACCTTTAGTC AGTAAAGATAAGAAAGCCCTGGTGAGTATCCACTTCCACAAACACACAGAAATATACACTTTTGGGAA ATTCCACTTAACCACTTGATTCTTCACTTTTATGATTTAAACTCTCCGTGG
WI-9758	135 A G ---	---	---	GATGGTCCCTTAAGGATTGCAATTGGTTAATGGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAAT TAGGAAACTGGGAGAAATCAATTCAAGAGAAATCTTGTTCGCAAGGTCAATTTTATACTATTTA A/AJTAATAAATAACTCTGTAGGTTCTATAGCAAAATGCTAAGTAAAGTAACCGTGGTTTCTAAAT ATTACG
WI-9778	127 G A ---	---	---	ATTTAATCCAGGCAGCGGGGAAAATGGATACATTTTCATATGCTCTGTACCCAACTATAAACTTTTG GTTCTCATGCACCATTTTCATTTGCTTCTCCTCACTCCAGTACCCTGATTTTACCAATTG/AJCTCTC ATAATTGACTTTGCTACTGGAAGAACTCTTAGAATGTTGGAATTTCTCTATACACACTTTGCCCTCA AAGAATGTGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116 C A ---	---	---	TCTCCCTTTGCTCCTCATGCCACTCCCTCAGCCTGCACAGAGCGTTTCTCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGTGACAATGCAGTTTTC/AJTGATCCACCCAGGA CTCAAAAACCTAGGAATTGGGAGAGAGGACCTGGAATCGGTGTTGCTAGCAAGCCGCCAGGTGG TTTGTAAAGTGGACTAAAGTTTGAGGACCAGACATGGAAAGTTGGCTTTGGC
WI-9841	101 A G ---	---	---	TGGAAAAATAGCTTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGAAATGGCATGA TATGAAATTCATTTTGAATGAATAAAATATAC/AJGTGTGTATGATATATATACTATTAAACACTT AGGATTATATACACACAATAAAACGCTGTGTAGGATAAACTAAGGTTCTATCAGTGGGAAATGAGA TTGAAAAGAGGGGATGTTACTTGATAIGCTGTTG
WI-9880c	222 G A ---	---	---	GAACTAACACCTTTCTGCATGGATTTTCTTGATTATGGCAGTTAAACAATAAAATGTTATTAGATC ACTGGTCTCTGTGTGGGTTGAGTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGGACTATAAGATCCTCTTTTAAATTTATATTTATATAAGCACATGAA AATGGAATGAAATAATGA/GAJTTGACATAGGAATTACCTACATATTTTG

WI-9880b	157	C A ---	---	GAAC TAACACCTTCTTG CATGGATTTTCTTGATTATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTCTTCTGTGGGGTGGATTTTATGATATCTCTGTTAGCCCATAGGGAGGCTGTGA GTTGTTTCTACATCCTTGA[C/A]TATATAAGATCCTCTTTTAAATATATTTTATATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATAATTTG
WI-9880a	108	C T ---	---	GAAC TAACACCTTCTTG CATGGATTTTCTTGATTATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTCTTCTGTGGGGTGGATTTTATGATATCTCTGTTAGCCCATAGGGAGGCTG TGAGTTGTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATATATTTTATATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATAATTTG
WI-10183	127	C T ---	---	ACACTGGAGGCACTCCAAATCCTNACAGACATATGCACTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTTATTTTAAAAACAACGCCCCAGTTATCACAGTTCTNTTTTGTCTCACC ATTTCCATAACAAAAGAAGCTACACAAAATTNNGGGGGAGANACTCTCTTTGGAGACTGACACATT TGCAGAGGGGTCATGAATAATGATTCAAA
FB25G10b	109	A G ---	---	TCCCTCAATGACAGATGAACATAAATTTCTCTTGGTAAGAAATACITTTATGTCCATTGTGATAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGA[A/G]TGATTTTAGATCCTCCCCCAG TGACAAGTAAACTGAAC TGACCATATTTATACATAAAATGGAATGTAAGAACCCTATTTTGGATATCC CGGAC
FB25G10	109	A G ---	---	TCCCTCAATGACAGATGAACATAAATTTCTCTTGGTAAGAAATACITTTATGTCCATTGTGATAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGA[A/G]TGATTTTAGATCCTCCCCCAG TGACAAGTAAACTGAAC TGACCATATTTATACATAAAATGGAATGTAAGAACCCTATTTTGGATATCC CGGAC
IB3071	102	C A ---	---	ACAACGGCTGAACCTCCATAACAGTCAATGGTACAGTCAAAACATCAGATGTACAGAACACAAATTTA GATGAAC TGAATTAAGNTAAATAAAATAAAATC[A/J]CAATTTAGNAAACAAAATCAAAAC ATTAAGGNTCCCTGNNATATCTTAAACCCTAATGAGATTTCACTGGNCTCAAGTCATTTTGTAGTGA GGCATTCACAATATGACCCTATTAAACCAGTCTAGGGATTCTG
NIB551	161	C T ---	---	CGTCTTTCTCTTTTGAGATTGCAATTAAGTAGATAATATGAGAGAGAACTGACAATGGGTTGTCCC TACTGAGCTTGGGGCCAGGTGTACTTAGGAACCAATCCACCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGT[C/J]TGACCACATACATCGGGCATTGGTTGATTCAGCTTT GCAAGCAGCGTAGTGAGAAAACAAAAGCTTGTC
S72904	51	G T ---	---	AGCATAGAAAGTGATTTATATTTTAAATGGTTTCAAGTGAAGTCTCTTTGTTAATTTGTGAGTTT ATTCTGGAAAATCTTTTGAGTTAAATAAGGATCCTAGGACAGCACCTCGAACTACAGGCCCTAAA GAGAAATGCCTCAACACCAAGTGCTGAAC TCTCCCTTTCTGTCAATGGTTGTTCTTTAAATA TTGCAAAAGTCTGATGCTAAACAGTATTTGGAGTGTTCAGTGTCTGTA

UTR-00481	115	C T	---	---	TATCTTTTATCTCTGGGCCACAGTTCTTGATTATTCCTCTTGTTAAAGACTGAATTTGTAAACC CATTCAGATAAATGGCAGTACTTTAGGACACACACAAACACAGAC/C/JACACCTTTTGATATGTA AGCTTGACCTAAAGTCAAAGGACCTGTGTAGCATTTTCAGATTGAGC
ESTC1	33	---	---	---	CCCTGTAGCAGTCTTCAGCCTCCTCTACCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	---	GCTACTACCACGGCTGCTTGGTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21	---	---	---	GCCATCAAAATTTCCCTTACANTCAATACTGTTGAACAACAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC107	20	---	---	---	TGCTGGCTCACTTCTCACANGCTGTATTACCTTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35	---	---	---	AAACCAGGAAGGCCCTGCCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGAOC
ESTC110	23	---	---	---	AAACCTCACACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	---	AAGGACACAGTGTGCTGACAAGGTGACACTGAACANACAGTTTTCCCTTAATTGTAAAGCGGG CATCG
ESTC117	24	---	---	---	AATTGGCTCTTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCTATCACAATTTACAAAAAGC CTCCA
ESTC119	24	---	---	---	TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTTT
ESTC122	34	---	---	---	GACAATAACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	---	GAAGCCAGTATGTTGGCAANATTCGAGAAAAACACACTGAAAAA
ESTC128	42	---	---	---	GCAGAGGCATCAGATAAGGCCCTCAGAAAGCCCAGGCCCATCATNTCCATGGGACCGGCTGGCTCAA TGTTGGAACCTGG
ESTC129	20	---	---	---	AGTCACCATGCCCCAGCCTAGNATGAGTTTAGTAAGATTGGTTATGCTGGGAG
ESTC13	46	---	---	---	GTGTATCTGGCTTCATGGGATGCATAAAATTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAAA
ESTC130	49	---	---	---	GCCTGCTCACAAGGTAGACAAAAACATAAATCTTCAGGAAAAATGAACACANGAGAGCTGAAACAAT CTACACCTGAATG

ESTC132	30	---	---	---	---	GGTAAAGTCTAAATTACTGCCTTAGCAAACNCTATGTTGICAGGTTTTCTGCTGCA
ESTC137	21	---	---	---	---	CCAGTTGGCTTCTGTCCTCANAGTCTCTCTCCATGTGGCAACA
ESTC139	45	---	---	---	---	AGGAGCAGCGCTAAGGACATGAAGGTCAGAGTTCTCAGAGAGNGGGCTGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	---	CCATTGTGGTACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTCCCTTGCATGGTTAGAAAGC TTGCCCTGGTG
ESTC142	72	---	---	---	---	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATAATCTATTTTATTCAATTTAAATC AAAGANACCATTCCTTTCTTAACAACA
ESTC143	29	---	---	---	---	GTTTACGAAAAGTACTGAAAATGCTATTANTAGCTGAATTTGTGATTTCTCTTTTG
ESTC144	26	---	---	---	---	AAATCCATATTTCTTGACATGAGGNGCTTTTAGCAGCATTTCCGG
ESTC146	20	---	---	---	---	CATGTCAGGATAAGGAGCANACACCAGGATTATACACGGTGGCAGCG
ESTC148	42	---	---	---	---	TCTTGGTTGTCTACACAGACACTTAAGTACTGTATCGCTGATGCAGCGGCTGTGGAGGCCCTG GGGTGGCTGGGCTGTGTCTCTGAG
ESTC149	28	---	---	---	---	TCAGTTCATTTATTTGCTTTAAGAGTTANATACCATGAGACACAGTTCTGCG
ESTC15	28	---	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAAGTTCTTCAGTGATCTT
ESTC150	20	---	---	---	---	CCAGGAAACAAGCAGACACANACTTATAGAATACTTTGGTTTAAAAATTATTCATAATCAATATT AACTCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	---	GAAGCTAAGGCCCATTTTTTTCTTTTAAATACAAATCTACTGGTGCNAAAACCTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	---	TTTTAATTGACAACCTCAATCTCTACATACATACAGTNTGCACGAATTATAAGTGGATCAACAATT ATATTATTGATACAAACTCATGAGCATTTACA
ESTC156	32	---	---	---	---	GCAGCATTTGTGACAGGAGAGCGCAAAACAANCCCTGGCTGCCTCGGATGGAGGGGGCGGCTCA CCACCACTGCAT
ESTC158	35	---	---	---	---	ACCAAGCCCTGGGATTTACTGTCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTCAGTGTGC AA
ESTC159	31	---	---	---	---	AGCTGGCAAGAGACTTCTGAGGCACATCAGNTACGTTGGTCAATTTAGGGCACGGTCTGGTTCTGCA GCTTTGAAAGG

ESTC16	23	---	---	---	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCACAGTGATCATCACCCACAAGGACAGGTT
ESTC160	38	---	---	---	---	TTCTAGCATTGCTGGTGAGTGGGGGCTGAGCTGGGNGCAGTCGGCAGTGTCAGTGGGCCCGTTTG GGACTGGGTGA
ESTC162	36	---	---	---	---	CTCTTCGTCGGTTGCAAGTTGCTGTTGTTTCCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	---	---	---	---	TCATTCTCCATAGAATAATTGGTTTGTAAACANCGAATACAATCCAATATAAACAATTAACAATCC GATACATACCA
ESTC169	22	---	---	---	---	GTCTCTGGTGTGCAGGGAATCANITTTGCTGGATTAGAGGAAGGTGCCCGCTGTTTCCATGACTT
ESTC176	23	---	---	---	---	CACCTCCTCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA
ESTC177	42	---	---	---	---	TGGTGGGCTCTTTAAATACCTTCCATTATATTTCAAATTTTNCCTTATTCTATTAAATACCTTTTAT TCTCTTTATCCCATAAAAAGCAACAA
ESTC18	29	---	---	---	---	TCAGACACTGCGACATCAGCATTGTCTCNTGTACAGCTCCCTTCCCTGCAGGGCGCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	---	---	---	---	TAGGGATTCCAAGTTGCCTGGNTTAAATATAATACATATTACAAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	---	---	---	---	GCCTGACTAGCGAGGCTACATCACAAATTTATAAAGTCCAGATNAGTGCTAATTGTCATTCAGCTTG ATTTTTCACCTCA
ESTC187	24	---	---	---	---	ACCATGATTGCTCCTCACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG
ESTC188	25	---	---	---	---	TCTATTAAACAGGGTTATGTCACACCNTGTCAACCTCAAACAGATGATCATCATCTTGTCTTCCAT CTTGC
ESTC189	27	---	---	---	---	AAAGTACAATCCAGTATATGCAGAAAGNTACTCAGCATCACACTCGTGATCA
ESTC196	42	---	---	---	---	TCCTCAAATACCACCTTTCCCTTAACCTTATCAGTCTAGTAAGCNCTTCAAGGAGGAAAATGGGTTAC CTTTCAGGGG
ESTC197	26	---	---	---	---	ATCTCCAGTGTCTGCTGCTCCTCCCGCAAAGTCTCCCAAGCACA
ESTC20	33	---	---	---	---	AAGATTAGACAGACCCGCGTATAGTAAGCTCTGNGGAACCTCAAGAATCTAGAGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC200	44	---	---	---	---	TTTGGTGAAAAATCCCAATATATGAGTTTAAAAAATAATCATTANCATCATTAACAGTACTTTAAAT CAATTACTCCTTTTGGCCTGCAACAG

ESTC201	35	---	---	---	TCCTACTGGGTAGTTAGCAACATTTTAAANCCACATCCAACAGATTGGTT
ESTC202	22	---	---	---	CTGCTGGAGGGAGGACAGACGNCAGGGCGCTGGGTGGCGCCAGAAAGGCTGGCGTGATGTT CGAGATGAGOC
ESTC203	27	---	---	---	ACACTTAACAGGTTAAATATCCAAATNAAATTTACTGCAACTTTTGTAGAAATTTATTGTGCTAC AAGACACGTTGCA
ESTC208	43	---	---	---	TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGATAANAGCAATAACTATTGTTTAAAGC CTAAGAGTGAAAA
ESTC210	29	---	---	---	GATGAAGTGGCTTCCTTTGGCGAAAGGATNAAGAGTGAGTGACGGTGACCTGTG
ESTC212	27	---	---	---	GGGTAACTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGCGTCTCAGAGCAGAGGGCTTGGT TCAAGTC
ESTC214	21	---	---	---	CTCCAGAGTCCCTCCTCTCANACCGGGGCGAGGGAGTTAGGGAAT
ESTC216	49	---	---	---	TGGCAAGAAATTTATTACACTAACAAATTAATTAATCACAGGTATTNTAGATTGGTCAGAAAA CAAAAGACCA
ESTC217	28	---	---	---	TTTTGTCAGTAATGAGCAATACACTGANTGGAATCTGCATGATTAATAACATTAAACAAGTTCAT AAACACACCCCA
ESTC219	32	---	---	---	GTACACATCTGGGGTGAGCACACAGCAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG GCAAGGAAGC
ESTC22	41	---	---	---	TCATTGAAGAAATATGGGTTTATTCTTATTCTAATTGNGAGAATGCTTAATGTCACAGGCTACA TAAGGOC
ESTC223	27	---	---	---	CTTCTGAAGCCCAAGAGAGGGGCGAGAANGTAGTTCTTGATTTAAAAAACAGAAAGGGGAGGGA
ESTC224	37	---	---	---	CGAAGGTAGATTTCCCTCACATATTACAAAATACACANAACACACACACACACACACACA
ESTC225	20	---	---	---	TGCACGTGTTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAGAGCATAAAGTGCTTCAGAAAGGA ATGTGTAGGATCG
ESTC23	27	---	---	---	TTCTACTTTATTTCATATCCACCACNATAACGACTCCCTTTAATTTAAACTAAAAACCATACAGGGT TCCTGAAGGG
ESTC230	43	---	---	---	GCTTCCTCCAGCAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGCAGGCCAGAAATTAAGA
ESTC231	24	---	---	---	CAAAAGGGTTAGTCATATTTCCCCANCAACAGCATGATAAAATAATTCAAC

ESTC28	23	---	---	---	GAAGAGCTGGGCAGGCATCTGACNTTCTCTCTATTCCTATAAAAAATAAAGGAAGCAGAAATCT GC
ESTC3	20	---	---	---	CAGACATGACCTACCGTCCNGGCCCTCAATTCATATTTTATTCTTGAGCCGCTTGGTCAGGTTTGAT TCGCACACTCC
ESTC31	32	---	---	---	ACAGCCCCACAGAACTATTGTAACAATATTNTCAGTCGGTGATCATTGTAATATACAAATACAAAG CAATTTCTCAGA
ESTC33	25	---	---	---	AGCACTCCAGCTCCTTGACGTTGTNGGACAGGGAACCTCCGGAA
ESTC39	26	---	---	---	AAGGAAAGGGAACCCACCTGGGCTTNGGTCACAGAACTCAGAGCCTGGGCATTA
ESTC4	23	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAAAICATTATGCTGATGGAAGAAACCATTT
ESTC40	22	---	---	---	GGCATGCTAGACAGAGGCATTANTTTGAAGATCTTTAAAAATATTTTGACTTGTCCCTTCAC
ESTC45	37	---	---	---	TTTGGAGGTTTGTGTGGAGTTTGTCTTTGTACNCTCTCATCATGAGGCTATATATTA
ESTC50	56	---	---	---	CTGTCCGTGTGAGCCCTGCCGTCTCCATGGCCAGGAGCCACTGTGCGGANCCTGGGCAGATG TTTACCCTGT
ESTC56	45	---	---	---	GTGCOCTGAAGATTAGCAGCAGCAGCAGCAGGTGGCAGGAAGNAGTGGAGGAAAGGACACCA AGT
ESTC57	20	---	---	---	AAGTGGCCCTCCAGTCCCTCTCTGGGCACAGATCCACCAGTCTGCTC
ESTC59	38	---	---	---	GAAACACAAAAGTGTGAGAAAAAACTTCTCAAAATTTGCCAGACTTCAGGAAAAATGATTTCC ACATGGTAAGGCC
ESTC6	27	---	---	---	TCTGCAGCACTTCACTACCAATGAGCNTTAGCTACTTTTCAGAAATTGAAGGAGAAAAATGCATTATG TGGACTGAACCG
ESTC61	57	---	---	---	AGTGATTTGGCTAGCGTGGTCTCATCTGTGAAATTCACAGCGCAATGACAGCANCCTCTCTCCC ACCCACTCAAG
ESTC63	20	---	---	---	ACAGACACAGCATCACACCANAGGGCCCGGAGGGTGGGGGAGACACACTTTTCCCTGGGAAA GGCAGCTCTAATC
ESTC69	20	---	---	---	GAGAGGCTAGTCAGGAGGGANACCCTCAAGTTAAATCCCCACACTTACTTACTGCTCATCCGT CACTTTCGCTAA
ESTC7	45	---	---	---	AGTTCCCTAGAGCTGTGGGCCAGATAGCTGTTCTGAGTTGCANGCAGATGGAGATTGGACACT G

ESTC72	37	---	---	---	GGGCTTCCAAAATGGGTATTGGGGCCAGGAGGCTGGGNTTGGCGTGACGCCCTAAAAGTGTGACC
ESTC74	49	---	---	---	AACAATTCACAGCTACAGGAAATCTAGAACAAAATCAAATATTCAACACNTTGGGTTGAAAAGTTG GAAGA
ESTC77	40	---	---	---	ATGACTTTCTGTCCCATCGGAACACAGAGTTTCCCCAGGNGAGCCCTTCTATCTGCGGTTA
ESTC81	20	---	---	---	GGCTCAGCACAGGATAAGANCCCCACTCCGCATGTCCCCAGAGGGCAGCACTCCAG
ESTC82	25	---	---	---	TTTCAGATGATGGGGTCTGAGATGNTCCTCAGGCTGCATCAGCTGTCTTCAGTCTCCAGAACAGAAA GAGCCTGACCCA
ESTC83	53	---	---	---	CAAAATCAAATACACAGATCCAGATATGTGAACCATATATACATACTATACANCCATTATTTAGAC TTTCACAAAACCT
ESTC85	28	---	---	---	TTTAGCTGCTATACCAAGTTTCCATAAANCTGTCTGTGTTGGGGAGGCTACAGCCTGACCACATTCT TTTGC
ESTC89	22	---	---	---	ATTGCAAAGGAAGTGGAAAGTGTNTCAAACAGAAATGGTGACAATGA
ESTC90	33	---	---	---	CTGGTCTCTTGCTTGGCATTGCTCTCCTCCTCNGGCCAGTGTCCACCCAAAGTGTCTTCCCGATGAT
ESTC93	29	---	---	---	CTCCCCCTCTCAGTTACAGTGGAGACTANGGAGATTTCAGGGCAGGATCC
ESTC95	32	---	---	---	GCACGTTCTTTGTTCTCCTCTCCAGAAGTTGNAGACGCTCTATTAGTTTGAATTCGTGCG
DWU-100	127	C	T	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCCTAATTCA GTGGATCTTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCTGACTGTTCTCCAC/TTGCCAG ATTCTTATCAATGATCTTTCACCTAAGAAACAGAAAGATTCTGGCAAGCACACGATCTAGAGATAC ATCTTATTGCGATTTTTCACAAAATCAAAGAAAGAAAGGCTTAGCTG
DWU-177	77	A	G	---	TTCCATCTAGATATCTACTCAAAAATAATTGAGACAAGTGTTCAAACAGAAAAGACGCTTGTGCTGAA TGTTTCATGGC/A/GJGCCCTATTACAGTAGCCAAACGATGAAAACAAACCCCAAGCTATATATTACCA GATGAAAGGATAAACAAAATGTGGTCCATCCATACAATGGAGTATTACACAGCCATAAAAAGGAAT GAAGCAGTGAATCCCTACTACTACTGTGGAT
DWU-286	213	A	C	---	CAAACTGGACTATCAACCTGTTGCTTAATCCCTGCAGCATTCAGGTTAATCCATCTAAGTGAC ATTTTGAATTCACGGGTGCCACCCCAATCATGCCAGCTTCTGTCAATGAATGAGATATACATTT ATGCTGACCTTCCCTCAAGACTGATTTTTCATGTCTGGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGG/A/CTGGGAAACCAAGCCCTATCTGAGTCTTTCGGCTCCCTCC

DWU-252	94 A G ---	---	AGTATACAAACATTTAAGCTGTGGTCAAGGCTACAGATGTGCTGACAAGGCACTTCATGTAAAGTGT CAGAAAGGAGCTACAAAACCTACCTCA/GJTGAGCATGGTACTTGGCCCTTGGAGGAACAATCGGC TGCAATTGAAGATCCAGCTGCCTATTGATTTAAGCTTTCCTGTTGAATGACAAGATATGIGGTTTTGTA AT
DWU-330	85 C T ---	---	GAACATTCCTCTGCAGCACTTCACTACCAATGAGCATTAGCTACTTTTCAGAAATTGAAGGAGAAAA TGCAATTATGTGGAAGTAA/C/TJCGACTTTTCTAAAGCTCTGAACAAAAGCTTTTCTTCTCTTTGCAA CAAGACAAAGCAAGCCACATTTTGCATTAGACAGATGACGGCTGCTCGAAGAACAATGTCAGAAA CTCGATGAATGTGTGATTTGAGAAATTTTACTGACAGAAATGCAATCTCCCT
DWU-370	231 A G ---	---	GAAAATGTTAATTGGGCAGGTGAAAAGGGTACAGATGTGCTGTAGCAGACCTTTGGTTTTAAAGAG AAGCATCATTTCCCAACAGGGCAACTGTAGAAGGCCAGCTGAAGAGTAAGGAAAAGGTCTGAGG ACTGAGCCTGTGGCTGGCTGGAAGAAAGGTGAATGTTGAGGGCCCTTCACTTCCATCACAAGAAAGTC ATTAGACGGTACCAATTCAGTGTCTGTTCC/TJAG/GCATCTATTTCCTCTGTGC
DWU-1537b	89 A G ---	---	CTCTTAACCTCAGTTCCTCATCTATAAGAAATAGGGATTCAGTTGTGATCACATAGCTCAGGTAATC CAGGACCAGAAACCCAGGAGC/JAGTGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGAAACACACAAGAAATCCAGTAAGCAGCACACACTGGCTGA
DWU-1537a	52 C T ---	---	CTCTTAACCTCAGTTCCTCATCTATAAGAAATAGGGATTCAGTTGTGATCA/C/TJTAGCTCAGGTA ATCCAGGACCAAGAACCCAGGAGCATGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGAAACACACAAGAAATCCAGTAAGCAGCACACACTGGCTGA
ESTD-ADAb	196 C G ---	---	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGAAATCCAGGGTCACTGTTCTCTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGCCCTCGGCACCTGAGCTG/C/GJAGA CCCGCAGACCAACTCCTGAGCTTTCTGGGCTCTGAGTCTTGTCTC
ESTD-ADAA	184 G A ---	---	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGAAATCCAGGGTCACTGTTCTCTCTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGCCCTC/GJAGCACTGAGCTGCAGA CCCGCAGACCAACTCCTGAGCTTTCTGGGCTCTGAGTCTTGTCTC
ESTD-ANT1	160 T C ---	---	TCCTCTGTCAATTCCTACTCCATTAGTTCAAGGTCAAGTGAAGAACTGGGGCAATTAACCAAGTAATCA TGGACTGCCCAACTCGAAACAAGAGGGCGCAGTGGAGCAGGATATTATGCTACGCGGTACCTT TTTTATGGAGGACCCAACTGAGGCT/CJGAGCTCAGATGATCCTGT
EST10398 2b	168 A' G ---	---	TGCTGGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGTTCACATTTGGGGCTTGACTTTCCACACCGGAGAAG CATGTGTTTCTTCGGGCCAAGAAGGTATCTACCTACC/JAG/JATAGTGTCTATTAGGCATTG

EST10398 2a	147 C T ---			TGCTGGGGTGGCAAGGCTGCAAAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTACATTTGGGGCTTGACTTTCCACACGGGAGAAAG CATTTGTTTCTTTC/TJGGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTG
ESTD-C7	14 G C ---			ATATCGTGGCCTTA/GCTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD- D4S95	90 T C ---			CTTTCATGCACGATAGGCTTCTCTACTAATCACAGAATTTGAGAAGAGCAAAACAACCTTTCAAGG ATAATGGGGCAATCACTTCTTTT/CJTCTTTAGAGTCTACCGG
ESTD- GPPK2L	38 G A ---			AGTCTTCATCTGCGGTGCCAGGTAGATCCCTTTCACC/GA/CCGAGAACTGCTCGATATC
ESTD- HRASb	82 A G ---			CTGGGCTGCGCCGACAGCTGCTGGCACCTGGACGGGGGCGGCGGAGGCTCACCTCTATAGTGGGGTGG TATTCGTCCACAAA/A/GTTCATCTGGATCAGCT
ESTD- HRASa	37 C T ---			CTGGGCTGCGCCGACAGCTGCTGGCACCTGGACGGG/CJTGCGGCCAGGCTCACCTCTATAGTGGGG TCGTATTCGTCCACAAAATGCATCTGGATCAGCT
ESTD- NRAMP	81 A G ---			GGAGGCAGGAGGTGGGAGGGGGTCTGCTGCTCCAGGTCCACAGACAGAGAGGCGGCTCAGTG TATCCACACCCCA/A/GTGTGGCGCTGGGAGATGAAGAGGATGATGCAGGT
ESTD-OTC	18 A G ---			GTGACCTTCTCCTTAA/GJAACTTTACCGGAGAGAAATTAATATATGCTATGGCTATCAGC AGATCTGAAATTTAGGATAAAACAGAGAGAGGATATGTAACA
EST36751 7	36 C T ---			CCAAGTCGTTCAATTTAGCTTTGCAGGTTTAACT/CJTGATTACTTTTCTATTCAAATCTCTGTA AAATTGAAATATGAACCTTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562	109 A G ---			CACGTGGAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAATCTGTCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAAGTTTCACTGGATGCATTAATAACAAAT/GJTTTTACCTTTTGAATAATAA ATGAAGGATTTGACCTGCTTCGCTCTGGAAGAGTATCCGTACCGTCTGACGTTTTGAAACAATACA GATGCTTCCCTTGTAGCAGTTTTCAGCTCCTCTACCTA
EST18288 3	121 C T ---			GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGTGAGAA GATTGACAGGTTTCATGCAGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGA/CJTGAGGAGCCAGT GTGGACAGCACCCCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAAGGCAACCTCTCTGCTGGCTC TGGCCCTAGGACTTAGTATCC
ESTD-AK- 168	31 C T ---			GGGAGTGACAGCTAGAGCACCAAGGGGGGCT/CJTACAGCTGTGTTCTCATGGAGGACAGGCTTCT GCTCATCTGG
ESTD-ALB	180 A G ---			AATCCCAGACCTTTAGGAGGCTGAGGCGGCATATCACAGAGGTGAGGAGTTTGAACACAGTCTGA CCAAACATGTTGAACCCCATCTCTACTAAAAATACAAATTTAGCCAGGATGGTGGTGCATGCCTGT AATCCCAGGAGGCTGAGGCGAGGAGATCGCTTGAACCTGGGAGCG/GJAGGTTGTGGTGAGCCGA GATGGCACCATTGCCTCCAGGCTGGGCAACAAGAGTAAACTCTGCTTC

EST70523 3	182 G T ---			TTCCGGCAGCCCCCATCTTGCCACCTGGTCCCTCAGGGGCCACCCCGGGCACTACCGCTCT CGCTCTCGGTAAATCCGGCGGGCGGCTCTTGAGACATAGCCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCCCGGGCTTGCCAGGGCCAGCCCTG/JCAGAGAGAGGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGGAGTGTCTCCACGTTG
ESTD- APOA2	101 C T ---			CCAGGTGTTGGCACGTGCCTGTAATCCAGCTACTCGGGGAGACTGAGGCATGAGAACTCTTTGAAC CGGGGAGGCGGAGGTTGCAGTGAGCTGACATCG/JTJGCCACTGCACCTCCAGCCTAGGTGACAGAGC AAGACTCC
EST58707 7	112 C T ---			CAGTGTATCTGGAAGCCTACAGGACACCAAAATACCTTAATCATCAATTGTTACAGGAGGCTTT AAGTTACAGCATCTTTGGCTCACATGAAGGCCAAATCCGAGAGAC/JTJTAGAAGATACACGAGAC CGAATGTATCAAAATGGACATTCAGCAGGAACITCAACGATACCTGTCTGTGAGGCCAGGTTTATA GCACACTTGTACCTACATTTCTGATTGGTGACTCTTGCTGCTAAGAACCTT
EST74167 6	137 C ---			AGACATGAAGGAGTTGAAGGCTACAAATCGGAACCTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGGGGCAGGCTGTCCAAAGAGCTGCAAGGCGCGCAGGCCCGGCTGGGCGCGACATGGAGGA CGTGGCGGGCGGCTGTGGTGCAGTACCGGGCGAGGTGCAGGCCATGTCTGGCCAGAGCACCGGAGGAGC TGCGGGTGGGCTCGCTCCCACTCGCAAGCTGCGTAAGCGGCTCTC
EST43211 8	132 C ---			CGCTGGTGCAGTACCGGGCGAGGTGCAGGCCATGTCTGGCCAGAGCACCGAGGAGCTGCGGGTGGC CTTCGCTCCACCTGCGCAAGCTGCGTAAGCGGCTCTCCCGATGCCGATGACCTGCAGAAAGCGCC TGGAGTGTACAGCGCGGGCGCGGAGGCGCGGAGCGGCTCAGCGCCATCCCGGAGCGGCTG GGGCGCTGTGTGAACAGGGCGCGGTGGCGGGCGCCACTGTGGGCTC
ESTD- ARSB	126 A ---			GGAGAAATGGAGCTGTGGAGGAGGCGTCCGAGGGTGGGCTTTGTGGCAAGCCCTTGCTGA AGCAGAAGGGCGTGAAGAACCGGGAGCTCATCCACATCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAACCATCAGTGAA GGAGGCCATCCCCCAGAAITGAGCTGCTGCATAATTGACCCAAAC
EST36770 4	144 C ---			TGTAGCCAAAGTCACTGCATCATTTGGCTGCTGGCAGGCTTGGCCAGTTTGCCAGCTATAATCC ATCGAAATGTAATTTTCAATTGAGAACACCAATATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAAT TCAACCTCCCGATAGGGCTGGGCTGACCAAAATATATACTGGTGTCTGTTTCTTCTGATCAT TCTTACAAGTTACTCTTATTGGAGGCCCTAAAGAGGCTTATG
EST26021 1	137 A ---			TAATGTAAGCTCATCCACCAAGAGCCTGCACCATGTTTGGAGTTGAGTGACATGTTGCAAACTGT CCATAAAGTAATTTGTGAAGAGGAGCAAGAGAACATCTCTGCAGCATTCTACTACCAAAATGA GCATTAGCTACTTTTTCAGAAATGAAGGAGAAATGCAATTATGTGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTCTTCTCTTTTGAACAAGACAAAGCAAGGCC
ESTD- BA511	29 A G ---			GGGCAACATAGTGAACCCCATCTCTACAI/GJAAAAATACAAAATTAGCCAGGTGTGGTAGCAAG TGCCTGTAGTCCAGCTACTTGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTG CAGTGAGCCAAAGTGGTGCCACTGCA

ESTD- BCL2	116 A G ---	---	---	AGCTGGATTAACTCCTCTTCTTCTGGGGCCGCTGGGGTGGAGCTGGGGCGAGAGGTGCCGTT GGCCCCGTTGCTTTCTCTGGGAAGGATGGCGACCGCTGGGAGAAC[A/G]GGGTACGACAAACCGGG AGATAGTATGAAGTACATCCATTATAAGCTGTCGACAGAGGGCTACGAGTGGATGCGGGAGATGT GGCGCGCGCCCCCGGGGGCCCGCCCGACCGGGCATCTCTCTCCCA
ESTD-BCR	69 C T ---	---	---	CAGTGGCTGAGTGGACGATGACATTAGAAACCCATAGAGCCCCGGAGACTCATCTCGGCAAGA GA[C/T]CAAGAGGTCAGCTTCTGTGTCCCGGAAAGGGAGGACGGTGACAAAGCTAACTCTGCTTC AAATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGCCCTGGCACA
ESTD- BRCA1aa	119 C T ---	---	---	AAGAAGAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGTTTTCAAACTGAAAGATCTGTAGAGTAGCAGTATTTC[A/C]TTGGTACCTGG TACTGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCACCTCTAGGAAAGGCAAAAACA GAACCAATAAAT
ESTD- BRCA1bb	139 A G ---	---	---	ACTAAATGTAGAAAAATCTGCTAGAGGAAACCTTTGAGGAAACATTCAATGTCACCTGAAAGAGAA ATGGGAATGAGAACATTCCTCAAGTACAGTGAGCACAATTAGCCGTAAATACATTAGAGAAAAATGTT TTTAAAG[A/G]AGCCAGCTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCA GTATTAAATGAAA
ESTD- BRCA1cc	126 A G ---	---	---	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGTTGTTGAAATAAAGGAAGATAC TAGTTTGTCTGAAAATGACATTAGGAAAGTTCTGCTGTTTATAGCAAAAGCGTCCAGAA[A/G]AGGA GAGCTTAGCAGGAGTCTAGCCCTTTCACCCATACACATTGCTCAGGTTACCGAAGAGGGGCCA AGAAATTAGAGTCTCAGAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
EST51212 0	122 A C ---	---	---	ATCCTGAGCTCGCCAAATAGCTTCTTGTTCTACTTCTCTCTCCACAGCCCCAATTTCATTCTCA GAGGAAATCCCAAGCTTAGAGCCCTGGAGCCCTTGTGCTCCCACTCAATACA[A/C]AAAGGCCCT CTCTACATCT
ESTD-C1R	40 A G ---	---	---	ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCCTCCCT[A/G]ATTGCTCCGGGAAGCACATTCA CAA
ESTD-C1R	40 A G ---	---	---	ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCCTCCCT[A/G]ATTGCTCCGGGAAGCACATTCA CAA
ESTD-C6	31 A C ---	---	---	CCAGTCAGTTTGGGGACAGCCATGCACCTG[A/C]GCCTCTGGTAGCCTTTCACCATGCATTCCATC TAAGCTCTGCAAAAT
EST20118 2	119 C ---	---	---	GTCCGAATCCTCCTCTGAAAGTGCCGGTTTAACTGCTCATGACGCTGCGGCTGTGTCCAGCT GAGGTGAGGGGCCCTTGAAGCTGGAGTGGGTTTAGGACGCGGGTCTCTGCGTGCATCTAAGCTCT GAGAGCAAACTCCCTTGAAGCTGGAGTGGGGTTTAGGACGCGGGTCTCTGCGTGATCCTAAGCT CTGAGA
EST53018 6	67 A G ---	---	---	ACAAATCCAGGTACACATTCAGAAAGAGGGGGTGGTCACTGAGCCTGGGTAGGTCCAGTAATCCA [A/G]GGATTGAGGAAGGAGGCCACAGGATCGAAGTTAGTGAAGTC

ESTD- CB22	119 C T	---	---	GGCAAGTTTTATTGATAGAGAGAAATCAAATATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGGATGGACAGACAATGGGAGTGCCAAACCCATAGGCTGGAATACAAAAG ACAGGCAAGGAGGGTAGAACCATCAAAGAGGAATAGGCTGGTACCCCAAGCAAGGAGGACCT AGTAACATAATTGTGCTTATTATGGTCTTTCCCGGCTTCTCTCACACAC
ESTD- CB23	136 C	---	---	TAGAACCATCAAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGTGCTTTCCCGGCTTCTCTCACACATACACAGAGCCCTACAGGACACAGACGCT CTCAGAGCAACCCTAGCCCATACCTCTTCCCTTCCAGAGGACCTGAAAAACGTGTTCCCAACCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAA
ESTD- CB24	145 A	---	---	ACAGGACACAGACAGCTCTCAGAGCAACCCCTAGCCCATACCTCTTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACCCGAGGTGGCTGTTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAAAG GCCACACTGGTATGCTGGCCACAGGCTTCTACCCGACACAGTGGAGCTGGTGGTGAATGG GAAGGAGGTGCACAGTGGGGTCAGCACAGACCCGACGCCCTCAAGGAG
ESTD- CB25	146 A G	---	---	GTTTTCTTCAGACTGTGGCTTCACTCCGGTAAGTGAGTCTCTCTTTCTCTCTATCTTTCGCCGTC TCGTCTCGAACCCAGGGCATGGAGATCCACGGACACAGGGCGTGAGGGAGGCCAGAGCCACCTG TGACAGGTAG/CJCTACATGCTCTGTTCTGTCAACAGAGTCTTACCAGCAAGGGGTCTGTCTGCC ACCATCTCTATGAGATCTTGTAGGGAAGGCCACCTGTATGCCGTG
ESTD- CB27	125 C T	---	---	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTTGTTGGGCTGTGTCATTTACAGAGTGCTGTGGAGTTCTGCTCATCACTGAC/CJTATCTTC TGATTTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTTTCTCTCCACCCCAATGCT GCTTCTCTGTTTCATCTGATGGAAGTCTCAACACCATTTCCATACC
ESTD- D4S338	59 A T	---	---	TTTTCTGTTTACCTTGTTCAGATCTTCAGAGGAATCCCTATATATGGCAGGTATATGA/TATGTA TTCTTAAACAATAAATTTGAAAGTCCAAATTTACTCCTTGATCCATGGACTGCAGATAAATGTTA TTTTAGCTGTCAGAAAAACAATACTAATCTTGATATGTTTCATCAGAGCCCTTGGGTGACCCAGGTGA TTGCCAATAAGCAGTAATTTTGGAGGAATCTGTTTCAATGCAGTAG
ESTD- CYP2D6	61 A G	---	---	CAGGCCAGCGTGGTCGAGGTGGTCACCATCCCGGAGAGAACAGGTACGCCACCACTATGC/JGJCA GGTTCATCATTTGAAGCTGCTCTCAGGGTCCCTTGGCTGAGCAGGGCCGAGAGCATACTCGG
ESTD- D11S1873	40 A C	---	---	AAAAAACATTTAACACCTTTTCAATCATATACACCATAJ/CJATTTCCATTTTTCACATAAGTCA GTTTGAGCTGAGTTTCCAAATTACTTGCAATCTAAAATGTCAACTGATTAACTGCAAGTTCAACAG ACAACTTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATATTGCCCA TATCTGCATGTC
ESTD- D17S33b	169 C T	---	---	CATCCCCAAGCCCATCTTAGCCACTGGCATTTTTCGCCCTTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCTTTGTAGTCCATGGAAAGGCTCCTCTGGGGCGGTG GGGTTGTGGCTATGGTGGTCTGTGTAGAJ/CJTTGGGGCTTTGGTTTCAGTTGCATATTGCGTT ATTGCAGATTGCTTGTCTTCCACCTGAGCGAGCCTC

ESTD- D17S33a	75 C T ---	---	CATCCCAAGCCCATCTCTAGCCACTGGCATTCTTTGCCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCTACACATCCAGGGGGCCCTACCCCTTTGTAGTCCATGGGAAAGGCTCCTCTGGGGCG GTGGGTTGTGGCTATGTGGTCTTGTGTAGACGGGGCTTTGGTTTCAGTTGCACACTATTGCGTT ATTGCAGATTGCTTTGCTTTCCACCTGAGCGAGCCTC
ESTD- D18S8	133 A G ---	---	TTTGAGACCACCCTGGCCAAACATGGCGAAATCACAATCTCTACCAAAATACAAAATTAGCTGGGTGT GGTGTACATGCTATCGTAATCCAGCTACATCGGAGGCTGAGCAGGAGAAATTGCTTGAACCCQA /GJGGAGGCAGAGCTTGACGTGAGCCAAAGATCACACCCTGCACTTACAGCCTGAGGTGACACAGTGA GACTGCTCTCAA
ESTD- D3S11	44 G ---	---	AACTGATTAGAACCTGAAATACATATTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCAATTAATAATCCAATAAAGTACACTGTAATAAGAAATTTAACAGAAATATCATTTG TTATTCAAACTATTATCACTTATTTATTTGTAAGCCATACTAAATTTCTAAAGCATGTTCTGAAAG TTTA
ESTD- D3S12	37 A G ---	---	AGGTTCCACATTATTGCTGATGTTTGTGATGTTTCCJAGJGGAGCCTTGATGTCATCTGTATCTCCT CAGGTATCCCACTTGAGACGTACTTTTCAAAAACCTCTCTACAGCCGTTGTTTATTAAATCAAGGT TGAACATAAAGTA
ESTD- D3S2b	247 C T ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAAACTGACAGCCATTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCC AGAAAGTGAACATACCTGCTCCTAGAACCCAGAGTCATACTGGATGTTCTGTTCCGGTCTTACCGATGG CAGGTATGAAATATAATACTGCTCTTATTGGAAGGATGCTGTTGGT
ESTD- D3S2a	248 G ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAAACTGACAGCCATTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCC AGAAAGTGAACATACCTGCTCCTAGAACCCAGAGTCATACTGGATGTTCTGTTCCGGTCTTACCGATGG CAGGTATGAAATATAATACTGCTCTTATTGGAAGGATGCTGTTGGT
ESTD- D7S399	83 A G ---	---	TGAATCTTAATTGCTATCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCJAGJGCTCTCTACATCATCTTTTCAAAACATTTTCATCCATGGACTCCATAC TAGAATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DMb	146 A C ---	---	GTGGGACACCGAGGGCTCCAGGCTGGGGCTTGACGTGTGGCTCAAGCAGCTGCTGGGCTCCACT TCCATGGGTGGGGCTGGGACCTCACTGCTCCCTGGGAGAGAGAGGGAGTGGGAGGGAGACA GAATGCTGATTACJCTGTGTGAGAACCAAGAACTTCTGGCCTGTGGTAGGGCAGCTGCTTCCAAG ACCTCTGATTGAGGAAGGGGAGCAGAGCGAAGAGAACAGAGT
ESTD-DMa	66 C G ---	---	GTGGGACACCGAGGGCTCCAGGCTGGGGCTTGACGTGTGGCTCAAGCAGCTGCTGGGCTCCACJ GJTCCATGGGTGGGGCTGGGACCTCACTGTCCCTGGGAGAGAGAGGGAGTGGGAGGGAGAGA CAGAATGCTGATTATCTGGTGGAGAACCAAGAACTTCTGGCCTGTGGTAGGGCAGCTGCTTCCAAGA CCTCCTGATTGAGGAAGGGGAGCAGAGCGAAGAGAACAGAGT

ESTD- DRD1	154 C T ---	---	---	TCCCCAGCCCTATCGGTATATTGGACTATGACACTGACGTCCTCTCTGGAGAAAGATCCAAACCATCAC ACAAACCGGTACAGCACCCCAACCTGAACCTGCAGATGAATCTTGCACACATGCTCATCCCAAAAGCT AGAGGAGATTGCTCTGGGIC/TTCGCTATTAGAAACTAAGGTAC
ESTD- DRD2	144 C ---	---	---	TCTGCCCTTGGTGCAGGAGGCTGCCGGGAGGCCAGGAGCTGGAGATGGATGCTCTCCAGCACCA GCCACCGAGAGACCCGGTACAGCCCCATCCACCCAGCCACCCAGCTGACTCTCCCGACCCG TCCCACACGGTCTCCACAGCACTCCCGACAGCCCGCCCAACACAGAGAAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T ---	---	---	AAGACGATGGCCAGGATAGGCGGCAGTAGGAGAGGCGATAGTAGGATGTGGCGGGCCCTGGCTGG CACCTGTGGAGTTCTCGCCACACAGGTGTAGTTCAGGTGGC/C/TACTCAGCTGGCTCAGAGATGCC ATAGCCAGAGGGAGGTGCGTGATGCCAAGGGCTTCTGTGAGGAGA
ESTD- ERBB2	93 C T ---	---	---	TCTTCAGGATCCGCATCTGCCCTGGTTGGGCATCGCTCCGCTAGGTGTACGGGCTCCACAGCTGG GGTGAGGGGGTGGTGGGTGAGTG/C/TGGGGGGCGGTGCAGACCCACGGGCTGGGAGGACTTCA CCCCGCCTCACTCCGTTTCTGCAGCAGTCTCCGCATCGTGACT
ESTD- ETS2	43 A G ---	---	---	ACTCACAGTGCTTTTAAGTGAATGTGCGAGAAAGAGGCACCI/AGGGAAGCCGCTCTGGCGCCTG GCAGTCGGTGGACGGGATGTTCTGGCTGTTGAGATTCTCAAGGAGCGAGCATGTCGTGGACACA CACAGACTATTTTGAATTTCTTTGCCCTTTTGCAACAGGACGCAATGCAAAAACCTCTTTGAG AGGTAGGAGGGTGGGAAGGAACAACCATGTCTTCAGAAAGTTAGTTTG
ESTD-F9	111 A G ---	---	---	AGATCCTGATGATTTTTCCTATTTTCTAAATGTTTACAGTTTGAAGTTTAGATTATGCCCA TGCTCCATTTGAGTTAATATTGTGTAAAGTATGATGTTT/AGTCAAACTCATTTTTTTTTTCC ATAGGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAC
EST68787 5	144 A ---	---	---	CTTCTATGGGATTTGACTTTATTTCTCCATGCTTACCTTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGAGCTCATGACAAATTTGAAGCTGACAAATACACAAGAGGAAATAAATTCACAGTCAA AGAATCAAGCACCTTTTCGAAACATTGAAGTTGTTTTGAACCTGGTGTCACCTTTAATTACAACCTAG CAGACGGAACTGAACCTCAGGGTAAGAAT
ESTD- GODH	200 C G ---	---	---	CGCAGACCGGTGAGTGGGGTGGGAGTGTGGAGGGAAGGAGGAACTGGGGGTTTAGGGACT TTCCGGGTGACTTTCCCGTTCTGTGCTTGCAGAGAAAGGGGGGAGAACACAGAGCCAACTGGCTAA GTGTAGGGACCTCTGGTCGACCGTGTGTTCTGCTGCCCTGTTTACGCTGCTGTCTGCCGCGAGT/C GIGACTCTGTCCCGAAATCCGAGAGCT
ESTD-GCK	88 A G ---	---	---	GTTTTATGCATGGCAGCTTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGGTCACCATGAC AACCACAGGCCCTCTCAGGA/AG/CACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGC TGGAGCAGGAAATGCCAGCGCGCCCTGAGCCCCCAGGAGGAGGCTAGGATGTGAGAGACACAGTC ACCTGCAGCCTAATTACTCAAAGCTGTCCCGAGGTACAG

[illegible]

EST45311 0	151 C T ---	---	GCCTCCTCTCTTCCAAATCTGTCCCTATAGTTTTCTCTATTAAAGTGAACACTACATGCATTCCTTTAGT GGATAGATGCACAAACACACAAAGCCATTATGGGAAGGATCCACGTGTGTGGCCATATTGTAACA CATTTTCTGCAAATC/TACCTCTTTCAITTTAAACAGCCCTATTCAATGGCCTTTTCTTTTTCAGTA GTACATACACATCTGTGTCAATTGTGAAT
EST65258 8	80 A G ---	---	TGCCCCATCAGCGCGCGAGACATGGCTTGGCACAGCTCTTGAGGATGTACCAATTAACCAGAAAT CCAGTTATTTTCQ/AGJCCCTCAAATGACAGCCATGGCGCGGGTGCTTCTGGGGCTCGTCGGG GGACAGCTCCACTCTGACTGGACAGCTTTTGCATGGAGACTTGAGGAGGAGGCTTGAGGTGGT GAGGTAGGTGGCTGTTCCCTGTGCAAGTCAGGACATCAGTCTGATTAAA
EST38216 3	26 A T ---	---	ATGCAGGATGAAGGTGGACAGGGAGGATJGAGGGCCAACTGTCTATCCAGGGGCTGCAGATGTGC CTGGACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782	149 G T ---	---	ATACTAGTACAAGTGGTAAATTTTGTACATTACACTAAATATTAGCAITTTGTTTAGCATTAACCTAA TTTTTTCCTGCTCCATGCAGACTGTTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGGAAAG TTTTTTTTCTCTG/TJAGTGCCAGTATCCAGAGTTTTGGTTTTTGAACATAGCAATGCCTGTGAA AAAGAACTGAATACCTAAGATTTCTGTCTGGGGTTTTTGTGTCATGCA
ESTD- KRT10b	183 C T ---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAAGTGTACCCTTTTGGCAATATT AAAGGAAGAAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACATACTTCTTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGC/TJTGCTTTTAAATAGT CTCTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT10a	133 A G ---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAAGTGTACCCTTTTGGCAATATT AAAGGAAGAAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACATACTTCTTAAG GJGAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTC TCTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT8b	231 C T ---	---	ACCCTCACCCCTCCCTTAGCCCGTGGGAAGCAGGAAATCTCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACCTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCCGTCTCAGGTTTACCA/C/TJGTCAACATTGACACA
ESTD- KRT8a	21 C T ---	---	ACCCTCACCCCTCCCTTAGCC/C/TJGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGAGGGCCTGACATGAGACCTCAGACAGAACCTTCTAGAG TTTGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCAT GGCTGCCTATCTCTCCCGTCTCAGGTTTACCACGTCACATTGACACA
EST75099 6	82 C T ---	---	CACTTGTGTGTAGATCTCCTCAGTGGCCGCTCTACTGGGTGACTCCAAATTCACCTCACTCACTCA AGCATCGATGTCAA/C/TJGGGGGCAACCCGGAAGACCATCTTGGAGGATGAAAAGAGGCTGGCCCAAC CCTTCTCCTTGGCCGTCTTTGAGGTGTGG

ESTD-LF79	142 A G ---			GGGTGATTTGAGGCTCAGTTAATATTTCAAATTTAAACCGTAGCAAACTGCATTGGTATTTAGA AAAAATAAAATTTCCAATATGTAGTGTCTGTATATACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACC[A/G]GGAGGGCTTCCTTACCACCCAGA
EST35879 9	142 A C ---			GAGATCGGTGTGTGAGTTATTAGGCATGTTACCTGTGATTTCTCCCAATCTTGTGCGTTCCACCGATG GAACTGCCGGCAATCTGACACGTGTGCACCCAGGCTGACCCAAATTAGGTGAACATGGCTTCGAG AGAGTTG[A/C]ACAGATTCTCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGAGCTGCTGGATGA A
ESTD-LMP2	35 C G ---			TACACACTTTCCTTACCCATTCACTGAAAACGACT[C/G]GCAAACTGGAGCCTTGTAGGAATGGAGT TGACCTTCCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	113 C T ---			TGTCAGTGTCCCCTAGGGGCACCTCACACATCCAGCTTCTCAGCTCTGCCCTGTCTGCTGCTGCTGCA AGGGTTTGTCTTAATCTCAATTCATGCTCTTTCATCTTTTAG[C/T]AGCTGTGGGTTTGTGTTG TTCTTCTGTTTTTGTCTAGTATCTGACTACTTTTAAATTATAAAAGAGATGATCTAAACAAAAATAG AGATTGTTATCAGAAGTTCACACATTTATTAAAAATTTTTCACCTG
ESTD-MCC	45 C T ---			TTGTCAGGAGTGTGCTGATGCTGCCTCCCGAGCTCTGTCCCTAGC[C/T]GAACTTCAGGACAAACGTGC AG
ESTD-METH	118 C T ---			CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCGAA TCTCAGGAAGTCTCTGCTTTCCAAAGGTTTGGTCTAAGTTGCTGATTACC[C/T]GGATTTTCTGACG ATCTTCAACTGCTAGAGCACTGCTGCTCTGTTTAGCATGG
ESTD-NF1	25 A G ---			ATTATCCAGATGAATTTACAAAAC[T/A]GTTACCAGATCCACAGACTGATATGGCTGGT AACATGGACTTGTATATTTGTACAAAAAAGTTTATTTTCTAAAAAAGAAAAAGAAAA AAATTTAAAGGGTGTACTTATATCCACACTGCACACTGCTT[A/G]GCCCCAAACGCTTATTGTGGT AGGATCAGCCCTCATTTTGTGCTTTTGTGAACCTTTTGTAGGGACGAGAAAGATCATTTGAAATCT GAGAAAACTTCTTTTAAACCTCACCTTTGTGGGTTTGTGGAGAAAGTTATCA
ESTD-NPPA	45 A G ---			TGTCCTTAGGCCCCAGCCCTGCTTGTCTCCTCCCTGGCTGTTATCTTC[A/G]GTACTGCAAGAGAACACA GACAT
ESTD-NPAS	202 C T ---			GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTTCTGCAGGTCATATAGAATTTGGT GGGTTTCTTTTATGTAGGGTGATATTGGATACTTTTGTGTTGATTATATATAGCAATTTGAGGG ACAAACCATAGAGCAGAAATGGGCTTGAATAGTAGTCTTATTTAACCTTGGCAATAGCATTTG CTTATCCCTGTGGTTTAAATAAAAT
ESTD-PAI1	100 A G ---			GCCACCACACCCACCCAGCACACCTCAACCTCAGCCAGACAGAGTTGTTGACACAAGAGAGCCC TCAGGGGCACAGAGAGAGTCTGGACACGTGGGG[A/G]GTCAGCCGTGTATCATCGGAGGCGCGGG CACATGGCAGGATGAGGGAAGACCAAGAGTCTCTGTGTTGGGCCCAAGTCTCTAGACAGACAAAAACC TAGACAAATCACGTGGCTGGCT

ESTD-PAR	120 A	---	---	CTCTTCAGGAACCAACAGCTCTTCTACCAAAACACGACCTATTGCTGTCCGAGAGGTACAACCCGTAGA
ESTD-Per/RDS	74 A	G	---	ACTTCTTCTAACTGTAATTTAGTTAAAGGAATCGAAACTGGCTCTGAAGACATGGAGATACTGCCT
EST68308	5	29 C	T	AATCGACTGGCTTTCATTAGCTCTGTAGTGTCTTCTTACCTTTCTGTGTTCTAGAACGTTTCTTAG
EST54045	6	39 A	G	GACTGGCAGTTTAAGCTTTCACITTAGGCTTCTGTATACCCATGCCC
EST54045	6	39 A	G	ACCTACAGACGTCGCTGGATGGTGTGTCCAAACCCGAGGAATCTGAGAGCGAGAGCAGGGCTGGCTG
EST54045	6	39 A	G	CTGGAGAGGAGCGTGGCGGAGACCTGGAAGGCTT
EST54045	6	39 A	G	GGAAAGAGATTAAAGAACTGATTGGAGTC/TAATCTGTTCTTTGAGTGTGGAAGAGTTTATGTC
EST54045	6	39 A	G	TCTGCTGAGTTACAAACAGATCCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAAT
EST54045	6	39 A	G	GGAGAAAGTAGACTTAAAGGTAAAGTAAGTAGTTATTTTTTA
EST54045	6	39 A	G	GGAATATTAAAAATATTTTAAATACCTCCATTTTGCTT/AGTTCCTTTTAGTGAAGATGATACCTGC
EST54045	6	39 A	G	AAAAGACATGGCTAAAGTTATGATTGTCTATGTTGGCAATTTGTTTCTTACAAAATCGGATGGGAAA
EST54045	6	39 A	G	TCTGTTAAGTAAGTACTGTTTGGCTTGGAAITGGATTTTAAATGTTGACTTTATCAT
ESTD-PXMP1	88 A	G	---	ATGAAACATGGTCTTTAATTTATGATATGTTTGTATAGCTATCTTAAAAGGGCTCTTTTTTTTA
ESTD-PXMP1	88 A	G	---	ATGCAGAAAGAGGGGAAA/AGGAGCGAGCTGTGGTGGACAAGGTGTTTTCTCAAGGCTCATAC
ESTD-PXMP1	88 A	G	---	AGATTCTGAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAGTCTTATGAAATATATACTT
ESTD-RDS	127 A	---	---	CCCGAGAACTCTGAGCGAGCGAGGGCTGGCTGTGAGAGAGCGTGGCGGAGACCTGGAAGG
ESTD-RDS	127 A	---	---	CCTTCTGGAGAGTGTGAAGAGCTGGGCAAGGGCAACCAAGTGAAGCCGAGGGCGCAGACGAGG
ESTD-RDS	127 A	---	---	CCAGGCCACAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCAC
ESTD-RDS	127 A	---	---	CCAGAAACGTGGATCTCCCCCTCATCCAACTCCGAAAGTCTGAA
ESTD-s14544	94 G	T	---	TTGGGAAGTTAGAGCCCTATATTAATTAACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA
ESTD-s14544	94 G	T	---	TATCCCAAAGTTGAAATGCTCAGTTG/CTGTGTGGTTAGATGCAGGATTTATATGATCCGTTA
ESTD-s14544	94 G	T	---	ACCTCT
ESTD-s14544	94 G	T	---	ATCACAGGCTCTGGTCTCTGGCCATCATTTCTCTGGGAGAGATGG/CTGTGGTGTCTGCAAGCCCTT
ESTD-s14544	94 G	T	---	TGGCAATGTGAGATTGATG
ESTD-s14544	94 G	T	---	AGGAGAAAGCTGAGGAGGGGAAAGAGAGACAAAGAAATGACATTGATGAGTGAAGATGTC/TTGGCTCAG
ESTD-s14544	94 G	T	---	GATGCCGGGAAATGAC
ESTD-s14544	94 G	T	---	TGAAGCTTCTGCCAGCTTGCAATTGTTCTAGGAGAACCT/CTGGCTCATACCTTTATCTATAGCCTT
ESTD-s14544	94 G	T	---	CCCCTAGGCTCT
ESTD-s14544	94 G	T	---	TGAAACACCTGTGTGTCGGAGCCAGGTGTGTTCTCTCTGGAGCCTGAGGAGTTTGTGTCTGTG
ESTD-s14544	94 G	T	---	CAGTCCCCCGGCCACCTGCTGTGTTGAGCCTGGACATACACCTTCACTCTTGGCCCGGAGAGAC
ESTD-s14544	94 G	T	---	ATTACCCACCTGGCCATGCCCTGGCTGTGTGACAC/CTTCTCTGTGAAGACCCCAACCCCTGC
ESTD-SPTB	176 C	T	---	CTCCCCACCAAGCCAGTTTCTAGCAAGGGCAGGAC

ESTD-TAT	224 C	---	---	AAATGGTCAGGACCCTGATCCACAAGAGTGGTACCATTTTCATCAGGGCCATCAGTTTCATTGAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCATTCATCTTAAATGACTTGTGGGACAGGATCA ATTTCCTCTCACCTAGAACGTTTGTTTACAACTTTTCTCCAGTATGGATGGGATTATGATGGGGG GAGAAGCAAAATTTTAAATAGGACCCATGAGACACATCA
ESTD- THFB	125 A C	---	---	TGGGGCTTTCTCCGGCAGGTAGACTTCTTACTTGGCTGTGATTTCCAGAGAAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAATCACACAGGATC/A/CJCTTCAT CCACACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG TAGTGAAGTTTTCATCTCCTGTGAGCTTCTGGATTCTTGTCCACCCGCAACAAGAGTCTATGC CAAGGCAGAAAAGCTGGTCTTCATGGGCAAAATCAATGTCTCTCCAGATTTCAGTATCCCCAA GCAGTGCATCCATTGACACATAATAATGCATCCAGACAAGAGGTCAATAATATTGATGTCGTTAAA CATGGGTGTGATCCATTTTTCATTTGGCCATAGGTCCCTATGGGGATGACA
ESTD-TYR	122 G T	---	---	AGTAGTGGATGAAGCTAACCCAGCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAATCCTAATCAGTCTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACA AACCACCTGGTGAATATAATAGATTGAGTTAATACTGTATTTCTTTCACITTTATTACCTTCTTCT AATACAAGCATATGTTAG/A/CJATTAAGTTCTAGGCATCTT
ESTD- TYRP1	222 A C	---	---	AGTAGTGGATGAAGCTAACCCAGCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAATCCTAATCAGTCTGGTCTAACAAATGCCCTACTCTTATGCATTAGTATCACA AACCACCTGGTGAATATAATAGATTGAGTTAATACTGTATTTCTTTCACITTTATTACCTTCTTCT AATACAAGCATATGTTAG/A/CJATTAAGTTCTAGGCATCTT
ESTD- TYRP1	222 A C	---	---	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCAGAGCCCAAGACACAAGGTACAGAGACAGGAACACCCAGTG ACTCTGAGATGTCA/CJTCAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12	148 C T	---	---	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCAGAGCCCAAGACACAAGGTACAGAGACAGGAACACCCAGTG ACTCTGAGATGTCA/CJTCAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148 C T	---	---	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACAC/A/GJTGATGCTGGAATCACCAGAGCCCAAGACACAAGGTACAGAGACAGGAACACCA GTGACTCTGAGATGTCAACAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74 A G	---	---	ATGGGCTGAGGCTGATCCATTACTCATAT

EST58607 0	105 A G ---	---	CTCTGGATGGGTTACAGGTGGCAGGCACAAGCCAGTCCTCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCTCACTGGAGAACAGGACAGCCACAGTGCGCGGGATGGCCGGCGGAGTTC TGGTTGCGGCCACGGCTGTGGCTCGTTGTGAACGGTAGCCTTTGCGGTTGCGATGCCTAAACCTTTGT TCTTGGCCAAAGGAGGGGGGGTGCATGCCTGAGATGTAGATGGGGC
ESTD-VWF	36 G ---	---	AGGTAGGAAAAGCAAGAGTTGATTAGTGAAGGAGAGAAATGGACCTACCTCCACACTGTCCTTTGG TCCCCTAGAGTCTG
EST71770 6	189 C G ---	---	AGCACCACTCTCAGCTCAAGCCTCAGACCAGATGCTGTTCTATAAGGATGACGTGCTGTTTACAA CATCTCTCCATGAAGAGCAGACAGAGTTATTTTCTCTGAAGTCCGGATCTATGACTCAGGGACAT ATAATGTACTGTGATTGTGAACAACAAGAGAAAACCACTGCAGAGTACCAAG[C/G]TGTGGTGGA AGGAGTGCCAGTCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAGG
ESTD- TNFAB	152 A G ---	---	TTCCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTGGGGGCATGAGGACGGGTTGAGCCTCCAGGGTCTACACACAAATCAGTCAGTG GCCCAGAAGACCCCTC[G/G]GAATCGAGCAGGGAGGATGGGAGTGTGAGGGGTATCCTTGATG CTGTGTGTCCTCAACTTCCAAATCCCCGCCCGCCGATGG
ESTD- TNFAa	88 A ---	---	TTCCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTGGGGGCATGAGGACGGGTTGAGCCTCCAGGGTCTACACACAAATCAGTCAGTG GCCCAGAAGACCCCTCAGAAATCGAGCAGGGAGGATGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGTCCTCAACTTCCAAATCCCCGCCCGCCGATGG
EST52418 6	113 A G ---	---	CAATTACAGGGTCAACTGCTATGATGTTTGGAGCCCACTGTCACCCCTTTGGTGCTACAAGATGTG GGGAGTGGCGGGAGTTGGCGAGTACGGGCTGCAGGCATACACT[G/G]AAGTGAAACCTGTGAGTG TGG
EST13586 3	89 A G ---	---	CCCCTCTATTGCCCCAGCCCCAGGGACAGAGCTGATCCTTGAACCTCTTAAGTTCACATGGCCAGGA CCAGTGAGCAGCAACAGGGCC[G/G]GGGCTGGCTTACAGCCTCCAGCCAGACCCCTGGCTGCAGA CATAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCTGCC CCGGTCACTC
EST51976 7	123 A T ---	---	AGGCAGAAACTGGGCCCCATCGGGGGACGTGGAAGGCCACTTGAGCTTCTGAGAGAGGACCTGA GGGACAAAGTCAACTCTCTTTCAGCACCTTCAAGGAGAAAGAGAGCAGGACAGAGTCTCTCTC CTCCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGCAGCAGGAGCAGGAGTGCAGATGCTG GCCCTTTGGAGAGCTGAGCTGCCCTGGTGC
EST11458 6	140 A G ---	---	CCACTTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGTCTATCTTCGAGTTTTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTTACCATTTTCCACAGTGGT CCC[G/G]TTAAACATTTCTATGAGCCAGGAGAGATACGTATTCCTGCAAGCCGGGCTATGTG TCCCGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC

ESTD- AT3aa	60	CT ---	---	AGACCTCAGTTTCTCTGTAAAAGGGAAGTTTGTCTTGATCTCCATGGGCCAGCCTJAGCA CTGGTGCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGACACAGGTGGAGGAAATTTGAAAGGGCA TTGGAATTCAGAGCAAGAGACAGATATTAAGAGCTGGGAAATGTGG
EST39852 8	106	C G ---	---	CGGTCTCTCCAGGTATTGTCAGAAAGCCGAGATGACCTCTATGTCTCAGATGCATTCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCACTCTTTCAGGTTACAGAAAGGAGATGCATGAACA GCAGGAACACCGTGGAAAAGCCCTGTTCCAGTGTAAAGGCATGCAAAAGGCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112	A G ---	---	ACCTGGTGTGCTGGTGTGGTGAACCTGGTCTCTTGCCATTCGCCGCCCTCTGGGGCCCGTGG TCCTCTGGTGTGGTAGTCTGGAGTCAACGGTGTCTTJAGTGAAGCTGGTGTGATGGCA ACCCTGGGAACGATGGTCCCAAGTCCGATGGTCAACCCGGACACAAGGGAGAGCGCGGTACCC TGGCAATAT
EST36027 2	120	A C ---	---	AGTGACTTCCAAGGAATGGCTACCAACCTGCTTCATGCGCCTGCTGGCCAACATATGCCTCTCAGA ACATCACCTACCACTGCAAGAACAGCATTCATACATGGATGAGGAGACTGGWCJAACTGAAAA AGGCTGTCAATCTACAGGGCTCTAATGATGTTGAACCTGTTGCTGAGGGCAACAGCAGGTTCACTTAC ACTGTTCTGTAGATGGTCTCTAAAAAGACAAATGAATGGGGAAAGACAA
ESTD- COL2A1cc	112	A G ---	---	AGATGTATATAGTCTCAAACCTGGCCATCTCCATTTTACGTCCAAAAGTTATACAGCTAGACAACA GTGGTACATACGTTGCTATTTATGCTCTCTTCTCTGTCACTTTCJAGJGGGTGTCAAGGTGAAAA GGTGAACAGGGTCCCGTGGTCTCCAGGCTCCAGGTAAGTCAACTCAAGCATATACAATACTGCCT TTGGTCAGCCTATTGAGCTGTAATCACCATACCGTACCT
ESTD- COL2A1dd	97	CT ---	---	TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTGGACCTGGAACA/CJTTGGACTTCTTCTACTGCAGCAGACAAGACTTA CCCAAGAGAGATTAAATGGCAAGATATACAATACAATTTTATTTGACCAAACTATCATGGAACA GCATT
ESTD- CPT2	150	A G ---	---	GCCGCAATGCCCGGAGTTTCTCAATGTGTGGAGAAGCCCTTAGAAGACATGTTTGTATGCCTTAGAA GGCAAAATCCATCAAAAAGTTAACTTCTGGGCAGATGAAAAGCTACCATCACTTCTCATCATGAAAAC TGGGAGGCCCGGCATJAGJGTGCTCATGCCTGTAATCCAGCATTTTGAGAGGCTGAGCGGGTGGAT CACTTGAGGTGAGGAGTTTGAGACCACCTGGCCAACAT
EST12274 0	135	A G ---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTGCTTCCAAATAGAGCCTTACCAAAGTGAT TACATAAAGAAGTCAAGTGTGTTTACTCTCATGACCAATAATCTTCCCTCCTTAGGATGAGGTG AVGTAGTAAATGACCGATGGGTGAGAACTGTTCTGTCACTGAGGAGTACTATAACTGTGAAGA TAAATTCAGCCACAGAGCTTGCCAGATC
EST76807	91	G ---	---	ATGCTAAGGGGATCGGACATGAAAGGACCCCTGTGAGCCGATTGTCTATCTCCAGCGGCCCTGTCAATC CAGCTCACTCATCAATGGGGCAGTCAGGCCAGGCACTGGGCTCCGGAGGACTCAACCACTGCCCCCT GCTGCCATGTGACTGGTGCAGTTGAGGACTTCTTG

ESTD-SSA1	111 C T ---	---	TTTGGCTTGGGCTGCTGCTTGGGATATTTGAAAGAGATC/TTTGCCAGTCCAAATGTCTTAGA GAGTTTCCCAATGTTTCTTGAATAGTTTCATAGTTGAGGCCCTAGATTTAAGTCTTTAATCCATT TTGATTTGATTTCTGTA
ESTD-RVR1	109 A G ---	---	CTTCGTGACGGGAGGTACGCTCCGCTCTTCATGGACATATGGATGAGTGTCTGAACATTTCCC CTGCTGACAGTATGACACGCGAGACTTGTCTACTATAGAG/GJGGGAGCTGTGTGCACTCATGCC CGCTCCCTCGGAGGCTGGAGCCACTGAGATCAGCTGGAGTGGAGCCACCTGCGTGGGGCCAGCC ACTCCGAGTCCGGCATGTCACTACCGGCGAGTACCTAGCGCTCACCGAGG
ESTD-WT1	70 A G ---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCTCCCTTCTCTTACTCTCTGCTGCAGGATGTG CG/GJCGTGTGCTGGAGTAGCCCGGACTCTTGTACGGTGGCATCTGAGACAGTGAGAAACGCC CTTCATGTGTGCTTACCGGCTGCAA
ESTD-F2 EST44438 7	100 C --- 62 C T ---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCCAACTGTGCATGCACGCTTAACCTCT GCACCAATGGCTCCAAAGCCCGTAGGGAACTGGGGGATCTAGGGATGGGTGAGGAATGGCCC AGCCAGTCCGGCGGTGCTGGTCCCAACAGAGGAGGCGGTGGAGGAGACAGGAGATGGGC TGGATGAG
ESTD-PBDA	103 A G ---	---	GCAGCCAGGAGCCGCTGCACATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGA/C/TG TCCTGCTCGACCTAAGCGAGCAGCTCAAGAGCCGAGCGAGGTGGG
EST12839 3	122 A G ---	---	CCCTCTCATGCCAGATGGAATTCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAT CTGAGCCGTGGCTGGGAAGGGCAGGACTAATCCAA/GJTCCTACCCGAGCTTGCTCGCATACAG ACGGACAGTGTGGTGCAACATTGAAAGCCCTCGTACC
ESTD-CTLA-4	48 A G ---	---	TGCAAAACACAAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAAACACAGCAGCTTACTCCAGAG/GJTCAGGTCCA AGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAAGGGAACCTTGAATGTTATTCAAC TGGATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACTTAGCTTAG
ESTD-ACE	96 C T ---	---	ATGGCTTGCTTGGATTTGAGCGGCACAAAGGCTCAGCTGAACCTGGT/GJCCAGGACCTGGCCCTG CACTCTCCTGTTTTCTCTCTTCATCCCTGTCTCTGCAAGCAATGCACGTGGCCAGCCGTGCTGT GGTACTGGCCAGCAGCCGAGGCATCGCCAGCTTGTGTGAGTATGCATCTCCAGGCAAGCCAC
EST54419 8	88 A G ---	---	GATCAAGCAGTGCACACGGGTACGATGGACAGCTCTCCAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGCAGTACAAGGATCTGCC/C/TGTCTCCCTGCGTGGGGGCCAACCCCGGTCCA TGAGGCCATTGGGACGTGCTGGCGCTCTCGGTCTCCACTCCTGAACATCTGCACAAATCGGCCTGC CTTCTGCCAATTTGAATGATATTGTTGCTGTGGGACCTGAGCACCTTTTATGGCACAAATGATCACTA TTTTCTGACCCCTACTTAC/GJATCCTGGGAGATGATTTGGGTTTAGCGTGGTGTGTTGTTCTA CTATAGTCCAAGTGAA

ESTD-PS-1	99 A G ---	---	GGGGAGTAAACTGGATTGGAGATTTCATTTCTACAGTGTCTGGTTGGTAAAGCCCTCAGCAACA GCCAGTGGAGACTGGAAACACACCATAGCCTT/GJTTCGTAGCCATATTAATTGGTTTGGCCTTAC ATTATTACTCCTTGCATTTTCAAGAAAGCATTGGCAGCTCTCCAATCCTCATCACCTTTGGGCTTGT TTTCTACTTTGGCCACAGATTATCTTGTA
ESTD- B3AR	104 C T ---	---	GGCTGCCAGGGTTCGGTGGAGGCGGCCCTAGCCGGGGCCCTGCTGGCGTGGGGTGTGGCCACC GTGGAGGCAACCTGCTGCTCATCTGGCCATCGCC/CJTGAGCTCCGAGACTCCAGACCATTGACCAA CGTGTCTGACTTGGCTGGCCGACGCGACCTGGTGATGGGACTCTGGTGGTGGCCGCGCGGGCCA CCTTGGGCG
WI-567b	48 A G ---	---	TCTCACACTGACCCCTTACCTTCATCCTCACCTCTGCTGCCCTTGGTTC/GJAGCCCTCATCTCTTTA CAGGGATCCGCCACAGCATCCCAACTGATCTGGCCTTAGGTCTCTTCTCCAATCCATCTTCAAAAG GCTGCCACTGTGATCTTCCCAAAGGTGATCTGATGCTACCATCTTGTCTCAAGCC
WI-801c	58 G T ---	---	ATGGAACATTTCTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTTCTG/JAGATGG TATTGGAGAAGTAGACAGAGAAGAAATTAAGTAGGCAATGCATGTTTGCAGGGGTGGGGCTGTGC ATCTGTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCAGAGAGTTAA CATTTCTGCCACCCCTC
WI-801b	58 G T ---	---	ATGGAACATTTCTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTTCTG/JAGATGG TATTGGAGAAGTAGACAGAGAAGAAATTAAGTAGGCAATGCATGTTTGCAGGGGTGGGGCTGTGC ATCTGTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCAGAGAGTTAA CATTTCTGCCACCCCTC
WI-1099b	76 A G ---	---	GAAATTCACCTATACAAGAACTATTTCTCTAATTATTACATTAGTCTCATTTCTGAAATATTAT TTTTACA/GJTACCCCTTGTATTATTTTGTATTCTTTGTAAAGAGAGATTACAATCAGTAACGC TGTTCAATTGATAGTGCTATCACAAATGCTAAAATACTTTTGGGTCAACATCAAAATTAGAAAGAAA CTTACAAAGTTTATTTGCTTTATGGTTA
WI-2529	71 C T ---	---	AGGAAATGGCTGATACCTCCTGGTGGCTTCATTATAGTAAAGGAGATGTAATTGCTTGATGAGCCTCT CAA[C/TTCTTAACCTGCTGCCCTCAGTCAGTGAAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAATGCTGAATAAGCTTGAATAAAGTGAAGAGGTAAGAGAGGAGACAACTGTGCTTT TTAAGAAATAGAAGAGTCACTTTTCATTAGAAATGGCTTTGGGGATGACAAGTA
WI-10088	205 C G ---	---	TAAGGGCTGTCTTCCCCAGAGGCCCCACGGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACTACATATAAGAGAGACCTGTACCCCTATAGGTAACTGAGGATGAAGGA GTGAGTCATATTGGGTGGCAATTAATGACCCAGCCTCTCTCTCAAGAAGACTTTTACATTTTAGAC AGG[C/GJAGCAGAAGCAGCAAGGAGAAAGGAAGT

WI-2625	98	G A ---	---	---	---	GGCAGTCTGGCTGTAGGTAGACAGCACTGAAGATGGAGGAAGAGAGAAACAGGCAGAA GCACGTGTGGTAGTTAAAGGCTATTATTAGGA[G/A]CAAAATTGATGATCTCCCTGAGGACTCGCAG AAATTACGACAGTGGACAGGGTTATCTGTGGTGAATTCAGTTATCCACTTGCAGGAGGAAAGCCA GCCAGCAAG
WI-2924	54	G A TAGG	TGACCTTCCTA GTCTTCTCTTA	GCCTAAGTGT AATCACAGGG	---	TCTGTTGTCATATTCCTCTTTGACTCTGACCTTCCTAGTCTTCTCTTATAGG[G/A]JACCCTGTGATT ACACTTAGGGCCCTACCTGGATTATTAGAACATC
WI-2939	72	G T GIGCCITT	GGCTTGTCTCA	CTTGTGAGGG AAGGCTTG	---	CCATTGTTGAGGTTGGTGGGTCACCTTGTCTTCCCTCGCACTCAACAAAGTGGCTGTCTCAGTGC CTTT[G/T]CAAGACCTTCCCTCAACAAGAATGTCTTCCATGCTCCCGTGTCTTTGAAAAATTCGACT TTATCCTGAAAACTCAGCTGCAGTGTATCTCCGGTATAAAGCCACTCCTG
WI-3203	99	G A AGACGAG	GGTTATGCCGC	TCAAGTATTGC CTTGTGGG	---	CTTGCTACCATGCAATTCACAGCATACAACCTTCAGTGAATGCCGTAAACCCCATTTATAAAACAT CTTGCCATCGAAGGGTTATGCCGACAGCAG[G/A]CCACACAAGGCAATACTTGAAGTGACTTGGGA GAATAAGATTITGGATGGATGAAAGCAGAGAAGGAGATGCTAAAAGTGA
WI-3473	101	A G GGCCTAGGGA	AAGCATTTTA	CTGATGTCAC CAACATTTTCT	---	GGAAAAAGAAACCTGAAGGATGAGTAGAAGTTAATGGGAGATAGTTGGTGATAGGCCCTGTTTGGGA GATTGCAGAGAAGGAAGCATTTAGCCCTAGGGA[G/T]AGAAAAATGTTGGTGACATCAGGGCT ACACACTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGGCTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATGTCTGGCTCCCC
WI-1796b	29	A G ---	---	---	---	ACACACTTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGGCTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATGTCTGGCTCCCC
WI-1796	29	A G ---	---	---	---	AGTCGTCCATCTTCAGGGTCTAACTCTGGATCTGGCTGCAGAGTAGGAAAGAGATGGGTGAGT AGTCACATTAGGTATTTCCAAATAA[C/T]JAAAATGCCTCTGAAAAATATCTCTCCCATGTCCCTGTC TAAATATAACATTTTCCC
WI-4360	93	C T AAATAA	GTAGTCACATT AGGTATTTTCC	GAGAGATATTT TTCAGAGGCAT TTT	---	GCTGAGCTTTGTGGCAGAGCCAGGGACAATTCAGCTGCCGGATTTTAAATAGATTCTGCAGCACTGCAA CAGGAACCAAAAATCAGTC[C/T]JGGGTAACCTGAGAGTGGTTTTCACACCCAAA
WI-1959b	87	C T ---	---	---	---	GTTGTGCTGTAGCAGACACAGAAGGCA[G/J]AGAGGAAAAAGCCCTTTTGGTCCAGGGGCTTACAC TGAATCCCTCAACAATGCAAGATGAGCTAATGGTCTTAGAGGTATAATCTAAGTGTGAGAAAAACA AAGGTATAGGGTTG
WI-1973b	28	A G ---	---	---	---	CTTGAGTATGCGTGGATTTGGTATACACAGAAATGGGAGAGCTGGAACATAATCCOCCATATACCA AGGGACAAATTGTATCTGTTCTTACAAATTATACAGTAGGAGACATTATGTTCCATGACAATGGTAAT TTTTAA[C/T]GACAGTTTTAAITGAGTGAAATTACCATAAAAAATAATAATAGTAGCAGCTAATATT TACTGAGCTGTACTAGGTGCCTATAAATAGC
WI-1980b	140	C T ---	---	---	---	

WI-2015b	190 A G ---				TGTCAGATAGTCGGTCTCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAAATTATGCT ATATATTTATACAATATACAATTACTTGCAGATAGCATGACCATGCTAGTGAACCCACACAAAGACTAT GTGTGAATCGTCTATTAGGGTTTGTCTATAAACTCTACATGGTGCTTTTCCAACT[A/G]CATATACCTT CTAATACCATAGAG
WI-754b	49 C T ---				GAAGGCACAGGGAGAAGATGGCTGTCTATCCAGCCAGGGAGAGAAGC[C/T]ACATTTATTGGTAA TCCTATAAGTGCATCTTTAAAATTTGTTACTTTAGA
WI-754	22 T C ---				GAAGGCACAGGGAGAAGATGGCT/CJGTCTATCTACCAGCCAGGGAGAGAAGCCACATTTATTGGTAA TCCTATAAGTGCATCTTTAAAATTTGTTACTTTAGA
WIR-1b	56 A G ---				AGGCAATCAGACCTACAGAAGGAACCCCAATAAAAACTCTGTATGATCGTACATCC[A/G]TGCCTG GAGGGTGATGCTCTCTGAGGACATGGAGCTTCATGTTTGGAGCCCTCCCTG
WIR-1	56 A G ---				AGGCAATCAGACCTACAGAAGGAACCCCAATAAAAACTCTGTATGATCGTACATCC[A/G]TGCCTG GAGGGTGATGCTCTCTGAGGACATGGAGCTTCATGTTTGGAGCCCTCCCTG
WIR-3b	72 A G ---				TAATTTAAAATGGGGCCAAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GAAGT[A/G]TCTAAAAGTTATTAGCTCAGAGCCCTCACACATCTCAGTGAAGTATAAACAAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-3a	69 A T ---				TAATTTAAAATGGGGCCAAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GAATGTATCTAAAAGTTATTAGCTCAGAGCCCTCACACATCTCAGTGAAGTATAAACAAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-4	47 T ---				GAGCCTTTCTAAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCTGCTCACACATGTGCA AGGCAGCAGCAAAATTTGCCAGCTGCC
WIR-5g	209 C ---				CGGGACAGAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCCTGTGGTCCCAGTGTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCCGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5f	196 C ---				CGGGACAGAGAGACAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCCTGTGGTCCCAGTGTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCCGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5e	194 C ---				CGGGACAGAGAGACAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCCTGTGGTCCCAGTGTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCCGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG

WIR-5d	191 A	---	---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTCAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGAGCCAGAGCCTGTGTCCCACTGTTAGG TTTTGAAGGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAACACACAGG TTTACGTCCAG
WIR-5c	177 C	---	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGAGCCAGAGCCTGTGTCCCACTGTTAGG TTTTGAAGGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAACACACAGG TTTACGTCCAG
WIR-5b	159 A	---	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGAGCCAGAGCCTGTGTCCCACTGTTAGG TTTTGAAGGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAACACACAGG TTTACGTCCAG
WIR-5a	37 A	G	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCAAGAGGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGAGCCAGAGCCTGTGTCCCACTGTT AGGTTTGAAGGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAACACAC AGTTTACGTCCAG
WIR-6	63 A	C	---	---	TAACCTGAAACTTGTCTTCTCTCATCTCAGGGAGAACACAGACTTCATGTTAAGACCCAGAA[A/C] CGCAGTCTGGGGTGGGCGAG
WIR-7	12 C	T	---	---	TTGTGACTATT[C]/AAGCATCTGTAGATATTGAATACATAGTCTTGAGATTGATC
WIR-8	46 C	T	---	---	GGCGTCTATGACTATCCTGGTCAATTGATTGACTAATGATTCTG[C]/TGGCCCTTG
WIR-2	56 C	G	---	---	AAACAGAAAAATAGAGGTTATAAGGATGGAACCTAAAGTTGTCAGAAGAGGATGA[C/G]CTGAAG AAAGAAATTACTCTCTTTTGACCAATAAATAACAATTGGGAAACACTGGAAACCATGGCTTGATTACT GACAAAC
WI-7069	93 G	A	---	---	TGTCTTGCTTATGCCTGCCTCTTTGGCTTGGCAGGATGATGCTGCTCATTAGTATTTACAAAGTA GCTTCAGAGGGTAACTTAACAGAGT[G/A]TCAGATCTATCTTGTCAATCCCAACGTTTACATAAAA TAAGAGATCCTTTAGTGCACCCAGTGACTGACATTAGCAGCATCTTTAACACAGCCGTGTGTTCAAAT GTACAGTGGTCTTTTCAGAGTTGGACTTCTAGACTCACCTGTCTCACTC
WI-18694	41 A	T	---	---	GGTCATTCTCTTTTATCTGTACAGGAGCCAGCTCTGACTT[A/T]CTCTCTGTTTCTGTCATCTCTCC CCACATACCAACTTCTTCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18612	37 A	G	TGC	TTGTATTGCTG CTTGCAAT	CACACTGTTACACCTATATTTCAAGTTTGGAAATGC[A/G]ATTGCAAGCAGCAATACAAAAGTA TTCATGAAGAATGCATAATCTCTGAAAATTATGAAAACATCCCT

WI-18517	87	C T	CAGGAATCAG CAGCCTGA	TGTTTGACAA GTGCAACA	TTAAAAATCAACTAGGGCTACCCCTCAACACCCCTCCATTGTCAACCTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCTGA[C/T]GTGTGCACTTGTCCTCAACACAACTGACTGC
WI-18668	76	C T	GGCGAAAAAC TAGGCAAAAA GC	GCTAAATTA CTGCACCTTTT GC	CGATTGACAACCTTTTATTTTCAACTTAGGTAACTAGGTCAAGTCCAAAAATCAGTGTAGATTGGCGAAAAACT AGGCAAAAA[C/T]AGCAAAAAAGTGCAGTTTAAATTTAGCAAGGCTCAAGACAGTATGTGGAAGGAA GGTGAGATTTCCTCTACT
WI-18680	75	T C A	AGCATCTGGA	CCTCTGAATA TACAACGGAGC	TAAACATACGAGTACTGTACACGCAAGCATGCATCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAAT[C/G]CTCCGTGTATATTCAGGAGGGA
WI-18704	99	A C	GGTTCTCCGA GGGGTAC	TGAAGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTTCTGTGCGAGCACACACCAAGGGCAGTTGGGCTTGAAGGAGCC CTTGAGGAAACAGGGTTCTCCAGGGGTAC[A/C]CCAGCAGGGCTTCAGCTTAAAGTCG
WI-18673	29	A G	---	---	TGTGGCAACCTTGTTTTAAATTGCAAC[A/G]JACTTAAATTTACAGCACATTCATAATGAACCAAC AGGAGAGTTGCTGACTTTGTACATATGAATATATAAAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGCATACAAGGAAG
WI-18640	121	T C	GTGTTGGGTG GGGG	GCAATACCAC TGAAGAGGAC A	ACCAGTCATGTTTATTTGGAGGTTAATTCCTATTAGGATATGAAAGGATTTCAGCAACGATTGAGATT GTGTTCTCAGGAGGGCTCGGGCCAAAGTCTGTTGGGGTGGGGTGCAGAT[C/G]GTGCTCTTC AGTGGTATTGGGACC
WI-18533b	91	T C	---	---	GGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTAACTCCCGAGATTTCCTTTTATT TATATTTTCAATTTTTCATCTTAAT[C/T]CTACTGAAGCCATTTCTTTGGTTAACTTTAGA
WI-18533a	59	T G	---	---	GGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTAACTCCCGAGATTTCCTTTGCTTTA TTTATATTTTCAATTTTTCATCTTAATTTACTGAAGCCATTTCTTTGGTTAACTTTAGA
D11734	83	A C	TCATCTGATAC CTTGTTTCAGAT TTT	AACCAGGATA AGGCTACAAC ATTT	GAGCATATGCTGTCATGAGGACCTTTCTATCTTACATTATGGCTGGGAATCTTACTTTTCATCTGATA CCTTGTTTCAGATTTC[A/C]AAATAGTTGTAGCCCTATCCTGGTTTACAGATGTGAAACTTT
D49493	159	A T	CCTGAAGGAA TCTGGGAATT	ACTTTCAGGCC AGGC	CAGGACTTGTGGTGCAGCTGCAGACACAGACAGCATGCTGCGCAACATCAGTGGGGCCAGAGAG AGCTGTCCGCCAGTGCATCATTAGGGGGTCTTTCATTGCTAGTACTAGCCCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAAT[A/T]GGCCCTGGCCTGAAAGTGGCCCATCATTCATACCCACTGTT CT
EST10030	98	T C	CATTTTGTTC TCTCAAGTCCC	GCAGTGTGTT ATGGATGA	TATTTATAGAGGAGACCTAGGAGGAGTTTGACACAGCACACTGCTCAGCAGATGACTTAAATTTT CCCTTAGCCATTTTGTCTCTCAAGTCCC[T/C]TCATCCATACCACCACTGCTGATTG
EST10052	24	G A	GAGGCTG	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCAGTCTCGGAGGCTG[A/G]GAAGTCTAAGATTGAGGTTCCACATCTTGTGAGGGCCTTC CTGTTGAGTCAATAACCTGTTGGAAGTCATCATGTGGCAAGAGAGAGGGCTACAGAGAGCAAGAGGAA A

EST10605 2	118 C G ---			CTTGGTAATACAGTTCTGTATTATACAAAAAATTTTCTCTGACAAAACGTACACATAGA AACAAATTTCCAAATGGACAGGAACCTAAATTTGTGGAGATGCCCATGT[C/G]TTGTGAGACTTAA AAAAAGAAAAGATCCC
EST11048 0	61 T G T A A T C T	CTCTCAAGTAG ATAAGAGGCA	GCTAAATTTTC AGAAAGAAAT TTGTTT	CATGTGTCATCCCATGATTGAAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCTT[G/JAA ACAAAATCTTTCTGAAAATTTAGCTTATGAACCTCATTACACTGCAACCCAGAGAGGAGCAC TATGGAGGCCAGAGGAAGTGACACTATATGTGGAAGTGCTGAAAGAAATGAAAGTGTCACACAAAA TTCTATATCCAGCTAAATATCATTTAAGAAATGAAG[G/T]GGAAATGAAGCAATATCAGATAAA TTGATGGAGAAATCCGAGGCTGCCAGCATCCCCACCAAGTAGATTTCTTTGGACGAAGAAATCCT TCTGTGATTGAGCTTTACCGCTTTTCCCTCATCTGCTGGTG[C/T]TCCCTCAGAGCTTTAATGTCCGT CCTGCTCTCCGAGTCAG
EST11349 9	109 C T ---			GAATCTGGGTATTAAATAGCGGTGCCACAGGACACATAGGAAGAGCATCCAACTACTTTGGAG CCCT[AG/JAGGAGTTTTAGAGAAAGCTGGAGCCCGAAGACCAGTAGTAGGAGGTAGCCAGACCAA AAGGGAGGAAGGAGTGGGA
WI- 16632a	71 A G T G G A C C C T	CCAACTACTT CTGAGCCCT	TCCAGCTTTCT CTAAAACTCC T	CCAGGAATAAAGAAAAGAGTCAGAGGAACAGTCTTTGATGTTATGAGGCTGAGACACTACTC TTCCCTCA[AG/G]GACTATTTCTGACTATAAGTGAATAAATACATTGAAGACTTCAGGAGCTCA CTTGCCATTTATTTGTGCATGTTGTTCTTAAAGGCTTGGAAGATAACTTTGGAATGTGGGAAC ACATAGATCCCAGA[G/A]TATTAAAGGGGCTGGAAAAGTAGCCCTTAAGAC
EST11772 6	74 A G ---			AGAGCAATGGTGGCATCTCAATAAGCAGCTCATTTTGATTAC[G/A]GGTATACATGAAGTAAAAATTC ATGAAGTAAAAATTCATTATACAAAAGCCCTCCACAGAACTTTTCATGCACCCTGAGCTATGTGAAC TGAAAAGTAACAGTGGGAT
EST11795 3	82 G A ---	CAATAAGCAG CTCATTTTGAT TAC	ACTTCATGAAT TTTACTTCATG TATACC	GCCTAGTAATTCCAAAAGGAACATGTTTGTATAATAACACTCAGTACAAAGTCTGT[AG/JATCCAGG AAGTGACCAGCCCGACGTGTGCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTTTGAAATC GTGGAATAATTTTATCTGTACGCTTTCC[T/C]ATTATATTTATCTTGTCCTTGATTTCAGCACCC CACCCGATTTGCAGGCAGTGCTTTCTAAACTGTGCCCTGTGAGCTGTTAAAAAGTCTTCT CCCTAGCAAAATGACTTGAGTGTGTCCAATACCAAGTTACATCTGTTGCCAAAATTAAGCTCTC TTCCCCAGAGGCATTAACTGAGATTAT[AG/G]GGAAACGCCACAGCAAAAATTGACGATGCAGCTTTTA CCTTTT
EST12005 9	56 A G C A A G T C T G T	TTGTATAATA ACACTCAGTA	GGCTGGTCACT TCCTGGAT	ATCTTGAGGTTCTGGCCTGTCAG[AG/JAAGTGACATCTTTTACTTACCACAGGTCAGGAACCTAT AAAGAACTGTGTAGAAAAGATATCAGGTCAGACTTTTAAAGGGCTTCTTATCAGCTCAATAAA
EST12055 9	32 T C ---			
EST12492 1b	95 A G ---			
EST12492 4	25 A G ---			

EST12502 2	52 C G ---			ATACTAGGGAGAAACCAACTGGAGGCAAGTCCACAGGTCCACACTTGTGCA[C/G]CAGCAAGTAT AAACAAAGTGGGTTTCGATGAAGAGAAATGCTCACGGGGAAATGACCAITTTTAAGGGCCATGTG GTCGTCGAGGCAGTTAGAGG
EST12619 8	105 T C ---			CCAGAGAAATAGAAATGATCGGTAAAGAAATAGGAATGCATATTTCAACTCACTGTCACAAA CAGGTGTTTATTATCCCAAATGACAGTGTGCCTGAGAT[C/G]GATGCATGTGGCAGACGAG
EST12620 0	67 A G ---			TTTCTCTCTCCTTCATTTATTCATTTGTTCAAAACACTGTCTAGTACCAACATTGTCCACCGGC[A /G]TTGAGAATACAAATATTGAAGAAGAGTCACTGCGCTGCGCTCTGGAATAATCAGAGTATTTGA
EST12817 9a	22 C A ---			TTGGGTTCTCCAGGATCCAG[C/A]CTCGTAGCTGATGTGCATGAGGTCTCATCCATGCTCCACGG GTCTTGGGAGTGACCGGGATGGGAATCCATGTTGCTTTGCGTACTCCATCAGGTCAITGGG
EST12941 8	23 T A ---			TCTCAGCTTCCACCTGACCTGCA[T/A]CAACAGCCCCAGTTATTTACCAGAAATTTTGTTGCGTTTCA ATGTAGTGTAGCTTTAATACACTGCACITGTTTG
EST12949 2a	52 A G ATACTGTT	GGCTTTAATCA TAACCTAATA	TGTGTCCCTGT GGGTCTC	AGGATTTTCATGAGGCTTTAATCATAACCTAATAATACTGTTAAAAACAACAC[A/G]TCTGTCACTTG CAGAGACCCACAGGACACACATCTCTCTCCTCCTCAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T ---			ATTTTTTTGTTTCTTAAATGAAGCATAATAAACAGTTAAAAATTCAGAAAAATCATCTATAGTTGA GTGTAAACTCCCTAAATCAGTCTTCTAGGGCCACA[C/T]GGAGCAGAAAGCAGCTTCCCACCCAAAG CACCTCTGAAC
EST13117 6	66 A G ---			TGCTGTCTGCATCAGTCCCTTTAAAAATTTAAATCGCTTTATACAATTGACACCAATAAATGCAC[A /G]TATTTAAAGTTTACAATTTGAGAAGCTGACACGTGTCCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T ---			TCTGCTTTAAAGATCTTCATAGCTGCTTAGGTTTGTCTTCC[C/T]AGCATATTCAGCTATAATCA CCTACATTCCTCCACAAATATTCCTGTGTGTGCCAGGCCAGTCTCCTCACTGTCCCATGAATAGCC AGTCTTATTCACCTCT
EST13226 6	74 T G ---			AACTGTTTACTAACAAGGTGCTTTAATTTGAAAAGCAATTTGAGGAAATAAATTAATGAAATAGTCT GGCCATTTT/GIGACTAACCAAGTTCTACAAATTTACATATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAAACAAAACATG
EST13230 6	72 G A AGAGACGC	GCTCAGATGTG	CCGGCTCCTGT ACAGAGA	GCATCATCAGCGGCTTTTACTGAATACACCAACTTGCCGCTCAATATGCAGCTCAGATGTGAGAG ACGC[G/A]TCTCTGTACAGGAGCGGTACTGTCTTCAATCCTTTGATGCAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C TCTCAGGCT	AACCAGATTT	ACAAGAGGGTT TGACAAAAGA G	AAAGATATAAAACAACCTCCCATCAGTAGCAATACAAGGTTATACATTTTAACCAGATTTTCTCAGG CCTT[C/T]TTGGATACCTTAGTAGTTAACTCTCTTTTGCAAAACCCTCTTGATATAACCA

EST13278 2a	51 A G	CTTCCACGAA CAATATTTAG	CATATCTGG GTGGTGAGAA	TTGCGAAGACGTTTTACAAGCTCCAAACCTTTTACCAGAAATATTTTAGGAGAGATTTGAAATAT TTCTGTAGTTCTCACCACCCCAAGATATGACAGCTTG
EST13282 0	99 A T	CCACACATTTT AGTCCAAAGA	GATGGAAAATT TGAGGAAGGTT	GCTCACTAGATGAGCATTGACCAATAATTTAGATAATACCTGTTGGGAAAGTGCTGAATTAAGCTC TGCCTGAGAATCCACACATTTTCACTCCAAAGATTAACCTTCTCAAATTTTCCATCTCCCATCAGA GG
EST13290 9		CAATTTTTAGA AGTTGGGTTT	AAATCAGTTCA TGGAAATTTCA	AGCTCATCTGCAAGCAATTTTAGAAGTTTGGGTTCTTGA/GCTGAAATTTCCATGAAGTGATTTTT TTTTCTGTGCTTAACCTTCACTTAAAGACCTAAAGACAAAGTGGTATCACATCACATATTTTGT ATGTGGGGCTTTTIG
EST13518 2	45 C G		---	GAAACATCTCCAGTAGTATTGAGGTTAAATGATTGAGCATTTA/C/GIACTTTAAAAATTACCTCA ATGTTCTCGGAGTCGTCATAGTTTAAATGACTTCTGCACCTTCCCTTAIAACCTTGATTG
EST13522 8a	66 A G		---	CAGGTTGGTATTCTCAACTAGGAGCTATTTGCCCCCATCCCGCCGAGTGCTGGAGAC/A G/GTTTTGATTGTCACAACTGCGAGAGGTGGTGCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	69 T C		---	CTTTAAGGAAGTGAGCCAGATGAATCCAATGACCAACCTGGTTGAGAGCCATTGGTCTAGGAGTAGA AAT/C/GCACACAAGGAATAAGGGAGAAGGAGTTGGTTAGTTGAGGGAGAGAAAGTTGGAAGCA TTTCAAGCTAAGTAAATGGT
EST13785 0	101 C G		---	AAGATTACGGACCATAGAAGAACTGCCCCCGACCCATACACACACAAATTTATAGCAGGTAAACCAA CTGAAAGGAACAAAGTAATGACTTTCTTGAACAAAC/G/GTGAATACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	25 A G		---	CCTCAACCATCTGTAAACCGAGCCCCAG/GIACGTGACCGGGGACTTGTGCTTCCCCCATCCCGCCCTCT CCTATCAGCATCCGCTAAGCGTCAGTCAGCAGGTG
EST14083 7	23 A G		---	CAATGGTGTCATGTGAACATATAGIACCTATTTCATAAAGTTAAAAATATCCCTTCTTGAATCA CAGTGCAAAAGGCATGAGGGTGAAAGTCATCTGCTAAATGACCGAACAGGAGGGTAGGAGG
EST14221 5	42 T C	GCATGCTAGA CAGAGGCATT	GGAACAAGTC AAAATATTTT AAAAGA	AATATCAATGCATCTTGTGGCATGCTAGACAGAGGCATTAT/C]TTTTGAAGATCTTTTAAAAAT ATTTTGACTTGTTCCTCCCTTCACTCATTTTAAATTTG
EST14812 2	50 A G	CAAGTCAGCTT CTACATTTCTGA	TAAAGATTTC TTAAATCCCAT TATGTACT	TTCACTTAGTACCAAGGATGCCCTTCAAGTCAGCTTCTACATCTGAATA/GIAGTACATAATGGG ATTTAAGTAAATCTTTAGAAGTCCCGGAGTTGGCTTTTCTAACATTTTCATATCAGGTGAAACAAAT TTTTTCATATGGGTGATT
EST14815 3	128 A T	CATCAOCCACC ATACTGGTT	CGGGAAAACA GTACCGGAA	TTTGGTTCGGCAATACATAGTGGCAATGCGAGCGTGAGTTCGGCCGCTGCCCACTGAACCAAGTAAT TCACCAGACAATGGCGCACCACTTAAATAAAGTTCGCCGCTCATCAOCCACCATACTGGTTT/TTTCC GGTACTGTTTCCCGTA

EST15420 6	109 C A ---	---	TTTAAACCCCAAGACCTTGATGTCAGGACTCCGATCATTTTCTCTGCCTATAGCTTGGATATCTTA ATCTCTCCCTTTTGTCATCATATAATCATATAGCCCAAGGGACTC/A/GGAAATTTGGCTGCTTCAAGTCA TTCCAAAACCTCTCAGG
EST15700 6	48 G C GGA	GAAAGACAA AGACAAACAGA TTATTCCTC	GGAATAGCTGA AACAGAGATA TTATTCCTC
WI-16739	57 G A CACAAGC	GGTTTGGCCAT CTATAA	GATAGTTGATG TTTATTTCC CTATAA
WI-16782	96 C T CACTGTAAGG TC	GGTGGGAGTCT CTGTTCTCTCA	CTTCTATCTTT CTGTTCTCTCA TC
WI-16783	64 A G G	TOCTGAGATGT CTTTTACCTGA	CTGCTTGGTTC AATCCTTATTA G
EST15948 2	58 T C ---	---	CAGGACTTAAGTCAATTTGCTGGAGACTTTAACTAAAGGTGAGGCAACATAGGAT/CJTGTGA CAGCACACTCGGACCAGGAAGTGTGCTGAAATCGTACACTAGCTGCCAGCCCTTTTCTCTGGC TGCTCTGCCTCCAGAGC
EST16088 8	89 G C ---	---	GGTTTGAAGACGCAGCTTTATCTCCACCTGCCACTGGGATTCATTTTGAGAGCTGTTTGTGACGCC TTTTCCAGAAAGGCCGCTC/G/C/GGGTTTCTGAACCCCTCTATGGGCAATTTTAGAAT
EST16089 9	96 C T ---	---	CGTCTGAAGTTTCTTTTATCACAAGTCACATCAATCCCTCGGGCCCTGCTCAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTCTC/TAAGAGAGCCATCCCTGCCCTTTCTTTGCT
EST16100 1	24 C G ---	---	ATCCAGCTGTGAAGGGACAGGAG/C/GGTAAACACAGTCCATTTATAAGGGGTGTGCACATTCOCA GGGGCTCCAAATAATGCAACATTGTTCACTCGTCCATGCTGATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGGTTGGCTC
EST16104 9a	83 A G ---	---	TTCTTTTAAATAACCCACAGACACCCCATGACACTTCCAAATTTACAGAGCAAAAAGTGATTGTCAG CTGGTTCTCCAGGGA/GJTTGGCCCCGAAGCTGGCTCAGTTCACCTCCAGGACCTCAGTC
EST16118 0b	119 T C ---	---	ATGGTATAACAAAAATCAGTCCAGGTTTTTCTGAACAAATGATCCTTTGGTCTTTCCCGTGGCATG CTCCTAAACAACTAAACAAACCCCTCTACGTCTAATCAGTCACCTAAGATA/T/CJGAGTGGCAAGT CTTTCACA
EST16118 0a	32 C G ---	---	ATGGTATAACAAAAATCAGTCCAGGTTTTTTC/GJTGAAACAAATGATCCTTTGGTCTTTCCCGTGGC ATGCTCCTAAACAACTAAACAAACCCCTCTACGTCTAATCAGTCACCTAAGATATCGAGTGGCAAGT CTTTCACA

EST16151 2	53 C T ---			AGCCAATTCAAACGAACTCTATCAAAACACACAAAGGCCTAGAGGAGAGATTAC/TAATGAACGT AAATAATTCAAGGCAATTTTGTATCTAAAGCAATTTGCTTAGCTCTACAAGGCATGAATGAGGTGT GGTCACGTTTTGTATAGGA
EST16182 6	54 G A ---			CATTGGTTGGGTAGGGAAGATAGTGTGCAAAATAAAATGGTAAACACAGCAG/G/AJAAATGGAA TTATAGCTTCTTTTCATATAGGGAATTGAAATTTATTTACTGAGGGTGATAGGCAGAAGTAGTA
EST16183 2b	59 A G ---			GCAGGTAAACTGTGGTTACAACGTTATTGTTCTTTTCATAAAGAAAGAAATATCTAGTTG/A/GJTAG AGGAAGGCACGTCTTCTGCGCCCTTCTCGTTTCATATTTTATGTCACGTCTCTAAGCGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	28 G A ---			AATCTTAGGCTCTTGGCTTCAAAATCA/G/ATACAGACAGATAAGAGCTTTAAGTATTTTCGCATTT CCCCAGAGGAAAAGTCAGCATCATAAACACATGGGTACATGCTCACGCACATGGTGTC
EST16229 2c	52 T C ---			TGTGAACCTGGAATTCGCTTGTCCAAAGTCTGAGTCACAGTTTCATTTGGGAGT/CJCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGCGAGGATACTCCACTAGCTGATTCAGACAGGCGAGGCTGCA
EST16229 2b	45 T C ---			TGTGAACCTGGAATTCGCTTGTCCAAAGTCTGAGTCACAGTTTCATTTCTGGGAGTCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGCGAGGATACTCCACTAGCTGATTCAGACAGGCGAGGCTGCA
WI-16816	124 A G TGGGTTA	GGAGCATTTGT	GCCTAGATTTT	CAGACTTTTCTCACACCTCATTTGGCTGGAACCTGGGTGCACATGCACATCCTTGAACATATCATTGGCAA AGGGAATGGGTCACTAAATTTGCTTAAGGCCAAGCAGGAGCCATTGTTGGGGTTA/GJACTGTCC TGAACAAATCTAGGCTC
EST16269 5b	49 G A ---			GCCTCTCTCTGTGGCTTGTCTCTCTGCTCCAGCTGCTGTCCAGTGCCACA/G/ATGGTCTAGCCTCATGG CAGAAGCATTTAGCCAACTCCTGGTCTGCTCCACTCTCTCTCTCTCCGCGCTGGGGCTCACCACC TCCTCTCTCTCAATC
WI-16824b	83 G A ---			GTCACCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCTGCGAGCTGTTGTTCTTATGAAGAAGTCAG AAGCTGATAAAGCTGG/G/AJCTTACACCTTTAGCACGGATAGTTTCTGGTCCCAAGTGGGTGTGGA GCCTTCCATTATGGGAATA
WI-16824a	47 T C CAGCTGT	TGATGGTGTG	CAGCTTCTGAC	GTCACCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCTGCGAGCTGTT/CJGTTCTTATGAAGAAGTC AGAAGCTGATAAAGCTGGGCTTACACCTTTAGCACGGATAGTTTCTGGTCCCAAGTGGGTGTGAGGC CTTCCATTATGGGAATA
EST16445 3	96 T C ---			TTGCTTTTATTATCCAGAAGGCGATGCTACAGATACTGTACAGCATGAACATTTTATTATTACAAA AATGGCTTCCAAACCAATTAAAATGAAC/T/CJGGAATAAGAGCATAAACGGAACAGTAACATCA
WI-16857	47 G A A	CAAATAAGCA GCTAATGGCA	TGTGAATGGG AAGACCACT	TATAATCCATCTCCAACACACACACAAATAAGCAGCTAATGGCAAT/G/AJTAGTGGTCTTCCCAA TTCACAAGACCTGTGCTTCAATTTTCTCTGATAATGTGGAGAAATCTGCTCTTTATGTA

WI-16879	79 C T	GATACAGGCC ATATTTCCCA	CAAGGCTTCT AGAACTAGAGT CC	AGACAGGTCAACAACTCCTAGGGATAAAGATATAAATCCAGCACAGCATTATTTCCAGATACAG GCCATATTTCCCA[C]ATAGGACTCTAGTTCTAGAAAGCCTTGGGAGAACAGGCCACCCAG
WI-16882	99 A G	GAAATGCCA CGTCTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCAACCTCTTAGTGGGAGAGACAAATCTCCCCCTTTCACCCAAAGGTTACTCTGAC AAGGCTATGAATGAAATGCCACGCTCTGAC[A/G]GCGATTACCTGACATGTGTCATCTCCCT
WI-16888	70 G A	GCTAACTTTGG GCAGGTC	AATGTTCTGAA TTGACCAAAT TAA	GTAGTAAATGTTTCATCACTACCCGGGAGAGCAAAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG TTC[G/A]TTAAATTTGGTCAATTCAGAACATTCCAAAT
WI-16905	75 C T	ACTGGCCTGT GTTGTTCA	GCTATACTCT TCTAGGCAGTG GG	TTTGTGTTGTTATTGCGCTCCCAACATCAGAACATAAGTTCCATGAAACAGGAACTTGGCCTGTG TTGTTCA[C]TCCCACTGCCTAGAGAGTATAGACA
WI-16910	74 G A	AAGAGTAAAG ATGGCGTAG AA	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTTCAGTATGTCTTAAGGAGGTTATATTCGCTATGACTTTTCATCTCAGAAAGAGTAAAGATGGCG CTAGAA[G/A]GTATCTGTTATAGAAACGATACCTCATTTTGGCCTGAACCAAGTGAAGGT
WI-16918	93 C T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAAATAAACTACCACCATCTCTCTGCTACACAGAGCACTAAAATCTAGGAAATTTGAC TTTACTGCAGCCATTAAACACCAGCAC[C/T]GATGCCACTTCTGTATCAGGAACCTTAACGTGACAACC ATGAAAGGTCCTCTGAAAG
WI-16947b	127 A C	GGAAAGCAGA CCTGGGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAATAGGCCTGGAG[C/G]ACAGG TGGCTGAGGCTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAAGCAGACCTGGGGACCA CGGGCAATCACATGAGATG
WI-16947a	58 C G	CATGAAATA GGCCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAATAGGCCTGGAG[C/G]ACAGG ATTTGGCTGAGGCTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAAGCAGACCTGGGGACCA CGGGCAATCACATGAGATG
WI-16966	43 T C	AAATGCACAC TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTGTTTTACTTTAAATGCACACTACATAACAACCTAATAT[C]CTTAACTTGGTCCAACTATTT AGTATAACTAATATGAGTTTTTATACTGATAACTTGCAATGCCATTAA
WI-16995	55 T C	GAGCAGTAGA GACTGAGGTA AATAGTATT	CATGTTGATTT CCAGCGGT	TTGAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAATAGTATT[C]ACGGCTGG AAATCAACATGCGCTCTCTCTGTGAAGTTGTGACATGGAGCTGAGAAGGCTGAGTCAATCT
WI-16992b	60 T G	---	---	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAAAGTACACTGTGCGCCCTCATCTGAGAT[C/G]GTG TAGGACTGTAAGGGAATGTGTTTGGGGTTTAGGAA
WI-16992a	46 G A	AAGCACCCAG AAGTACACTG TC	CACATTCCTTT ACAGTCTTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAAAGTACACTGT[C/G]CCCTCATCTGAGATGTG TAGGACTGTAAGGGAATGTGTTTGGGGTTTAGGAA

WI-17010	23 T	TTCAACAGGA AAAGCCATG	AATAATACGGT GTTTGAATGT CA	ATGTTTCAACAGGAAAGCCATGTCATGACATTCAAACACCGTATTATTAGAAAGCTCATTTAAT TGTTTAATGCAGACAAAAATCAAGGCTAACTAAAGCAGATCCAATGACCCAGTGATCAACCTAGA GGTCCACG
EST17127 9b	74 C	CACCTGGCAC TAGACAGAGT	GGGAGGGCAGG GGTG	ATTCGGTCTCCAAACAGATCCAGGCCGGGCATCTCCCCACGATTTTATAATACACTCGGCACAGA CAGAGTCCTTGGGAGCCATGGGCACCCCTGCCCTCCCCAGGCTTCCTAAGTAACAAC
WI-17040	94 T	AATTCTTTAT CATCTCAAGCC	GGACTATGGCT TATTCAGTGAT G	CACGCGTTCAATAAATTTGGTACAAAGCATGAACACTCAGGACAGATTGGCACAATACATGCAGTTC GAGAAATCTCTTATCATCTCAAGCCAGTCATCATCACTGAATAAGCCATAGTCCCGTCTCGTTTCC AAATCTTCTCATATTGT
WI-17044	47 G	GCAAGGGAT TAACGTATAG	GGGATCCOCT TGTTAAGA	TGTTTGGTTTGTCTCTCTCTGCCAAGGGATTAACGTATAGGCTTCTTTAAACAAGGGGATC CCCCACTTATAGCTGACAGCAGCAGCTGCAACCACTGACTCTCTGCAGAAATGGCAGGGAATCGAAT CAAAAAGAAAGCAAGTG
WI-17021	62 T	TGGACTTGTCA GCCTATAACT	TGTAGAGTTAG TGGCAGCTGC	GCATGTGTGGAGCAGATCTCCATGGTAAGCCAAAAGTGGACTTGTGAGCCCTATAACTACTCTT/AJG CAGCTGCCACTAACTCTACAGGCACAGTAACACTTATACAGGAGCACATGCCAAAAGTGCCTGG GAGGTGCCAATAAAATCAA
WI-17065	90 T	CCAGAAAGGA AAAGCATAAA	CCCAAGAGAC AATGAAATCCT	TGTAAAAATGTAGACATGGGGAAAAAACATTCGTAATCAACATGTGCTGTTTTCTACTTCCGGTA CCAGAAAGGAAAGCATAAACTT/CJAGGATTTCAITGTCTCTGGGT
WI-17066	32 A	TGTACAGCCA ACATCACTGTT	GAGATGTTGAA AATGTTCTGGA A	TTCATAAGGTTGTACAGCCCAACATCACTGTTT/CJATTCAGAAACATTTCAACATCTCAAAAAGA AACTCTGCACCCATTAGCAGTCATTCCTGTAGCTTCCCTCATAGGCAATGGCAACTGCTGATC
WI-17074	86 T	---	---	TGCTGACTGTCTGACTTAGTAAGGCCATCACAGGTTGCCAGAACATCTACTCAACTGTTCCAAGCAT AACCTCCTACACAGGCCCTT/GCTACATAGGAGTATATTGGCCAAGACTACCACACTAGAAGTGATT
WI-17104b	108 T	---	---	CAGATGAGAACTCATGTGGCTCATCTGCAAGCTTCCCTGATGCTTTGCGAGCTTCCCATTCATTCCA AATCAGAAAGCAGTCAGTGGCCCGTGGTTCCAGACGGCTT/CJCTCTTTGTTAAGAAATTA
WI-17114a	37 T	TTCCATCAAG GACTTTGTTT	TTGTATTATAA ATAGCAGAGTG AAGAGAC	AGCGTCCAACAGATGTTCCATCAAGGACTTTGTTT/CJGTCCTCTCACTCTGCTATTATAATAC AAGCTACCTCCCAAGGCCAGATGCTAAGTGTCTAAAGAGAGACTGCAGCCACAATCAGAGTTACAT GGGA
WI-17150	76 T	GATGAAATTC AGATAGTCTTC	TTCTCAGAATC CTGGAAGATAT G	CGTGGCTGGACTAAGTGCTCTTTCCATGTGGACACATCTCCACTGAACAGGATGAAATTCAGATAGTC TTCTCTTTT/GCATATCTTCCAGGATCTGAGAAAGGCCCTCTTGTCTGCTCTAATTT
WI-17163	43 A	CATTCCTTGT AAAATAACAA	CAGAACTTTGG TTTTGCTT	GAAATCGAATACGTCCATTCTTTGTAAAATAACAATAACGTTT/GJAGGGCAAAAGCAAGATTCTG TAAACCAACATTGAAAAGGGGACACAGGGGAGGGGAGGAAAGGCCAGATTTTCAACGGTTT CCTCCACATCTGCAGACAAA

WI-17178	127 T C	GGACTCCCTCA	CCCTCAATTTT	AGCAATGTCCCTCCAAATTTCAATTAGCTATGAGGATTATCAGTTTCATTTTCAGAGCGCAATTA	CTGCG
WI-17180b	81 C G	---	---	GGCAGGGGGTTTAATATCTCTGATGGTTTAATTCAGTGAGGACTCCCTCATGAGGAGCTTC/JAGAA	CTGCG
WI-17180a	47 T C	TGCA	TGCGACGAGAC	GCAGTTGAAATGAGGG	CTGCG
WI-17156	54 G C	TOCCA	TGTGGAA	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACATTC/JCCCCAAGTCTCGTCGCA	CTGCG
WI-17149b	79 T C	---	---	CAGGCTTCAACAAATACCAACATCTTGCCCATTTTGTTTCATTATCCGCACCCACACTGACACAGATGAG	CTGCG
WI-17149a	48 C G	CAAGGTTTGA	CCACGCACGTG	GGAGTGCAGGGCATCTTAAGAAATGTTCTCTAAACTTTAGATATCTCCCATG/JTTCCACAGA	CTGCG
WI-17197	67 G A	CTGGGGCTAC	GCATACC	ATCAATATATATTTCTTGTTGGTGGAAATTTAAATGTTCTTAACATCTGCCTACCATCCACCTCAAT	CTGCG
WI-17198	38 A C	CCTAGTTT	ACTGAGAAATTT	TAATATCTTG	CTGCG
EST18753	27 C T	GGTCTCAT	GGTGCATGA	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACATTC/JTTTCATGCACGTGCGTG	CTGCG
WI-17108b	74 C T	CA	CC	GAACCCAAATTTGTCATGTGTATGAACACTACAAAGGATGGGGAAGAACACATTTCTCTCACA	CTGCG
EST19067	41 A G	---	---	ATTTTGCTATGTTCCCTGGGCTGGACTCCAGCAATCCTCCTGCCCTCAGCAGAAAGTAGCTGGGGCTAC/G	CTGCG
EST19067	40 A C	TTC	CCA	/AJGGTATGCACCACCTCACCTGCTTATCAGTTTCGTTTAAATAGAATATTTTGACTTTTAGATGGCGCA	CTGCG
EST19125	28 A G	---	---	TGATTTTCAGTACTTTTCTCCCTGTCCTAGTTTTC/JTAATTTCTCAGTGGACAAATGGACAA	CTGCG
				ACCATCTCTGTTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAAATGCACATCC	CTGCG
				TTC	CTGCG
				TCGCTATGCTACCCAGGCTGGTCTCATTC/JTTCAGGCTCATGGATCCTCCTGCCCTGCAGTGGCTGG	CTGCG
				GATAAGACACAACTGCCACCGCTGCCCTAGGAGTAGTCTTAATGCCGTGATGGTGGG	CTGCG
				TTATTTTAAACATAACAGATGCACCTTGGTTTTTACATTTCTGGTTGCCATTACGTCCTCAAAGT	CTGCG
				AAACAC/JTGGGAGCATATGATAAATCGTAGTTTAAAGGAAGCATAGCAGTACAGAGT	CTGCG
				ACACAAAAATTTACCATCGTGACCATTTAAGGGTATAGTTCA/JGJTGCGCAATTAAGTACATTTCAACT	CTGCG
				TTTTGAGCAACCCGCCATCACCATTCATCATCCATCTCCGTT	CTGCG
				ACACAAAAATTTACCATCGTGACCATTTAAGGGTATAGTTCA/JAGTGGCAATTAAGTACATTTCAACT	CTGCG
				TTTTGAGCAACCCGCCATCACCATTCATCATCCATCTCCGTT	CTGCG
				CTGTTTCTCAGAGATGACACTGCCAACA/JGJTCACAGATTTGCATACAAATACAGTTATGTATTGGC	CTGCG
				TATTCACAAATTTACAGTAGTGTTTTTTCCTCTGAAAAA	CTGCG

EST20824 8	115 T G	AGTCGGGAGT GCTGATTG	AAGATTTTATC TTGGACCCGA	GTGTGAAGCCGGAGTTTATTATTATCAATCAGTCTCTCTGAAAACTCAGGGATTGAGGTTTTTA AGGATAACTTGGTGAGTAGAGGGCCAGTAAGTCGGGAGTGCTGATTG[T/G]TCGGGTCCAAGATAAA ATCTAGG
WI-17347	50 A G	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGCTA	TTGGTTAAATGATGCCAGATGGGGTCACATCCTCAGAACTTCTCAGCCTT[A/G]GTAGCACAAAGTGG ATGCTTGAAGAAACTCAGTCTTGGAACTCAGACAGCAATGGAGACGGGATGTGAGTGGGACCA
EST21904 b	128 G A G T G	TCATATGGCC ATTTTAATAA G T G	GGCAGGTGTC AGAAAGCAT	TGATTGGGCTCTGGGAGCAGGTGGGCAGTTCAGTGAGGAGCAGAGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAAATGTACTAGGCTTTTCATATGGCCATTTTAAATAAGTG[G/A]TA TGCTTTCTGAACACCTGCC
EST22111 3	82 T C T	GAAGATCTGT CTGGCATTCTT	TGGA AAAACA GCCCCAC	CAACAAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTGCTAAGAGAAGAT CTGCTGGCATTCTTTT[C/G]TGGGGCTGTTTTTCCAAGGCACA
EST22197 2	78 T C T	AATTATCTGC TATTCCTGCCA	ACCATGAAGG ATGGGT	GTTTAAATGATCACTCAACAAAATCCACAGGAGAACTTTAAATGTTTACAAGCACCAATATTCTGCT ATTCTGCGCAAT[C/G]ACCGCATCCTTCATGGTAGAGTATCACAAAGTAAAGATTTCTGGTTGTTTCATC TACTTAAACCA
EST22311 9c	92 T C ---		---	TTTTCCATGGATTAGATCATCTTTTTTATTGAGTTATAATATACATAAAAAATCCACCACCTGTAAACAG TAGCATTCAATGGTTTTTACTCTAT[C/G]GTCAAAGCTGGGCAACTATCACTACTATCTATAATTGAGAA CACITTCATCATTCAG
EST22311 9b	54 A G ---		---	TTTTCCATGGATTAGATCATCTTTTTTATTGAGTTATAATATACATAAAAAATCC[A/G]CCACTGTAAA CAGTAGCATTCAATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTATAATTGAGAA CACITTCATCATTCAG
EST22311 9a	41 T C GAGTTATAA G	GGATTAGATC ATCTTTTATT	TTGAATGCTAC TGTTTACAGTG	TTTTCCATGGATTAGATCATCTTTTTTATTGAGTTATAAT[C/J]ACATAAAAAATCCACCACCTGTAAA CAGTAGCATTCAATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTATAATTGAGAA CACITTCATCATTCAG
EST22319	19 A C ---		---	TCGAGGAGCTCTGAGGAGC[A/C]ACCAAGGGACGTGTGTCCAGGGCCACCCGTGCAGGCAAGTGTG GTCCAACTCCTTCCTCCCTTTACAAAACCTCCAGCCTCACCCACACAAACACTGGCTGACAGGCTTCT TAAGCCTTTTTTAACTGT
EST22433 c	103 A G AA	AAGACATGTT CACCAAGTGA	CAGCTTCAGCT TAAC TGACAGA	GATGTTAATGACTTTCCTTTGAGATATGATGGAAAAATATTCAGGTACACATGGA AAAAGACATGTT CACCAAGTGAACCAATCTAACCCAGAAAGCTTTACC[A/G]TCTGTGAGTTAAGCTGAAGCTGAAATTT CTGGGAGCTTGACATGCTG
EST22657 9	71 A G	AAATGGATCC TTATCTGCACAT	GCATGAATTTT	TATCCATTTCAAGAAAAAAAATGACTTAAAAAATACAAATCTATCCCAGAAATGGATCCTTATCTG CACA[A/G]CCATTGAAGAAAAAAAATTCATGCAAACTGAAACTATGCTTT

EST22993 5b	71 T C	ATCCTTTTGT TCTACCCC	TTGCCTGTTAA TTTGACTGTAA TG	GCCTTTTATTGCTCCTTTTAAACATCAATGTTTATAACACACTTGATCCTTTTGTCTACCCCCA ATTTCATTACAGTCAAAATTACAGGCAATATAATAGGTCTAACAGAATGCTTGCAATTT
EST23021 0	108 T A	---	---	TTATTTCTCAGCTTACCAATTTGTGTAATCTATCTCTGTACAAGGTGTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAAATTTATTAATCTTTGCCTTTTATGTTTACAGATTTGTGCTTTCT T
WI-17387	55 C G	CCTTTCAGAT TGAAGAAAA	GCTTTTGCTTA AGATTAATAGT AACTACT	ACAGAAATTTAACATGCAAGTTTCATTTACATTACCTTTGCAGATTGAAGAAAAA[C/G]AATATTAG TAGTTACTATTAAATCTTAGGCAAAAGCCATTTCTTTG
EST23669 1	101 A C	AATGTAAGCT CCAGAGGCAG	CCTTCCCTCC TGTAAGC	TTTTTGGCTTGCTGCAGAAATAGATGAAAGAGAGAAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGCACACTAGGCAATGTAAAGCTCCAGAGGCAG[C/G]CTTACAGGAGGGGAAGGACGCTGAGGC CAAGAGTGCTGGCTCACTG
EST23733 9	31 T G TT	GGCTGTTAGTT TTGTTTTGTTT	TGCACITTTAA TCCCATCAAT	AAAGGCTGTTAGTTTGTGTTTTTGTCTTTTCTTT[G/T]ATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAAGGCCTAGAGAAAGATATAGGCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA
WI-17470	83 A G	GTCCCGTCCCG CCAG	CCAGTGACGAG GOOGA	CTGACACGTCCCTGTGTGCGGGGTGCTCATGTGCGGTGTGTGAGTGAGACTTTTTTAAGTGGTCCG GTCCCGCAGCCCTA[G/T]CGGCCCTCGTCACTGGCCCTGGTCACTTTGTATTCTGCTTGGTTGGAAA TACCATCAGCCCTTCC
WI-17519	55 T C A	GTGTCCTAGC TAATGAATGC	AATTAATTAT TGCAGGCAATA CTC	TTTTTAACGAAATCTCACTACTGCAAAATGCAATGTTTGTCTAGCTAATGAATGCAAT/CJAGAGTATTG CCTGCAAAATAATAATTGAGATTCTATTTTAAAGACTTAGAACAGTACATGGTGATAG
EST25356 3b	95 C G	---	---	TCITTTGATACAGGTAACCAATTTGTAACTATTTCAGAACTTCACTGTATCTTCAAGTTTTTGATAT CAGCATCTCTGTGGAGAAAGCAGTGTG[C/G]ATATAATGTCACATCAGGATTTCTTTTT
EST25356 3a	26 A C	---	---	TCITTTGATACAGGTAACCAATTTGTAACTATTTCAGAACTTCACTGTATCTTCAAGTTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCACATCAGGATTTCTTTTT
WI-17581c	99 C T	---	---	GGGTGACGCTCCAGAAATGGAGACAAAGCCAAATTTGGAGCAGATTGGATCCAGCTTCAATCAACATT ACTACCAGTTATTGATAAT/CJGATAGAACCCCACTAGGCGCAATTTACATTGACGCGTCATGC
WI-17581b	86 T C	ATTCAACATT ACTACCAGTT ATTGATAA	CGTCAATGTAA ATTGCGCCT	GGGTGACGCTCCAGAAATGGAGACAAAGCCAAATTTGGAGCAGATTGGATCCAGCTTCAATCAACATT ACTACCAGTTATTGATAAT/CJGATAGAACCCCACTAGGCGCAATTTACATTGACGCGTCATGC
WI-17596	86 A G C	ACTTCCITGTG TAAACACTCC	CATTCTTATAG CTAGAAATCGA CAATAT	GTGTGCTGGTAAATGGATAATAGCAGTCTCTCATCTCTGAAGGGTGGGAAGTAGGAGAGGCGCTACT TCCITGTGTAACACTCCCA/GJATATTGTGCTGATTCTAGCTATAAGAAATGGGCCACTAAGTGGGTC

WI-17623	46 T C ---	---	TG TGG TTTTAA TTTTAA TTTCCCATATAATTAATGGTGGGCACATTTC/GCATGTGCTTACTGGGTC ATTCATATATCTTTTGGAAGCATCTGCTCCAATCTTTTGCTGACTTTGGAGTTTTTGGT
EST26419 1b	46 T C ---	---	ATTTACATACAGAGATACAAAGGCAACTATGTGCAGCAACAATCTGA/T/C/GGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTTAAATGTCATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAAATG
EST26419 1a	35 C A A G	CAAGAAAGTTTG GACTGCCC	ATTTACATACAGAGATACAAAGGCAACTATGTGCAG/C/A/AACAATCTGATGGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTTAAATGTCATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAAATG
EST26780 5	69 G C ---	---	TCAGCTTTAA TTTAAGGGACATGTAATAAATAAGATGCATTTGACAGGACAGCAGACTAGTTCAAAGC AG/GC/JAGGTTAGACCAGTAACAACAACCAAGAAAGCAAGTGTCTGCTTTCCATCTTTGGCTTTACCA CACTTACAAACTGATACCC
EST26900 7	39 A G ---	---	TACTTCAGTTTAAAGGCAAAATTCACACAGAGACTGTCTC/A/G/GAGACGGGCACAGAACCCAGACACC GTAGAAACACCACCACCACCATGTCATGACGGGAAGCAGAG
EST27152 1	101 C T ---	---	CAAAGGATTTTATTTGTTCCCTAAAAAGTAAAAATCTAGAAAAATAGCAACCCCACTGCAAGAAGAGTT CTATACATAAACAATTTTCAATCAATCTCTCTCTC/T/T/TTCACATGGTGTACTCTTTTCATGTACACAT CATCGGAAAACAGACTGA
EST27504 0a	33 G A ATTT	GCTGGTGTGAT GCTACTGTAAAT G	TTTTGCAC TTTGCAACAATTTAATAATTTATC/G/A/CATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAGCTTTTCAGTATTTCTGTACACATTTCTGTTAACAAAGAACCCCATACATT GGTAAATTCATTCT
EST27662 4	51 C T CTCCAGTCTTG	TTATGGAAATG GCTTATGTAAC C	ATCTTAAAGGACCATTAGAAAAGGCCAGTCACATTTCTTCTCCAGTCTTG/C/T/JAGGTTACATAAG CCATTTCCATAAATTTCTATAGCCTTCTTCTTAGAGTAACACACACTCTTGTTTAGGAATGTTT
EST27788 3	100 A G ---	---	ATTTTATTAGGCGGTACAAATTCAGGGTGGTAAGGGTGAAGGAAAGGCGAAGGCGAGGCAAAATACAT TATTGAGCTGAAAACAAC TTTACATTCAAGGAC/A/G/GCTTCCAGACAAGCCATGTAGAACCAGCAT GCCTTGGGACTGTGGAT
EST27828 4	58 G A AGAAGTCTATC	GTGCAGAGAGG TACTCCAAGTA C	TCTTCTAAAC TTTCTCTGTTGGATCCCAAGTACGTTGGAAGTCATCAGAACCCCAAC/G/A/JGTACTT GGAGTACCTCTCTGCACCAAGATAGCTGGCTGATTTTCTGCTCAGTCACAAATTTTACTTGAA
WI-18369	58 G A ACAATC	TCAAGAAGGCC TTATCCATT	TAAAAATTTGAGATACATTTCCCAATGTAAACAATAAATTTCAATCTGTACACAATC/G/A/JAAATG GATAAGGCTTCTTGACAAATTTCTGCCACCTCCGTTTAACGCATCAGAACTCAATCTTATCTC
EST28036 4	37 T C ---	---	TCCCGCTTCCAAAAGCTTTATTGGCAAAATGCTCTA/T/C/JAAAAGAAATGATCAATCCTGTTGCCTCT AAGTCAATGGAATGAAGAGCTGTGTCCAGGGACACACCACGCCGCTGTGAAGGAGACTGCTGTTGTG TCCACCTCTTATTCATAG

EST28483 7			GGAGTAAAG GTGTTCTTCT CA	TTTCTCGCATT TATTTTATAG CA	CATTTGGAGTAAAGGTTTCTCTTTAAAT/AJATGGTATAAAAAATAAATGCGAGAAACATTAAAC GGAGATGTACAGACAACAGACGAGACATGAGTTGTTCTGACTGTGACACATTGGTGAAA
WI-17724	31 T A		TGGGOCCTCC TGTC	TGGTTGGCAG TGTC	AGAATTGGTCTAGTAATCGTTCCAGGATTCGGTGATGGGCCCTCCCTGTC/CJGGACACTGCCAACCC CACAGCTGGAGGGGCACTTAAGGCACGTCATTTTGATTAGA
WI-17730b	50 T C			---	TGAGCCTGGGAGAAAGACACAGAAAGTGAAGTGTATAGTTACATCATACCAAGTGTACATACTG TT/CJACATGATTTATGGCTGTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGTCA
WI-17730a	68 T C		GACCACAGAA GTGAAGTGCT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGAGAAAGACACAGAAAGTGAAGTGTATTA/CJGTTACATCATACCAAGTGTACATA CTGTTACATGATTTATGGCTGTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGTCA
EST29041 5b	39 A C		GGAACAAACA CATTAAAGCAT	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTTATGAGGAACAAACACATTAAGCATCATTGTCACT/G/AJGCTAACTCCT CAATCAACAATACCCCTTATTTTAGCCATGAAAAC
EST29128 4	53 G A			---	CTTTAGAAAGGACACACAGTCTTGTGGACTTAGGGCCTACCCCTATTCAGCAGGTGCC/A/GJTTATTT TCACTTGGTTACGTCGTAAAGGACCGTTTCCAAATGAGGTTACAGTCACAGGTTCTGAGCAGACATGA GTTTGTCTGGGACACT
EST29912 3	58 A G		TCTGCCAGCTT ACAGGCT	GCGTAAGTGTC TCATTCCTCTG T	ATTATTAGGTATCTGCTGTGGGGTGGGGAGAGATTGTTGAGATACTGCAACAGACACAAA AGCAAAGAAAGAAACATTCTGCCAGCTTACAGGCT/CJACAGAAAGAAATGAGACACTTACGCATG GCCATGATACACAGCAGTGA
EST29936 8	103 C T			---	TATTGGTATGCTTAGGGAAGATTCTGATTTAGAGATATTAATCTTAAAAGTTAACTCACCATGAAA TTTAACCTTCTGTACTGGCTTCACTGATGAGGCAGTAACTACATAGGGATAAA/G/CJAGCTCAGTA TCTGGAATCATGCTTCTCTG
EST30223 2	121 G C			---	AAATAATACATCATGGGGAATGGGATATCCATCCCTCAAGCATTTATCTTTGAGTTACAAGCAA TCCAATTACACTCTAAGTTATTTTAAATATCC/A/GJGGATTTAATTTCTCCTAGTTCAATCTTGGGA GG
WI-16260b	99 A G			---	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAGACCCAGA GTTTCAATATAGGTAGC/G/AJATAACCAGGCTCACTTTCCCTTCCGTGAGAACTTCTGTTGGGAC
WI-16260a	86 G A		TGAGGTGGATT CAAGAAGAAA	CTACCTATATT GTGAAACTCTG GGT	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAGAA/G/JACCC AGAGTTTCAATATAGGTAGCGATAACCCAGGCTCACTTTCCCTTCCGTGAGAACTTCTGTTGGGAC
WI-17835	59 G T		ACAGGAAATA TTGTGCTTTCT	TGGGGTATAGG AAACAGGC	AAGAGAAACAGGAAATATTGTGCTTTCTTG/AJGCTGTTTCTTATACCCCAATATCATAAAGAAAT GTTGTGCTTCTAATGTTACAGCTTCAAAATCTTTGTCTTAATCAATCCAAATGAATTACCTGAAT TTCTCCTCTTGTTCAAA
	30 G A	TG			

EST31951 4	87 C T	GGGTGTCCAG CCAACA	CCCACCAAAAT CACTCC	ACAGCCATTTATTATGTTTACTTGGTAATATCAGAGACTGAACAACTTTTCACTCTTTTAGCAATGACA TCGGGTTGCCAGCCCAACA/C/TGGAGGTGATTTTGGTGGGAATTCCTTATCACAATTAATCT
EST31968 8b	95 T G ---		---	CGAATTTGTCCTCTTATTTTGTGATTCTAGTAATCCTAAAGATTTGGGGGGGGGTTACTATAAGT GCATTTTATAATGGGATTTTCTGCTT/GJAAGTCCCACTGATTCCTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTGCC
EST31968 8a	75 T C T	GCGGGTTACTA TAAGTGCAATTT	TGTAAGAATCA GTGGCAGTT	CGAATTTGTCCTCTTATTTTGTGATTCTAGTAATCCTAAAGATTTGGGGGGGGGTTACTATAAGT GCATTTT/CJATAATGGGATTTTCTGCTTAAGTCCCACTGATTCCTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTGCC
EST32063 2	103 C T ---		---	TCCATGGATGAACAGACGCTACCATGCCACATCCCACCTCCCTCCGACCAGATGTCGTGGCCAGAGC TGGCTTCCCTTCCAGACCTAGCTGGCTTTGTAGT/C/TGTTGAGGCCCATTTGAAATAGCAAAACGCAC AGTCATGTAGCACTCGG
WI-16303	65 A G ---		---	AAGGCTTTCCAAAGCAATTCAAAGGCACCTTGGGTGTTGTGCTCTAAGTTTCTGTCACCTGCAGCCCCA/G TCTGTATTAGGGAGACCCCAAGCCAGTAACAATATGGTTCTTGCAAG
WI-17800	29 C G	GGGAGCACAA GAGAACTCA	TTTCCCTACAAT TAATCCCAGTC TT	TGGACATGGGAGCACAAAGAGAACTCACT/C/GJAAGACTGGGATTAATTGTAGGAAATATTTACACAG TTTCCAAAGTCAGAGAGCTAATCCCAACCCCTCTGTATCTGGAACATACACTGCTGCCATTTTCTGC CCATGAAGGGAAATACCC
WI-17857	34 T G C	CCTAAAGTCTG GGATGACTTTC	TGGCTTAGGT TCTACTTGATG T	AAACTGTCATTCCTAAAGTCTGGGATGACTTTCCTT/GJATTCATACATCAAGTAGAACCTAAGCCAAAT TCAGAATCAGAATCCTTTTGTCCATCAAAATCCAGCTAAGTCCCAAGCTGAATTAATTTTCAATCT
WI-17860	121 T A	TTTGGCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	GTATCTGATGTAGTTAACCATGGCCTGTGATGATTATATTGCTATAAGGAAGGGAAACAAATCTTTA TAGTGCCAAAGATAATTAATCTTGGTTAAATCTTTGCCAGCAAGCAAAATAT/AJCCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17866	43 A T	TTTATAGCCT ACTTCTCAA	CCGTTGTCACT AATCACACAA A	CAGCAACCTTTTGTGTTTATAGCCTACTTCTCAAAATTTGTI/A/TJTTGTGTGATTAGTGACAAGG GGGGAATCTACAATGCTCACATCACAGTAAACTACCA
EST33301 4c	80 G A ---		---	GAAAAAAAAGTCAAAATGTTCCTTTATGGGTGATGCCACCATGATTGCCCTCACACAAGCATGATC AATCGCCACGAGAG/GJA/ACTGGATGCCAAAGAGTATGG
EST33301 4b	63 G A ---		---	GAAAAAAAAGTCAAAATGTTCCTTTATGGGTGATGCCACCATGATTGCCCTCACACAAGCAT/G/AJ ATCAATGCCACGAGAGACTGGATGCCAAAGAGTATGG
EST33460 1	44 G A CA	AGCGTGGTTTT CAATACTAAA	CTGTATTATT GTTAAATATTT GCATTGTT	CTATCCAAAGATATTTATTGCAGCGTGGTTTTCATATACTAAACA/G/AJGTAAACAATGCAAAATATT TAACAATAATACAGTGATTAAATAAGCCATGCCATATCCAGTTGATGTAATACCTTTTGCAA

WI-17904	50 A G	AAAGCATGAC AATAAAATGA ACAC	CGCTTATGTTA ATAGTAATTCC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAATAAAATGAACACIAGJTAGGGGAATTAC TATTAACATAAGCGATAAACATCAAAACATCTGGTAAATGCAGTTAAACAAACACAAACATGA
EST34149 5	69 A G A T	TGCCAAATAC TCAAGTGIGA GAT	AACTACTAGCG AGAACAACTA ATAAAATC	GTCTTTCTTTGAGTGACACAAGCTTGTTCAITTTTGAGAAAATGTGTGCCAAATACTCAAGTGTGAA TJAGJGATTTTATTAGTTGTTCTCGCTAGTAGTTTGGTATTTCTATGAAAAAAGCAGCTAGTTTCAGC TTACAAATCACACAAGT
EST34343 8	95 C A ---	---	---	TGGGAAACATAAGTTAACTCAAGAAATATATCCAGTCTTTATGTTACTAAAACATTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCTCJAJTACAAAGATTAAAGAACTTACCATCAAAACACTTC CAGTGCATCAA
WI-17982	98 C T C C T A A A A G C	GGACCATATG ATATATAACT CCTAAAAGC	CAGAAATTATG TGATAATAACT CCTTCC	GGTACACAAATTTAATGGAGGAACACACAGGTATGTTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATACTCCTAAAAGCJCJTGGAAGGAGTTATTATCACATAAATTTCTGGGC GCTACAGAAAGTTTTTCATCA
WI-17993	118 A C ---	---	---	CTCAGTAACTCCGGGTATAATCTGCCATTTATTGATTTATTTATGATAAAACACCTCTCATTGTGA AAAACAGCTAAGGGTGACATCTCCAGACCCCAACCACTGTCCCTGTAATGTJAJCJCTGCTGAGAGTCC ACATTTTGGAAATCCAAT
WI-17996	84 A G A G G G A A C A G	GTAGAGCGA AGGGAACAG	AGGCACATGGG CAGC	CCCATCCAGAAACCCAGTGTGATGGTGAAGCAGCATGAAAACAACATCTCCCCAGGCCTCGCAGT AGAGGCGAAGGGAACAGJAJGJCTGCCATGTGCCTGTCTCTAAAGACGCCACCTCAGGTTGATGT CACCTGTGGAGACCGGT
WI-17136	33 C G ---	---	---	ATTCTTTATAAAACACCATGTCCCTAAAATGTJAJTTCACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGTCCCT
WI-18041	24 A C ---	---	---	GCCACTGAAAAAAGGTGCTCTTCCJAJCJGTTCTAACTCCCTGGACTCCCTCATTTGGAACTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAATACTTAATCA
EST35164 8a	57 A G C C C C	CACAGCCCTGC C C C C	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCCTTCAAGCACAGCCCTGCCCCCAJAJGJCTTGA GATTCAGAAATCCAGAGGGTGTCTCAGTCCCTTGGTTAGGTGCTTCTGTGACATTTCTCTTG
WI-18052b	67 A G ---	---	---	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTCTTTTATGTCGATGCATGCTCAGCACAGTGTGCTGGC AJGACAGCAGAGCTGCCTGAGGGAGGTTGTGTTAATGTGCTATGCGATGCTCAGCACAGTGTGCTGGC ATGGCCCATCCATGCTTT
WI-18052a	50 T C A T C	CCTGAGTTCTT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTCTTTTATGTCGATGCATGCTCAGCACAGTGTGCTGGC AGAACAGCAGAGCTGCCTGAGGGAGGTTGTGTTAATGTGCTATGCGATGCTCAGCACAGTGTGCTGGC ATGGCCCATCCATGCTTT
WI-18054	46 G A G A G T A A A A	GGGAGTGGG G A G A G T A A A A	CGTCAACCTGC TTCCA	CTGTTGTGCTGAGAACAGAGGGGTCAAGGGAGTGGGGAGTAAAJGJTAGGAAAGCAGGGGTGACG CATGCGAGGAGTCCAGACAAAAGACGGGTGATTTTGCTCAGGTTGGTAGCAACAGAGGTAATG

WI-18064	54 G A	GTAGTGTCTA AGCTGTATTC	CCAGTGGTATG ATTGTGACATT C	CAGTGGCAATCATCTCTCAAAACCCCTGTGGGTAGCTAGCTAAGCTGTATTTTCAGAG/GA/GAATGTAC AATCATACCACCTGGGGAGAAAGAGTAAGCACAGTGCTTATTAGGTGCCAAACTGGGGTACCTGGGAG GCAGAAA
EST35347 2	97 T C A A	GCATAAAATT TTCCAGTTGGT	COCTGGCAOC TGCT	TTAGCACCATCTTAGTGGAGCAGGATCTTGATCATGGGGTGAATTTTGTGTATCTGGGCTTCAT GGGATGCATAAAATTTCCAGTTGGTAAGT/CJAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28 A C	AACCCACTAC TTACTCAGAGT	AAAACTAATA AGAACTGGA GGTTTT	AAACCCACTACTTACTCAGAGTGTGTAT/CJATATTAAACACATGAAAGATATAATCTTAGAAAA ACCTCCAGTTCTTATTAGTTTGATATTTCTGTACTCAGAAGCATTTTAGGTGCAAGGATATAA
WI-18080c	80 C T	---	---	TGGCATAAAGTTTGCATAATCAATATCAAACTAGTCTCTCTTTGTAATTAATACTACTATGCCGTG TTTGACITTTAT/CJTTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18080b	65 G A	---	---	TGGCATAAAGTTTGCATAATCAATATCAAACTAGTCTCTCTTTGTAATTAATACTACTATGCC/G/ ATGTTTGACITTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18080a	41 T C	GCAATATCA ATATCAAACT AGTCTCTC	CAATTTACATA AGAGATAAAA GTCAACA	TGGCATAAAGTTTGCATAATCAATATCAAACTAGTCTCTCT/CJTGTAAATTAAATCTACTATGC CGTGTGGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT GTGGCATCCTATAAAAGCAGCCATGTGTGAAACAAATGATATGCACAGAAAGCATCTTCT/GA/ TGGCTTGTACACGGGTTTCTTCAAGAGGAAGATGACTCAGCCCTCCAGCTTCTGCAGCTAGC TTAGGAGAGGTGTTGAA
WI-18115b	71 C T	---	---	AACTACATAGTATGGTGGCTGGCTTAGAATCAATGGGTAAAGCCCTTAGTGACCTTTGGTATCCCC TT/C/JTTTGGTATGAAAGACAGACACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGTGAG TCAGT
WI-18115a	70 C T T	TTAGTGTACCT TTGGTATCCC	AGAGGTCTGTC TTTCATACCAA A	AACTACATAGTATGGTGGCTTAGAATCAATGGGTAAAGCCCTTAGTGACCTTTGGTATCCCC TT/C/JCTTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGTGAG TCAGT
WI-18136	78 A G	---	---	TTTTGAGAAGCACTCTGTAAAGCAAGGATGCATTCAAAAATGGCTTTGAGGATTAATCTTCTCTTTA GGTAATTTGC/JA/GJTAAGAACATAAAAGCATTTTAAAGTCCACTGCCGCTTAGAACT
WI-18169	115 A G	CCATCTTCCG GAAGCTC	GAGTTCTGCTT GTGCTCCA	GGCAAAATATTTTACATCACACCTGGAATCTGCCAAGCTTTCCACTATGAAGGCAATCGTAGAG TGTGCAGGAGGAAAGGTGTTATCCAAGCAGCCATCTTCCGGAAGCTC/JA/JTGGAGCAACAAGCAGA ACTCGGTGGGTAGGTGA
WI-18190b	26 G A	---	---	TGAAAGAAGTCGACACAGGGGACACT/GA/JTCATAAGTGGAAACAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGATGAGCTGGAGACATTAATCCTGGCGA

WI-18190	62 G A ---	AAATATATAC AACACTCCCTT CAGATC	--- CGTTTTACCAT TTGTTAAGCTT TTG	---	TGAAAGAAGTCGACACAGCGGACACTGTCATAAGTGGAAACAAAGGATGAAGCTAATCATGTGA[G/A] GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGATGAGCTGGAGACATTAATCTCTGGCGA
WI-18181	100 A C	AGCAGAGTTT CTGCCCTC	OCTCCTCTCT OCTCCTCTCT OCTCCTCTCT	TTGTTAAGCTT TTG	GACAGTGAAACACATTGAAACACAAATACAAACAAACATTAGGAACAAAGAAATGTGTAAATCCAA TGTGTGAAACAAATATATACAAACACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAACGTA TGTGTTCTTGAAC
WI-18215	78 G A	AGCAGAGTTT CTGCCCTC	OCTCCTCTCT OCTCCTCTCT OCTCCTCTCT	TTGTTAAGCTT TTG	ATTACATACAAAGCAATTCCTGAGTACAACTAGGGGACAGGTATTTTACAAAAACAAATAGAGCAGA GTTCTGCCCTC[G/A]GTGTGCGGGGGAGAGAGGGGATTCAGCATTTGGTGGAGTATGTTAATTT CCCTCAAGTTAATTCCTTC
WI-18232	60 T A A A	TGGTGTGATT GTGATACACTT	AAATAAAGGT TTTCAGGGGTT C	---	CATTTCCGAAAAATCTGATAGTTAAATATCCCGTCTGGTGTGATTGTGATACACTTAAGTT[A/GAA CCCTCGAAAAACCTTTATTTTGAATTTGAAGTTTGTCTCAGAAACTGGGCAGAACTTTTCACATTCTG AC
WI-17892	76 T C A C A	GGAAACTTG AGTTTGAGATC ACA	CACAGAAGTG AATAGACTAGT GAGACA	---	TTTAAATAGCTTAGAATTTTCTCAGTATTTTATCAATAGTGTGAAGCTGGAACCTTGAGTTTGAG ATCACAATAT[C/G]TGTCTCACTAGTCTATTCACITCTGTGGGCAITTCGGCAGAGTGCGC
WI-18242	30 G A AATCGTAACA	CCCCAAATGTT AATCGTAACA	GCTAACACTTC TACTGTAACAG CTTTC	---	AATATCCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTAGCAAAAAT TGGATGCCACAACTTATCTACCACTTCTTCAAGCAAGTGAGGTCAGAATGTTCTTGCCTATATC TGCAAAAGATCGAACAAG
WI-18266c	119 C T ---	---	---	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAATTGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATC[C/T]ACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124 T C ---	---	---	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAATTGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[C/G]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97 C T TTCAAA	AAATAGGAAA TATGGACTATC TTCAAA	TTTCATGCATCA TTTGCGCA	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAATTGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGACACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73 A G A A	GCTGTCAGCTA TTGTTATTCA	GGAGAAAAGG GAGCAGAAGA	---	CTGAGCCTCTTGGATATGGTTTAGTGTCTATCATTAATTTTGGAAAGCTGTGAGCTATTGTTATTTT AAAT[A/G]TATCTTCTGCTCCCTTTTCTCTTTTCTGGGATTTCTATTCTGCAATGTTTATA
WI-18330b	66 A G ---	---	---	---	AAACATCTACAGCTGTCTTAGGCCATCTGTAAAGAAATCAGGGATAAGAGCTGAGGAACAAGAGGGI A/GTATGTAGGCAGTGAGTCAGGACTATGCAAAACCATATAAAATAAAGAACATAATTTTTTTGTTGAT TCACA

WI-18330a	49	TCCTGTAAGA AATCAGGGAT AAGA	AGTCTGACTC ACTGCTACA	AAACATCTACAGCTGCTTAGGCCATCCTGTGAAGAAATCAGGGATAAGA[G/A]CTGAGGAACAAGA GGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAATAAGAAACATAATTTTGTGAT TCACA
EST37564 5	85	AAATTC AAGC CATCTACAAA T C A G A	CTATGGAGGCC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAATTGCTGTTAGTAATACTGCATGTTATTTAAGCTAAATTC AAGCCATCTACAAAAGATT[C/T]CTCATTTAGGCCCTCCATAGGCTGCAAAACACATCAAAGGCATTAC TGTACTGGAGAGGACTGAG
WI-18327	104	AAACAGCTTT CGTTAGGCTAG TT	CGCATACAATG GCTCAGC	CAAGGGATTTTATTACCTACAAAGTAAGGAGGACAGCTGGGGCAGTTTCCCAAAGCAGTACCTC CCAAACAATGGTGAAACACAGCTTCGTTAGGCTAGTT[G/A]GCTGAGCCATTGTATCGGAGGCAGA GT
EST37624 6b	102	---	---	GTGGCAAGAGCAGCTAAACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCACGCTGATGG CCTGCAGTCTCTGCCGTGCTTGGCTCTCTGGACG[G/A]TTCAATCTACATGGCTGCTTGGCGTCC TCTGACCTCCCATTC
EST37624 6a	58	CT ---	---	GTGGCAAGAGCAGCTAAACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCACGCTGATGG TGGCCTGCAGTCTCTGCCGTGCTTGGCTCTCTGGACGTTTCAATCTACATGGCTGCTTGGCGTCC TCTGACCTCCCATTC
WI-18357	89	CCAGCCCTTA GCATCAA	AAGACTCAA AGACTGAAGAT GA	AATGTTTTAAAGTCTACCGTCTGAGGTGGCCATGAAGCCAGCCCATGGAGAGACATTTTCAGA TAATCCAGCCCTTAGCATCAA[C/G]TCATCTTCACTTTGAGTCTTCCAGCCAGGTCCTCAAGCTT GTGGACCAGAGACAAGCC
WI-18012g	117	AG ---	---	TTTTATCTGGGTCAGCTCCTTCTTAATGGCCTGAAGGTCATCTCCTTCAACTTCCAGACTTGAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTCGTGA[G/A]GTGTTTCCGTGATACA CGCTGACGTTTCGAGGG
WI-18012f	113	GA ---	---	TTTTATCTGGGTCAGCTCCTTCTTAATGGCCTGAAGGTCATCTCCTTCAACTTCCAGACTTGAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTCGTGA[G/A]GTGTTTCCGTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112	GCCACTTTTGC CCCTT	TCAGCGTGAT CAGGAACA	TTTTATCTGGGTCAGCTCCTTCTTAATGGCCTGAAGGTCATCTCCTTCAACTTCCAGACTTGAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTCGTGA[G/A]GTGTTTCCGTGATACA CGCTGACGTTTCGAGGG
WI-18012b	46	T C ---	---	TTTTATCTGGGTCAGCTCCTTCTTAATGGCCTGAAGGTCATCTCCTTCAACTTCCAGACTTGAAG AGATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTCGTGA[G/A]GTGTTTCCGTGATACA GCTGACGTTTCGAGGG
EST38390 4	75	GCAAAAAGGA CTCTGCATTG	GCTAAAGTCAG CTGATTATAA ACTTAA	CATATCATAGCCAGATCTACAACCCAGAGTAATCCCATGGTTATGTTACATGGCAAAAAGGACTC TGCATTG[G/A]TTAAGTTTATTATCAGCTGACTTTAGCATTGGGAGATTATCTGGAT

EST38512 7	91	T G	TGACGATGCC AATACTTCG	CACGCACTCT GGGAAGC	TAATAAAACCTGACCCAAATTGGTAAACTGTGTGCTGACTGAGAGAAACAATGAAAAATCTGTAAAT ACCTGATGACGATGCCAATACTTCGT/G/GCTTCCAGAGTGCAGTGATAACTGTTATAGCC
EST38519 0	24	C T T	CCTGCACTCC TAAAAGATCT	TCTGTAGGAC TTGGGGA	CCTGCACTCCATAAAGATCTTTT/C/TJCCCCCAAGCTCTAACAGAAATGGTATATTCCTCTGGA AGATGAACGTCATCAATGGATTGTGCTGCTCTCGTTTACAGCTTTGATTTTTTGTCCCTTGAGAACCTTG TCCTCCCTGCTGATTT
EST38575 1	66	T C A A	GAACATCCCA TGTTCTGTTT	AGGGAAGGA GTATAACACAT	AGTGGTCAATGTAAACTAATGGGGACACCAAGCCTCAGGAAGAACATCCCATGTTTCTGTTTAA T/CJCTCTTATGTGTTATACTACCTCCCTTCTCTTCTTATACACATAGATTTTCTTAATTGCAGC CCA
EST38616 9	101	C G C T T C	CCTGCTCGCC CTTC	GAGGAATGGAT GGTGGC	CCATCTAGGAGGCTACCTGAGCTCTCTGTGCTCCAGAGTGGTGCTCAGGCCGGGGCCCCCGTGG AGTCTCCGGGGCCCGCCTGCTCGCCCTT/C/G/GCCACCATCCATTCCTCCAGGGG
EST38652 8	59	T C	TCGAACTGGG CATTTCAA	TTGCAAAAATG AAAGGAAAAA	TATAGTAGGTACTTTCTTGTGCTGACGAGGAATATTACAGTCTGAACCTGGGCATTTCAA/T/CJGCGTG GTATTTTTTCTTTTCATTTTTGCAAGTAAAAAATCAT
EST38654 5	42	T C	AATGGTCATTT TAATATATCA	CAGTGATGGTC CTTAATCTTCT	CTCAAGCTGAGAAATGGTCATTTTAAATATATACAGTTTACATAT/CJAGATAGAAGATTAAGGACCAT CACTGAGGTACATAGCTCAGAGGCAGAGTTAAGATTTGGACCCAGGAGGTGGTTCCAGCATATA
EST38707 9	75	A G ---		ATC	GGATCCTCACTCACTGGGACAGCCTGAGAAAGGACATCCACCAGACCTACTGATCTGGAGTCCCA CGTCCCCA/GJAGGCCAGGGGATGTGTGCCCTCTCTCCCACTCATCTTTTCAGGAACACAGGAGG ATCTTGTCTTCTGGAAA
EST38759 2	86	A G	TGTCCTCCTGA GGTGATATGG	TCACCATCGTG GACTTAAGG	TGACCTTGATTTCTTACTAGAGGGGAGAAGATCACCTACCTTTTGGATGCCCTCCACTCTACTTGT CTCCCTGAGGTGATATGG/GJ/CCTTAAGTCCACGATGGTGACCTAAACTCAGTTTAAAATCTTGCC TAGCAGCAAC
EST38775 1	40	T A C	AATCAATAGG AGAGGATTGG	GGCTTTGCTCT GAATTCAAA	GACTCTCAACCAAGAGAAAAATCAATAGGAGAGGATTGGC/T/AJTTTGAATTCAGAGCAAAGCCCT CTTACTGAGAGGTGAGCCCCCAGCCCCCTCCAAATGCCCTTTCATGAGTTAGGATCTCCTAAGTGGTAG AAACAAACCAACATGGTGG
EST38815 4	91	C A C A	TGTTATGAGA ACCCATTACA	GCTGACTGGCA CATGCTTT	CACCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTTCACCTTATGTGTGTTTCATTCACAAG TGTTTATGAGAACCCATTACACA/C/AJAAAGCATGTGCCAGTGCAGAGATTCTGTAATAA
EST38858 4	98	C T T G A C	CACAGTAAA AAGAAACTCA	GGAGCGAGTCC AAGGAGAA	TCCTTACTGTGCTTACAACCTTCTCCCAAGTTTCGGGTGGTTCCATATTTGTTATTGTTATTATTA TTCAACACGAGTAAAAAGAAACTCATGAC/C/JTCTCCTTGGACTCGCTCTCTCCCAATCTCGAT ACCGACTGCACGTGG
EST38865 2	72	T C T G T G C A T G C	GCTGTAGAATT AGGACACAG	GGAAGGACGG AGGACACAG	CCCTAATGGATTTACAGCTCATCTGAGTCTGCTGTGTTCTCTGAGGAGCTGTAGAATTTGTGTG ATGCT/CJCTGTGCTCCTCCCTTCCCAAAATGAGCACATATGCAGGGCAGGCAAGAGCATGCTGGA TTTGTCTTAGTTGTAA

EST38878 9	47 T C	AAACATCATT ACTAGCCTAG ATCCTAA	CCTTCAATAAA TCTCATGTCT CA	CCAAATGAGAACCAAGTAATTAACATCATTACTAGCCTAGATCCTAA[T/C]TGAGGACATGAGATTT ATTGAAGGGAAATCCTCAATTAATATGAACATTTCTTGAGAAATGGGAAATTTGAAAACATTCOC TTATCAATGTCTATCTACACATCTTTATTTTATTTTATTTTCTCCTTTCTCAATATCGGATTGTTGC TCATGAGAATAATGGCTGAGGGAGCTGGCAGGAGCTTCTCA[G/C]GCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 G C	---	---	TTATCAATGTCTATCTACACATCTTTATTTTATTTTATTTTCTCCTTTCTCAATATCGGATTGT TGCTCATGAGAATAATGGCTGAGGGAGCTGGCAGGAGCTTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38882 6a	35 T C	TGTCATCTCAC ACATTCTTTAT TTTT	CGATATTTGAG AAAGTGAAAA CAA	TTATCAATGTCTATCTACACATCTTTATTTTATTTTATTTTCTCCTTTCTCAATATCGGATTGT TGCTCATGAGAATAATGGCTGAGGGAGCTGGCAGGAGCTTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38909 5	47 A G	GCACAGCATG GCTAAACG	GGTATTTGTG ATCCCATCTT T	GCACTAACTAACTTTCAATTTGTGGATTGCACAGCATGGCTAAACG[A/G]TAAAGATGGGAATCAA CAAATACCATTTGAAGATATGGAGCAAGAGAACTCTCACATACTGCTGGAGGGAATATAAAT
EST38911 9	85 A G	GTTGAGGAA ACTTATAACCT CAC	TGTTGTTTGT GAAACAAGCG	AACCTGAATGGCAGTGAAACACTACACATCAAACTTAGGAAATGTGGTTAGTGGTACGTTGAG GGAAACTTATAACCTCAC[A/G]CGCTTGTTCACAAAACAACAGCAGACAAGAGATTTCCAACTC CAGCAATGACAGGCTAGGG
EST38955 5	30 G C	TGAATCCCTT GGTGG	CACTGCAATCT CACCCC	TAAACATCCCATTTGAATCCCTTTGGTGG[G/C]GGGGGGGGTGAGATTGCAGTGTCTCAAGATAAA TATCACAAATATATCAAAAACCTTCAAAATTTGTCTATGCATTCACACACTGACATGAGCCACAACAT CCTTCACAGGGACTGTAC
EST39002 0	42 G A	GGACCTTCGG TGACC	CTGGCAGGGAG CCTG	CCTGCTATGATGCCTGGGAGATCCCGACCTTGGTGACQ[G/A]CAGGCTCCCTGCCAGGCTTGG CCCCTGACCGGGCTCCCGAGCTCGGCCCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39004 8	79 T G	GGTGGTAAGG CCTAAGGAAT	ATCTCGGCTGG CGC	CACGTGGCCCTAAGTTCCGGGTCTTCCCTCAGTCTGGATGGCTGTGGAAAAAGCTTGGTGGTAAG GCCTAAGGAATTTGAGGGGAGGGGGCGATGCCCGCAGCGAGATGGTCTCTGTAAGCCTGTGGGTC AAAGACCTAACTTCTGGA
WI-16398	90 T C	TCCCTATTATT CCATGATATTT TCA	GAATGGTTGT GAAAAATATA TTGATAT	AAAGATAATGTCTATCACACGCAACATATAGAAACATAAAAGAAAAATAAGTATCCACCCATAAAT CCCTATTATTCATGATATTTTCA[T/C]AGCAACTAGTATATATATCAATATATTTTTCACAAACCAT TCAGTTACAC
WI-16403	69 T C	CCTTTGCTCTC AATTTTAAAC ACT	TAAGGCTAAT TCCCTATATAA AAAG	GGTTGCTTTTCATGATTTTCTCATTTCCCTATCAGGTTTCTGGTCTTGTCTCTCAATTTTAAACAT T/C]CTTTTATATAGGGAATTAGCCCTTAAACTGTGGTACATGCTGCCAAAAATTTCTCCCAAGTT
WI-16406	24 C T	GCTTTAATGGC TACAGAAAGA AGG	CCAGAACCCAG ATGTGTTTAAA AA	GCTTTAATGGCTACAGAAAGAGG[C/T]GGTTTATTTTCTTTTAAACACATCTGGTTCTGGCAGC AAGTTATATTATGCAATTAGAGCAATAGGTGCCCTGAA

EST39236 0b	57 C G	TCATCTGAGA ATAAACTTCCT GTCT	CATTATAGGTA CTGAGTCAATC ATTAAACA	TCCTTTTATTCATGATTTGTTTCATCTGAGAATAAACTTCCTGTCTAATTTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATAATGAGACTGGAAATATATTACCTGGCAATGAATGAGGTGTCTC TTT
EST39294 4	63 G T	CCTGAACACAG GGATGCC	GCACAAATTAA ACATAGTACCG AGAA	CAAAACAGACCTTTGGTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAACAGGGATGCC[G/T] TTCTCGGTACTATGTTTAAATTGCTGAGCCAGCAACCCCTCGAGTTACCCGGCCTTTTACCCACAGCC AGCTCTGCTTGTCTGCAT
EST39366 2	72 T C	---	---	AGAAAACATTCTGTCTGATCAGAGGAAGATGTATGTAGAAAATCAGAATCTGACTGAATTCCTAAA ATCTATT[C/J]ACACTGAGAGGAAAATGGAAAAGAAAATGTTTGCATAAAAGCTTTTCCCTGACTCTCA GAGGGGTTTCAGA
EST39371 9	86 A G	CATTGGATTA GGTGAGG	TGATTTGAGAC ATTTACATTT TT	AAAAAGCTGTAGCTGGCAAGTCAAAAGTTTATTTATGTGTGTAATTTCCAGTTGAGCATTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAATGTCTCAAATCAAATGCTTCTCTTAAAGATTAA GACATTGCCCAACCCCTGC
WI-17177	23 A G	---	---	ACAAAGTGACATATCCAAACCAACC[A/G]TCCATCCCACTGTGCCCTATTCTTTCTTGTGTTCTTT AGAGCCCTTTTCAGCTATTCTCTGTGAAGCAAACTGCAGGAAGGCCCTCCCGTACTCCTCCCTGGAA G
EST39428 8	31 C T	GCTCCCCACA ATTGATT	GGTCCCTTAG AAGCCACC	AGGTTCCCTGGTTGCTCCCCACAATTTTATTGTTGTTGTTTCTAAGGGACCCAGGATTCTGCATT TTCTGGGTGGGCTAGGTAATCTGTTGCTTTGGTCCACAGAGCACAAATTAAGAAGATCAGGTCT GGCTGTTGC
EST39430 2	45 A C	GGCAGAGGAA TAACTGATGTT	CAGGGGTGGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAAATGATGTT[C/A/C]CAATAACCCGACCCCTGA CCAGTACCTTTCCCTCAGGCCAGGCTCCGGTGAGGATGTCTGGG
EST39446 7b	117 C T	CTACTGACAT AGGACTTCA	TCCTGGAAAAC TGACATAAAC	AAAGCCCTGTAAACTGAAGCTAGACAACGTCAACTTTGGAAGAAAATAACAGGAACCTATTATAT ACGTAAATCACTTTTCATACCTGCCTACTGACATAGGGACTTCAGAGTAATA[C/T]GGTTTATGTCACT TTTCCAGGATTGTTCTCCC
EST39465 2	80 A G	AATGCAGGAG GGTGGC	CAATCTGGGC CCTCT	ATGGTGTCAATTAGAGGGCCACAGGGGATGGGGAGTAAAAATAACATAAACGAACGTAAACAGAAA TGCAGGAGGGTGGC[A/G]AGAGGGGCCGAGATTGGGTGTTTCAGGGCAGAGGGTGAAGACAG
EST39501 0	81 A G	AAAGATTCT GTAGACATCT	CAC TTGCAATT CTGAAGGCT	TGCTTACAACCCATAACCATAGGCCATGTGTTTCAGACATTCTTGACCAAGCCTAAAGATTCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAAATTGCAAGTGAAGTTCAAGTCAACCAATTTC
WI-18387b	84 A C	---	---	CACAAAATGGGACTGCTGAAGAGTGACAGTTGGACCTTACTTTGGTGACCCCATACATTGTTGGTCA CATGCTTTAGCATAC[A/C]CATGGTAACATTGACTATGGAGTCTTGTGAAAGTGTATGTGCGATG GCTATGTAGACATAAAGA

WI-18387a	57 A G	CTTACTTTGG TGACCCCAT	GCTAAAGCATG TGACCACAAA	CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATAC/A/GJTITGTG GTCACATGCTTTAGCCATACACATGGTAACATTGACTATGGAGTCTTGTGAAAGTGTAAATGTGCGCATG GCTATGTAGACATAAAGA
EST40601 9	78 A G	GGGTGAACCT GAAACAC	TTCTTGAAGA AAGCGTC	TCCCAGGATGGTTTATCCAAAGCTGTGGACGGTGAACATTAGACGAAAGAGGTGACTCGCGTGGA ACCTGAACAC/A/GJGACGCCCTTCTCCAAAGAGGGCTGTGGCGATCAGGCCACTCAAGG
EST41935	32 A G	AGTGATCAC ATCTCAGGAT AGGT	GCACACCTTC ACACTGTTA	TCATTCAAGTGATCACATCTTCAGGATAGGT/A/GJATAACAGTGTGAAGGGTGTGCTCATTTTCTTC AGCTGTAGTAGAGGAGTCTCCCGAGAGTAGCAGTTGTGA
EST43091	28 C T	CATTCTGGTCT TTATTTTGGG CA	AAAACGATTT GTTAAACATG CTAC	ATGTCATTCTGGTCTTTATTTTGGACA/C/JGTAGCATGTTTAAACAAATCAGTTTTCATAGGCAA CCTTTGAACATCAAAAGAAATACAATATATTTTCAAAAATTTCTCATCACTGTAAATTCA
WI-18420c	108 T C	TTCCATTAAAC AGGAAGTTTC C	AAATTCACAG ATTGCTATAAG C	AGAGAGACAACAAGAAATAAGGAAATGGGAAGAACAGAGTGAAATTAAGCAAATCTTGGA TTCAGATTCCATTAAACAGGAAGTTTCTCAAAAAAATCAAAT/C/JGCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18420a	38 C T	GAATAAGGGA AAATGGGAAG AA	CCAAGATTTC TTTAAATTCAC TC	AGAGAGACAACAAGAAATAAGGAAATGGGAAGAA/C/JTAGAGTGAATTAAGCAAATCTT GGATTCAAGTTCATTAAACAGGAAGTTTCTCAAAAAAATCAAATGCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18425b	101 T C	AGCTGATCAGCTGCTGTTACTGTTTATGTGTGGCCAGGGAAGCCAAAAGATCAGACACCTGTGTC CTAGACAGATTCAATGCACACAACAACAGGAGGTGGGGTCAACACGGCGGAGAGCCAAAAGAC TAGGGC
WI-18425	81 A C	CACCTGTCT AGACAGATT A	OCTCCTGTTGT TGTGTGCA	AGCTGATCAGCTGCTGTTACTGTTTATGTGTGGCCAGGGAAGCCAAAAGATCAGACACCTGTGTC CTAGACAGATTCA/C/JTGACACAACAACAGGAGGTGGGGTCAACACGGCGGAGAGCCAAAAGAC TAGGGC
WI-18449	129 C T	CTTTTGGCTCT AAGTGGGACT	CTCCCTGACT GTATCCAGA	AAATTGAGGTCCGGGTGGAACATATAAAAGGAAAGGAAGAGAAATCAATCAAGGGAGGCCAAAGTG GGAAGCTGTATTGCTGATCTAACGTGCTGTCCAGTTCCTCTTTTGGCTCTAAGTGGGACTA/C/JTTC TGGATACAGTCAGGGGAG
WI-18457	120 T C	ATCGCTTCATTGAAGCCTGCTTAATTTCTCTCAGTCAACTGGTGCCCCCAAGACATTATTTTATTTCTT AAATGTCCAATATCTGCCTGATGTCTGTGTTTGTGCACATTGGGGCCACAGT/C/JAAATAGGCTAAA AGGCAGTCCCACTGCT
WI-18462	39 A G	CCACAATGGC AGAGGTGA	TTTAGGCTTTG AGATGGTTTCT	GGTGCTATAGTCTGTGTACACCACAAATGGCAGAGGTGA/A/GJTAGAAACCATCTCAAAGCCTAAAA TATTTACCATACATCCCTCACAGCAAAAGTTTGCTAATCTCGGGTTTAGGGACTCCATTGAG
WI-18476	60 C T	GGTGGGGTGC GAGG	GCACGATGGGA GTGACC	TGAGGACGTGTGACAAGCTCCAGCAGGGGTGGGGCCGGGCTGAGGGTGGGGTGGGAGG/C/JGGT CACTCCCATCGTGGCCCTGGCCGTCCCTCCACTCACCCACACCTGGCCCGAGTCCACGTTGAGGT

WI-18491	109	A	AACAAATGGT AGGTGGTATT AATACTATT	CGTGTGCATT TCCTGTAATCC	CTAATGAGATGAATACATGAAGGCGTTTAGCACAGTGCCTAAACACACAGTAAGTAACCAACAAAT GGTAGGTGGTATTAACTATTATTATTAATCCAGAAATGAC[G/A]GGATTACAAGAAAAATGCACA CGT
EST50757 b	79	C	GAGCTGAGG CTGCTTCT	AOCCTTCAACC GACC	AGCCCCCTCCACTCCACTCTGCTTCCACAAAGTCGGTCCCGAGAGCTCGAGGGCTGCTCTTTTATAT GTGACGGGCG[CT]GGGCGGGTGAAGGTCAGAGA
WI-17675	103	T	GGACATTTGG CATGGTGACTT	GGGGAACCAAC CAGG	GATCTTGAAAGCACTAGAAACTAAACATCTTACCAGGTGCTGAAGAAAGTGTCTCGTTTTAAT TGCCAAAGCAGGGATGTGGACATTTGGATGGTACTTT[C]CCTGGTGGTTCCCCATAGATTCACCAT TGCTCTAATGGTGCTA
WI-16543	67	G	AGATAAACTA CATTTGGGTTT TGG	GATTCATCAT ACAGGGGACTT	GATCCATTACCTAGGGTAAAAATCTCCTGAATGTCAACAAAGAGATAAACTACATTTGGGTTTGG[G/TAAGTCCCTGTAAATGATGAATCAAGAAATCCTCAAGTCTGTCTTGCCACCCATTTAATACGTATT TTTGTTAAGGCTGAAGTT
WI-17687	107	C	GCCAAAAAGG TTGGGAA	TTACTTTTGT CCGACCAACA	ATCTGAGATGGAAAGAGTTTCATCCAAAAACCATCTCCCCCTGACCCCCAGTCCATGGAATAATGTC TTCCACAAAAACCGTCCCTGGTGCCAAAAAGGTTGGGGA[C/G]TGCTGGTCCGTACAAAAAGTAATT G
WI-17690b	79	A	AGGCATTTTC TAGCTGTGTTT	...	ACAACATGTGAAGAAGATATGTTGCTTTACTCACAGTGGAGGCAATTTTCTAGCTGTGTTGATTT GGCTTCCCTA[G/G]ATTACAGGACCCATACTCTGTTCTCACTCATCTGCTATGCTGCTG
WI-17690a	63	A	AGGCATTTTC TAGCTGTGTTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAGAAGATATGTTGCTTTACTCACAGTGGAGGCAATTTTCTAGCTGTGTT[G/A]A TTTGGCTTCCCTATAGATTACAGGACCCATACTCTGTTCTCACTCATCTGCTATGCTGCTG
EST51717 b	128	C	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	GATCCAACTCTCAGTGTCTAACTCATCATCCAGATTATTCTGAAGTGGAAACCCCTCCGACCCAA TGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGGCGGAAGACAGTGAGCTGT[C/T]GAG CTGGATTATTGCCCTCAA
EST51717 a	39	C	GATCCAACTCTCAGTGTCTAACTCATCATCCAGATTATT[C/T]TGAAGTGGAAACCCCTCCGACCC CAATGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGGCGGAAGACAGTGAGCTGTTCGAG CTGGATTATTGCCCTCAA
EST53012	97	C	TGGTCACTTTG GGGOC	GGCTCTGOCCA GGOC	TTTCCAGTTGACAGGTTTATTCCACCCCTTCCATCCCATGGCCACCCCGAGGAGGAGACAG GTGTGCTGGAGTGTGTCACTTTGGGGCC[C/T]GGCGTGGCAGAGCCCACTGGGTTTACATTCTCTGT GGGACGGTGTGGACAC
EST53349	96	A	TGTTGAAAGC AGTCACAATG GTAC	CATCTGGATAT CTTGTACATT TT	AAACTGCAAAATAACAAAAACAGAAAGTCCAAGAGGCTAAAGTCTAAGCTATAATTACACATG AAGTATATGTTGAAAGCAGTCACATGTAC[A/G]AAAAATGTGACAAGATATCCAGATGTTTAA
EST53389	74	A	GGAGACCTGC AGAACTTAA CA	GGCCTTTCTAA CAATAAATGCT C	TTTCGAAATGTCCTCCATGACTTGACAGACTGAGAGCCAGCCAGCCAGGAGACCTGCAGAACT TAAACACIAGIAGACATTTATTGTTAGAAAGGGCAAGCTTACACTCAAATAGGTTTTAACATGAAC ACATTAAGGGAGATGGCC

TIGR- A003P30	117 C G ---				ACAAGTTCAAAGGAGAACTTCCTTTGTTTAAATGCAGCTGTGCTCAGAAAGCCTGTGATTTCTCTAGGA AACCATCTGGGTTTAGCCATTAGAAAAATGCAGTTTAAAGCAGTGTCA[C/G]ACTGGCTGCCTGAA GGTACCCCTTGGAGATACT
TIGR- A004S34	156 C T A				GCTTGCTTTTATGTTAGGTTCCGGGGAAGGAGGGGCTGACAAACCGCAGACATCTGGACACCAGC AAGGTCACAGGGGAGTTTGCAGAACTCTTTGCTTGGCTAACAGTCTGTCATGTGACAATAGGCA AACCTCCTCATCTCCTATAAA[C/T]CTTTAACAAAAACAGTTAGCTGTTTACAAAAACAGTTAGCTGTT TACATG
TIGR- A004T44b	97 A C ---				AACAACAGTGAATCTTTAACAGGGGATGTTAAAGGTAAGATCAGGAAGATAAACCCAAAAATGAT TGAGTATGATAAAGAAATTTTGCATGGCGATT[A/C]AAATAGAAAACTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TIGR- A004T44a	69 G A TGA				AACAACAGTGAATCTTTAACAGGGGATGTTAAAGGTAAGATCAGGAAGATAAACCCAAAAATGAT TGA[G/A]TATGATAAAGAAATTTTGCATGGCGATTAAATAGAAAACTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TIGR- A004V08	60 T C GGCATTCTCTT				CCTACAATCCTATAATATTGCAAGGGTTGGGAAGGATGCAGGAAAAACAGGCATTCTCTTAT[C/G]GCC TTTTGTGGGAAGGATCAATTTGGTGCATGCACITTAGGGGACAAATTTGGGCAGTAGCTGTCAAATTTTC AGTAGCTGTCAAAATTTCAAA
TIGR- A004V26	125 A G ---				TCTAGCTATAAGACCAGATTTTAAATATTCTAGATATAGAAATATCCAGAATAATTCTATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAACGGTAAATATGCATTATCTTCACATGA[A/G]AAGGT TTCAGTTTATAATGCTTAAATACTGTATCTATTGCTTAAATACTGTATCTATTGG
TIGR- A004V28 a	29 A G CGATCTC				CCAGGCTATAATGTTGGGTGGGATCTC[A/G]GCTCACTGCAACCTCCGCCCTCCAGGTTCAAGCAA TTCTCCTGCCTCAGCCTCTTGAGTAGCCGGGACTACAGGCACCCGCCACCGCACCTAACTAATTTTGTG TATTTTATAGTAGAGACATTTGATTTTTTTAGTAGAGACAGG
TIGR- A004X20	25 T C GA				TAAGTTTCCCTCTCTCTGTAGGAT[C/G]GCTCCATGTTACAGTCAACTATAAACATGGCTCATGT TCACTCTGGGCTTCGCTTCAGAGGAGTTGATATTTTGGAAAGTGGTACCCTTTGTTCTGTGCTTTTCA GACCAACCCGCTCTCTTCAATTTCTCAAGGCTTCCCTCCAAAGGAGTTAAATCATCATCATGTCCAATC ATCATCATGTCCCT
TIGR- A004X30	26 T C CCAC				TTTTGAAATCTTAGAGTAGAACCCACAT[C/G]ACTCTAGTAATACTTGTATAAAATTTAAAAATAGTTTT AAACACTTCCATAAAGAAATAGGGTGCCAGCTCCTTGATTTCCCCCTAGGGATAAAGATATCCAT GTTAGGGATAAAGATATCCATGTAC
TIGR- A004Z04	102 T G ATGCAAAACT				CACGGTATATGCCCTTATATAGGTATATATACAGATCGTACACAATATATTTAACAGTTTGACATG GGGTCCACAGTACCTTCATTTGGGTATGCAAAACTT[G/T]TTCCTTCATGAAATTTCTAATTATAAGG ACTGTTGCTTCTTCATATTCATGGACATTATACAAAAATACAGTCTCTTTAGTGATTTAAGACGTC TCITTAGTGATTAAAGACTG

X57830	106	G C C T	AGTGGAAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC A	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTTCACCTATCTGGAAAAAATAATGAGATTGGA AAAAATTAGACAAGTCTAGTGGAAACCAACGATCATATCTG/CJTATGGCTCATTTTATTCTGTCAAT GAAAAGCGGGGTTCAATGCTACAAAATGTGCTTGGAAAATGTTCTGACAGCATTTACAGCTGTGAG CTTTC
X74070b	72	T G T G G A T C	CTTTTAAAGAA ATTTTGTTTA	GGGCTTAAAAA TATTAGAGATC TAGATTT	AACCTGAAGAAGTTACTGGGAGCTGCTATTTTATATTATGACTGCTTTTTAAGAAAATTTTTGTTTATG GATCT/GJGATAAAACTAGATCTCTAATATTTTAAAGCCCAAGCCCTTGGACACTGCAGCTCTTTT CAGTTTTTTCCTTATACACAATTCATTTCTGCAGCTAAITTAAGCCGAAGAAGCCTGGGAATCAAGTTT GAA
Z48804	44	C T ---	---	---	ACTGCCGAAGTGTAGCGGCCCCCAACCTTGCCTCATCACCAG/CJTJTAGAGCTTCTTCCCCGAAGGG CCTTTAGGATAGGAGAAAGGGTTTCATGCACACACACGTTGAGAAATGGAAGAGCCCCCTCCAGACCACT CTACAGCTGCTCTAGCCTTAGTTGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAGTAAGTAAGG TCCA
D28513b	133	A G ---	---	---	ATGACCAAGCCACCACATTTAGAACCTTTGGCTGGCTTTGGAAGTCCAGAGCTGGATCTCTCAGCTCC CGCCCCAGAGGGTCAGCACTTTGGACATGGCTCACAAGCAGTTTTTGTGACTGCATGAATGC/A GJTGCGGTGCAAGCATGAACCTTGTAAATCAAGAGGCTTACATAATTTTAAACCAGTTCTGTCTTC AGCTGTACATA
D29833b	85	A G ---	---	---	CCACTCCATCTGTATGCCCAAGTTATCCACAGCCTCCTTCCGACCAAGACCCCTATCCACCTGG TCCATTTTCCCTGTAA/A/GJTTCTCCAAGTATCCTACCTCCCTACTCCTGCAACCCCAATATGAA CAACTGCAGCAGGTGCGACCAACCAACCAACCAACCAACCAACCACTACCTTGTAACTACTGCTTCTGCTAC
D29833a	21	A G ---	---	---	CCACTCCATCCTGTATGCCCA/A/GJTTATCCACAGCCTCCTTCCGACCAAGACCCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATTTCTCCAAGTATCCTACCTCCCTACTCCTGCAACCCCAATATGAA CAACTGCAGCAGGTGCGACCAACCAACCAACCAACCAACCACTACCTTGTAACTACTGCTTCTGCTAC
D31762	82	G A ---	---	---	CTCCCTGCTCCTCCTTCCCTGCTGTATGCTCCGTCTCAACAGCCGAAACCTGTCTTGCATGGGGG GAGGGGGCGTTTC/GA/CJTTCCTTCTTCTTGGCTTCTCTTATTTCCACAAACCATTTCTCAATAAA GCCAAAATCTTCTCTTCTCCCTCCTCAGGCCACCTCCTGTCTCCTACTCCTGTCTGTGCTGGGCTTTT CTGGA
D37931	64	T C ---	---	---	ATTATCGCGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTG/T/C CCCAGGCTCTGTCTCCTCAGCTCAITTCCTACTCTTTTCTCTATATACTCATTTCTATTAATACATT GCACCAAGAGATATGGAGACATAAACCTGTAATGAATGAGGCTGGGCTTTTCTGTAAATAGCTTCC TTT

D63807	101	CT	---			CAGGCAGGACTTCAGTGTCAAGTATCCCTGCCTTCAGTCTCTTTAGAAATCACATCTGTGTTCAATCC ATTGTTTAGAGGGAGTGATTTTCCCTGTTCCA/C/TTGAAGAGGACTTTTGTTTACAAATTTGGATCAC AATGCAGAGGAGTCTGTTCTCCCGCTGCTCTCGGTGCTGGAGGGTGAOCTGTCCAGATGAC
D90145	21	TC	---			TGGGAACATGCGTGTGACCTCT/CJACAGCTACCTCTCTATGGACTGGTTATTGCCAACAGCCACA CTGTGGGACTCTTAACTTAAATTTTAAATTTATTTATCTATTTAGTTTTTAAATTTATTTTGGAT TTCACAGTGTGTTGTGATTGTTTGTCTGAGAGTTCCCGCTGCTCCCTCCACCTTCCCTCACAGTGTG TCTGGTG
EST14035 1a	59	TC	---			ATTATCACTCTCAAAAATTTTGGTGTGTGTTTAAAGTACTTTCTTATTATGAGCCCCCT/CJGAGGA CCAGACATGTTATTCAAGCCCCCTTATATACCATCTAAT
EST16868 5	71	CT	---			GCATTTTAAATTCACATTTGAATCATTATTACTATTATGATGTTTACATAACAATTCAGTATCATTT ATG/C/TTGTAGATTTTCAAGTGTAGGTGCTCAATCTGAGCACTTATCT
EST16904 7	57	CT	---			ACAGACTATCGCCAACTTATAATGCTTAAACTTTTATGATCAATAGTAATAAATTACAT/C/TTGAGATA TTCACACTTTTATTATAAATAGGGTTTGTGTAAGATGATTTTCCCAACTGTAGGTTAACAT
EST21863 9	49	AG	---			TTTTTAAGTACCAGAGGCACTGCTGGAACAGGATGAAAACGTGATACACC/CJGTTACTACTTACTG TTCACCTCTTCAAACTGATCCCTAAAGACTTCTACTTAGCAAA
EST21885 6	80	GA	---			GGCTGTAAGTAGAATCAAAGTTTAAAGAACATTTTATGCCTTATCCACAAACATTTACTGAGCATA CTAGGTGCTGGGA/CJ/TTGACAGTGAGCAAAAAACACAA
EST22623 8a	26	AG	---			ATTTTAGTGCAATGACAAAGCCCAA/CJ/AGAACAGAGGATCAAAATAGATTGAAATGTATTACC TTCTCATAAGTATACGAAGTTTAAACAAAGTATGGGAGT
EST22644 2	98	AG	---			AAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTTGTTAAACAGCACTAAAAATAA AAATTTTAAATGATTATCCATTATTACAG/CJ/AAATGTGAAAGATGGCTTTTAAACCC
EST23587 1	31	TA	---			CCTCATTTATTTAAAAAGACGGACATAAAAAAT/ATATACAACAAAAAACCCCAAGTCACATTTTCAG GAGTAAAAACTAAAAAGTCTGATATGAAAAATATGGTGG
EST24246 7	106	TC	---			AAAGATCTGGCATTATTCACATCATCTTAAATATTTTGTAAATTTTCCATGAGTATTTTTTCA TGTCGAAGCATTTTAACTATCATTTTAGCGTAAATACC/CJ/GAATAACCCATAGTTACAGAAATGG GTCTGTGTAACCTCAATT
EST24308 3	45	AG	---			TAGTTTAAATTTCTGAACCTTTGGCTTATAAATTTTCTCAACTT/CJ/GCATTTAAAAATGTATCAAT GCACCTTCTTCAGTAGTACCACATGAAAAATATAAACCTCGTTC
EST24435 6	73	GA	---			CTTGAACCTTCTGGTCTCAAGTGTAGTCCGCTCAACCTCCCAAAATGATGGGATTACAGGCATAAG CAGCC/CJ/ATGCCCTGACCCACATTTCTTTATCCGATCTGTGATGGACATTCAGGTTGTTTC
EST25089 6	25	TC	---			TATTGTTGCATTATCAAAATGGTTAT/CJ/AGTTTTCATTTAAACTGTAAATGATTTCTATGTATAAA ACAGCTTTGAAGTTGTAATGTAGTTTCCAACTCGTTAGTTAATGCTACATT

EST25476 9	33 GA ---	---	---	AATGATCTTTATTTTCAGACCTGCTCCTAAAA[G/A]CTTTCTCCTCCTAAAAACCAACACA AGAGGTCTCTTGCTGCTTTTCCATGGACTGTGGCGGCTGGACTTGGACCGTCTGCTGA
EST26183 2	70 TA ---	---	---	AGATAATGCATTAGAGCCTGCCCTCATTGTATCTTGATTAACCTTTGTAAAGATTGATCTCTAAATAAG ATT/AJACATTCTGGGGTACTGGGAGTTAGAACAA
EST27231 1a	28 TC ---	---	---	AGAAATAAGGTGCTACCGAAGCTCATGTC/GATAGCGCTTTCTTTAGGCACATATTATAGCATT CAGATGAAAGTTCTGTAATCACACACACACTGTGCTCTAACACAAACACGGTGACTCTGA
EST27816 5a	26 TC ---	---	---	CAACTCAAGGTACAAAGACAAATTCATTC/CJTAACATTGTTATAAATAAAGGAACATCAGATCAAT CATTAAAGGCTCCAGAGTGAACAGCATCTTCATACTTCCATGTT
EST28588 0	78 AT ---	---	---	GTTTAATTGGCGTATGGTCCACAGGCTGTACAGAAAGCATGATGGCTTCTGGGAGGTCTCAGGAA ACTTACAATCA/TJGGTAGAAGGCAAAAGAGAGCAGGCATCTCTCCATGACCACAGCAGGAGG AACAGACAGAGGGGGGAT
EST30226 5	25 AC ---	---	---	TACTCACACCGACATACATATCTCA/CJGTAGAATTAGCTATAGCTATGCTACTAATCTTCAATTTGATG AGGGAATATAAACTACTGAACAAGACAGACACTTGCTAACTTAACAAGACAGACTCATTTCCCTTTGA G
EST30935 9a	59 CG ---	---	---	AGCTATGGTAGAGCAAAATTCAGTGGTAAATCAAGAACTCTAAAGTTCAAGTAGAGAG/C/GJAGGT GTTTTGAATGTCAAGGAATCACTGAGGTAGATTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTTGAGG
EST32515 7	25 GA ---	---	---	CCGAATATAAGGAAAAAATGGTGGC[G/A]TGCCTCTAAACCTGTTGAATAGAATAATGGCCAAAT ATTACAGTTTCTCCTCTCTATGAATACTGGCACGTTTATTTTCATGTTTATATGTGAGTTTCTATGC ATAAAATCCCAGTAAGA
EST33274 4	27 TC ---	---	---	TGCTTTGTTTCCCTCCAAATCCTAAAAT/CJGTGTGCTCTTCAAAGAAATTCGTGGAAAGGACTTTGAA TACGAGTTTGTACCATATTCAAGTATTCTTGAATACAGGTTTCAGATAACTATGGAGATGATACCATTT GGACTAGGTA
EST33352 7b	75 CG ---	---	---	TACACATTATTCAAGAGACCACCTGACATGCATCTCCTCCGCAAGATACTTCGTCCTCTCTTAGAGA AGTTTAA/CJ/GGCACATAGTATTATTTTACTAAGAGAAATATCTTGGTGTATATCTAGGGG
EST33424 1	126 AC ---	---	---	ATTTTCCACAGCAGAGTATATTATTGTGCTGAAATCAGGTAGCAGGGAATGAATAGCTCTTGG GAACAGTACAGAAATGTTCAAAAGATTACAAATCTCAGTCATTACACACTGAGCAAC/C/AJAA CAAAGGTGTGAATCCTCTT
EST33488 7	90 AG ---	---	---	CCTTTGGGGGAGTTTAAAGCCAGAATGTGACAAAGTCACITACAGGAAGACTGGAATGTAGCCATAG TTGAACTCTAACATCGTCTATAG[A/G]ACCATTTCCCGTCTCCAGTTAGGTTCTAGGCATACTAAGCT GCTC
EST33508 1b	45 CT ---	---	---	AAAAACATGCTATTTGAACAAACTTTTTTATAAAGAAATAAGTTGA[C/T]TGAAAAAGCAGTTTAAAT AACATCAACTCACAAATGACTTTTAGAAGCCAAATAA

EST33508 1a	36 A G ---			AAAAACATGCTATTGAACAAACCTTTTATAAAGA[A/G]TAAGTTGACTGAAAGCAGTTTTAAAT AACATCAACTACAAATGACTTTTAGAAGCCAAATAA
EST33863 4	77 C T ---			ACAACATAGGACTGGTTATCTTGGTTTGAAGAAATATGTTGCCACTTCCTATTGTTTTAAATGA TCATTTAAC[C/T]CTTTGAACCTACAGCCTGAATCCCCC
EST34739 3	97 T A ---			GAAGTATCCTCCAGTGGCAGGAACCTGAAGACTCCAGATCAACCAGGTGGACCTTTTCGTTGATGA GCTGATAGCTTCTAGGCTGTGGGGAACCTC[T/A]GGTGCCTTACAACCTCAACTACTGCAGAAATTTCT TGTTGTGCCTCATAAACA
EST34792 6b	104 A G ---			ACCTGACTGCTTTAAAGCTCTTTGTAAGCTGACCGTAGCACAGATCACGTGGCATCCCACTATCAATA CTCATAAGTCTAAATTTATCCTCAGGATGTTCCCTGA[A/G]GTATTCAGGAATTCCTAGTCCCTATTACA AAGATTTTGTGCTGTG
EST34835 9b	93 T G ---			GGAAATGTTCCCTTTGCAAAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGGAGTCTATGTTGCTTTCTGGT[G/G]GCCCTTAAAGAAACAGACAAATTTGTGCTAAAGAT
EST34835 9a	82 G A ---			GGAAATGTTCCCTTTGCAAAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGGAGTCTATGTT[G/A]GCTTTCTGGTGGCCTTAAAGAAACAGACAAATTTGTGCTAAAGAT
EST35230 0	93 G T ---			CACAAAGTCCACTTTACTTACATGAAGGAACATAAAGGCATGAGAAACAGTCATCTCAATAAATG CAAGACATGAGCATAAAGAGGTTCTC[G/T]GCCCTTCCAGCGTTGTTATTACAGAGAGAGAAACCT
EST35337 9	33 C T ---			CTTTTCAAATTTTGTATGAGGCATTTAATG[C/T]TATAAATTCCTGCTTAGGAATGTATCTGCT ATATCTCAGAAGTTGGGCATGTTGTTGTTCCATTTTACTAGTTCAGAACTTTTTCATTTTCATCT
EST35708 9	32 C T ---			CTGCCCCAAATTAACTTTAGGCAATGGAA[C/T]AGACTTACTGTATGGGACATTTTAAAGAG ACAGCTTAGTAATATGTCATATGCAGCGTGTGCTCCCTCTCGAGGTGGCACCTTTCTGTTGTG ATGTGCAAGTGTGGCT
EST35747 9	51 C G ---			ATCCAGTGCAGAGTTGAGCTGGAGACATATTTCAACCCACAAAGGCTCCA[C/G]ATGTTAAACGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCCCCCTCCAGTAGGGTTGAGATT G
EST35751 9	89 C A ---			TGGTCCATTATATAAACTGAGGGAACAAACGGTGTGACATGGCAGACATTTATTTCAATGGAGA AGTCTCCCTCCATGAACCAAGA[C/A]CTTGCTCCTCATGATAAAGTGGAGACAATAAGAAAGCCAGGT ATATAATTAGGCCTGTGA
EST36301 4	93 C T ---			CACCTGTTTCATGGTTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTCTCAGCCTACAGC AGTCAGGAGGCAGCCATGGCCCCCTG[C/T]GCTGATGGAGCTTGTAAATTTAGCCCCAAACTGATCTTCA GAAAGAGGTACAACAAA
EST36519 0a	33 G T ---			GCCATCAGCCCCACAAGACATGACTACCAACGC[G/T]GGCCCCCTTGCAACCCATCTGGCCTCAGCAC CTAAGACTGGACAACCTTTGTACCTAATGACCGCCCCCACCTGGCATATACTGGCTGGCCTCTTCTCTGT CACAGGGGTCTTAGTGT

EST36620 6	50 G A ---			GACTTTATTAGATAAGGGGTTTTCGGTACCCTCAAAGCTCTCAGGACTGG[G/A]GCTAGGGTITTAAGG AAGGCTTATTTAAATATGGGAATAAAATACAAAAGGCCACACCCGATGCAAAAGACTTT CCTGTGATGTGCATGGTGCTGAGCAGTCGTACTTACTATCGTCAGACAGCTCACGTATGTCAGGA AAGGAAGTCTGGGATTCTA[C/G]JAGGGGACATATCACACATATCTAAGTCACTGTGTGACTCGG CTTGAGCAAGTCATTTCA
EST36690 0a	89 C G ---			GAGACAGAAGCCCATCAGTTAAATGAGGTTAGGCCCTCTCCTCTTAATATACTGATTGACAATG[C/T] TATTAGCCAGGTAATGCACCTTAGCTACCTGGACAATGCTATCAAGTGTCTGGGAAGGGAG ACTGTCTGGCCGATGATTGGAGCTTGAAAAAACTAACATGCCAGATCOCACCCCAGACCAATTAG GTCAGTATCTCTGGGGTGCTATTCAAGCAACAATT[AT/J]CTTTTATGTTCTTAAGCTCATCATGAG TTAA
EST36729 9	62 C T ---			ATGATCGCTTATGTAATTTGAGGCGACATGGTAAATGGGAGATACCCACAGGACCTGTAAATATT TAAATAATATTTAACAGCTGATCAGAGGCTAAATTAACAATGACATTTTGATGCAGTTT[C/G]GTTA GGGAATTAAGACAATGCAG
EST36823 6	103 A T ---			GGTCTCACTCTCTTGCCCAGGACGGTTTGAAACTCCTGAGCTCAAGTGACCCCTCCACCTTGGCTTCC GAAAGTGCTAGGATTACAGG[T/C]GTGAGCCACCACACCTGGTCTTGTTTAAAGTAACCACCTGAA C
EST36987 4	126 C G ---			AATAGTCTATGGCTACGGGCCCGTGGGATGTTAAAAATTTGGGATTTTAAATTAAGATTGTGAACATG CAAAACCAGCAATTTCTCAGCTTATATTTTGAAGTCT[G/C]CAGGAGAAAAAATGGGGTCC
EST37054 3	88 T C ---			AAAAGACCTTTCTCAAGCAGTAAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCCAGGAA GCTCTCTGGATAATGTCACCTCTAGGAA[G/T]AGTAAACAGGTGTTAAACCCTGAGATAGCAACCCT CTTGGCTTGTGAGGAATA
EST37284 2	93 G T ---			AGATGGGGTCTTGCTAGCTTGCTGGGCTGAACATAAGATATCCTCCTCAGCCTCCAGGTAGT TGAACTATAGTAGGAGTATC[A/G]CCCTGCCCTGCTAGAACTTCAAGTTTGTATGGGCAAAATCCA CCCCAGAGGACAGGACAA
EST37315 2a	90 A G ---			CCTGCCATGATAATGTTAAAAACATATCAAGATCCTCTCAAACACTT[C/T]AAGGGTGAAAAGCATACC ATTCCATTTTAGTTGAAATATTCTTCACATAGCCAAACACATTTTTTCAAGGCACTCTAGCTACTACA GGA
EST37374 1	45 C T ---			GTGACATCATGCTCTTCAATGCCCTTTCAATTAATAGTAGTTGAGCGCTGGGGCTGAAGTCAGACT CTCTGGGTTCAAATCACAGTGCTGTGCTGCA[G/C]GCTGTCTCAGGCAAGTTGCTGACTTCTCTG TGTCAGG
EST37376 8b	101 G C ---			GTGACATCATGCTCTTCAATGCCCTTTCAATTAATAGTAGT[C/J]TAGCGGCTGGGGCTGAAGTCAG ACTCTCTGGGTTCAAATCACAGTGCTGTGTCTCCTGCAGGCTGTCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG
EST37376 8a	41 T C ---			

EST37378 9	63 T G ---			ACACACAAAAAATGGTGGCAGAAAAATCTGGAAGATTCTAATAACCTCAATTCTGTGAAAACT/G JAACATGCCTCAAAAAAGAGGGGAAAAAATTTAACAGAAACACTGTGCTGACATGATTAGCTT
EST37452 4	46 G A ---			AAGACATAAATCTGCAATGAAATCAGTTATGAAATATTAACCTCTG/AJCTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATGCAATTTAAACACCCCTAAATCAATGACGTAGAA
EST37613 6	34 A G ---			CTAGGCATGGGGCTTTTACAGTCATTTATTTACC/AJGTCATGAATTCATTAAAAACACACGCGAT ATAGCAATGAGCAAAACAGACCCCTCCCAAAATCACCCCTGGTTTCATGGATCTCCATTCTAA
EST38025 4	56 T G ---			TTATTGAGTAGCTACACTGTGGCCAGAACTAAGCTTTACATGTTTTATACATTA/TGTTATCTCA ACAATCTTGAAAGGGTGGTATTTTCCCGTCTTATAGGTGAAGACTCTGAGGTTTCAGAA
EST38068 6	57 C T ---			TCTACCAGGTCACCAAGTATCTGTATATGCTTTAAGTGGCATTTTCATGTCACTTA/C/TJCGCATGG AAGAACGCTCTCCTTTAATCCCTAACTCTCTCTCTCTGGAAGACAGAACGTGCACAA
EST38420 6a	100 T C ---			TAAATCAAGGCCCTCTTTTACATTAACCAAAACAAAAAAGGGAACAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGTCTGCTGACTGACTGAC/TGTCCTGCAGTGCCCATGGTCCCGTGCCT TATTCATTCTCTCTCTCTCA
EST38950 5	25 T C ---			TTTATTTGCAAAAGTAAGCAGCCGGT/CJGGTCCCTGGATTGAGGCTGAGGAAGACATTACTTCCTG CTGGAATACTTGGGACTTACATTTGACACAGGCTAAAGTATGGGATGAGAGAGGAACAAAAGCTT ACAAACAAAGAGCAGCCA
EST39053 6	90 T C ---			TTTTTTGTACTCTGTAGCCAGTCATTAACTCTGAAGTTTAAATATATCATTTTATTTGGGATGAGATCA TAGCTTTACACAATGCTATG/TCAACAAGTTACTGAATATTTTACCTCGTGGAGTTG
EST39331 1	70 G C ---			TCCTCTTGCTCTCTAGCACTCAGACCACCAAGAAAGCCCTGGAAGACCAGCCCATGGAAGGAAAGTA TGC/GCJGTGTTTAGGGAGAGCTGGCACCTGGCCTCTAATCTTCCCTCTGCCATTGACACAGATGGGT GCCITTTGGATACATCACT
EST40544 7	31 C A ---			GTCACCATGACCTTACATAGTGCCTCTAGT/C/AJACCTATGAGGCACCTAGAACCTCTATTGTACTTCT CACTTTATCACATTAGCTATCGAAGTTTGAAATTT
EST40548 4	37 T C ---			TTCTAATAGCATGCCCTGTGACAGGGGAAACTAAGCTC/T/CJCAAAAATAACTGAAACTAAATCTGTA AGATAAAATGCTGGAAATTTGAGAAGGCACATGCGCTTTTGTAGTTTTCTCCAGAAGGCTCAAGGTGTTG AATAATCTGTGGGACTCA
EST40549 1	42 A G ---			TGTTTCTCTAGAGAACCCCTGTGTGATACACTACGCATGCAACA/GATAAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTTGTACCACCATTTCTCACTTTGAACCTAGCTCCCTGCAAGCACCTTTCTA CCCTGCACCTTTGGGGAG
EST40579 1	81 A C ---			TGTGAATTACACATCAGTAAGGCAGTTTACAGAAATTTTCATCTCTACCTAAAGCTGTGCTATCTG AGCTGGTGGAAAAA/CJGGACITGGAGACAGCGATTTAAATACGGAACAAGGTCTTCCAGGAAG
EST40584 3	68 A G ---			TTGTATGGTTGTAGGAATTTGGGAAGAAATTAATCTGTGAAGGAAATTTGCCACTGTAAATGCACACCC A/AJG/TCTGTACTCCCAATATCTCTATGTTTAAAGCT

EST51340	51 GA ---	---	GATCAAACTGTATTGCCAGGCCAGCTCCTGAAGAACTGTGAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATCCATTGTCTCTTTCAAACTAAGAGCCTCTCTAAGCTA GATAGGCCAAGGATTATT
J04162	134 TC ---	---	CATGGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTGCAACCCCATCAT CCTCAGGCCCTCTACAAAGCAGCAGGAACATAGAACTCAGAGCCAGATCCTTTATCCAACCTCTCGA T/CJTTCCTTGGTCTCCAGTGGAAAGGGGAAAAGCCCATGATCTTCAAGCAGGGAAGCCCAAGTGTGAGT AGCTG
K01506	63 TC ---	---	CTGAATCCAGCTGCCCTACAACTCCATCTCAGCTTTTCTCTCCTCATGTGAAAACACTAC[T/C]C CAGTGGCTGACTGAATTGCTGACCCCTCAAGCTCTGTCTTATCCATTACCTCAAGCAGTCAATTCCT TAGTAAAGTTTCCAAATAGAAATTAATGACACTTTGGTAGCACTAATATGGAGATTATCCTTTC ATTGAGCCTTTTATCCT
L18877	69 TC ---	---	TGAGTCTGAGCAGCAGTTCAGCCAGGCCAGTGGAGGGAGTCTGGCCAGTGCACCTTCCAGGCO C[T/C]ATCCATTAGTTTCCACTGCCTCGTGTGACATGAGGCCCATTTCTCACTCTTTGAAGAGAGCAG TCAGTATTGTTAGTAGTGAGTTTCTGTCTATTGGATGACTTTGAGATTATCTTTGTTTCTGTTTGA ATTGTTCAAATGTT
L31848	36 TC ---	---	GCATTTTACATATCCCAAGCCCTTAGGGCTACAGT[C/C]CTCTTGCTGGACCTGTAGGGTGCCA TTTGGAGTTACAGCCTAGAAAGAAAGGCTTTGGCCCTGGTGTGGTCATAGGCCCTGTAAATCGT AGCGCTTTGAGAGGCTGAGGAGGAAGATAGCTTGAGCTCAGGAAGTTTCGAGACAAACCTGGGCAAT GT
L38517	137 GC ---	---	GGTCCAGAAGCCTCTCAGCCAGGAGGGAGCTGGCCCTGGAAGGGACCTGAGCTGGGGGACACTGGC TCCTGCCATCTCTCTGCCATGAAGATACACCATTGAGACTTGACTGGGCAACACCAGCGTCCCCAC CC[G/C]CGTCGTGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGTTGTTGACCCCTCT CTCCTAGAGACCTTGAG
L39059	123 TG ---	---	ACTTGAGAAGCAGAGCTGCCACCTTCTGGAGGCCACTGTGATGATGAGCCAAGCAATTTGGAGCCA AGTTGAAGGGACAGGGCAACAAAATACAGTAGTCTTTCTTTGTATTTGTATAT[T/G]CGCCTGA AGATCATCCCGCAAGCAGGCTGGAGGTGCGGTGGGCTGTGTGCTGGGATTTAGTCTGTGCTGG GAG
L41268d	173 GA ---	---	CAAAGTTGCTCTCTGCCATGAGCACCACAGTCAGGCCCTTGAAGGGATCTTCTAGGGAGACAACAGC CCTGTCTCAAACTGGTTGCCAGCTCCAATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTGCAT CTTAGGGCATCGCTCTTCTCCTCACACCACAAAATCTGAAC[G/A]TGCCTCTCCCTTGCCTTACAAATGTCT AAGGT

L48728b	111 T C ---	---	---	AAGTGAACAGAAAAGCATGGATTGTGTTCTCTATAAAAGCACATAGTTATGTTTACTGGTATCGT AAGAAAGCTGGAAAGAGAGCTCAAGTTTTTGGTTTACTTTTCTCAGAAATTCGAAAGAACTTATTCAGAAAG CAGAAATAATCAATGAGCGATTTTAGCCCAATGCTCCAAAACATCATCTGTACCTTGGAGATCCA GTC
M18079	52 G A ---	---	---	GCGCACAGTCCAAAATACAAAATTGGACAGAAAGATCTATATTGTACCAGAACTGGAAJTTTATTTCACC CCATCAAGTATAAGGTTACTGATTGATGGTCCCTTTATAAACATTGGTATATTTCATTTCATGCGAA AGCAAAAGAAAGTAAAAGCTAA
M19169	113 T C ---	---	---	TAGGATCTGTGCCAGGCCATTGCGACAGCCACCCACTCCACCCCTGTAGTGTCTCCACCCCG TGGACTGGTGGCCCCCAGCCCTGCGGAGGCCCTCCCATGTGCTGTTCGCGCAAGAGACAGACAGAG AAGGCTGCAGGAGTCTTTGTTGCTCAGCAGGGGGCTCCGCCCTCCCTCTCTCGCTTCTAATA GC
M21539	114 T G ---	---	---	TCACCTGTTCCACAGCTCCACCTGCATCTTCTCATAAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCTTAGCCTGTGATCTGCCCATGATGATCCCGACAGCAAAATTCGTTTCTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAAAGGAAGTCTCAGCTGTACCGGCCCTTCAGAGCT TCTCTTTGGGTGC
M26041c	173 A G ---	---	---	CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATATTTCCTCTGACTTC CTGATTTTCTCTTTCTCAAGTGTACCTACTAAGAGTGGAGTAAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157 A G ---	---	---	CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATATTTCCTCTGACTTC CTGATTTTCTCTTTCTCAAGTGTACCTACTAAGAGTGGAGTAAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45 C G ---	---	---	CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCTCCCTTCGCTCTCTCCTCACC TCTCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATATTTCCTCTGAC TTCTGATTTTCTCTTTCTCAAGTGTACCTACTAAGAGTGGAGTAAAGCCACCCAGCTACC TAATTCCTCAGTAA
M53967	57 G C ---	---	---	TAAGGCAGCTGTACGGGAGGCCAGTCCAGTCCAGCAATTCACAAACCACCTTGAGCGJJAATGCT TGCCAAAGCTGTTTAAAGCCCAAGAACCCCTTTCTTTGTTCCAAATTAACCTTTAGAAGAAACCCCA CAAAATAAGCAATTCATC
M81695	34 G A ---	---	---	ACTTACTACCCCTCACCTGTGAGGCTGACGGGGA[G/A]GAACCACTGCACCCAGAGAGGCTGGG ATGGCCTGCTCTCTGCTTTGGGAGAAAACGCTGTGCTGGGAGGGGCTTTGCTTTGTCAAGGTTG CAACTGGAAACCCCTTAGGACAGGGTCCCTGCTGTGTTCCCAAAAGGACTTGACTTGCATTTCTACC T

U06641d	166 C T ---	---	CTCCTCCTTTATTTCAGCATGGAGGGTTAAATGGAGGATCTCCTTTTCTGTGACAAAACATCTTTC ACAACTTACCCTTTTAAGACAAATTTAAAAAGATCTTTTCACAACTTACCCTTGTTAAGACAAAATTT TATTTCCAGGCTATTTAATACGTACTTTAG[C/T]TGGAAATTTCTATGTCAATGATTTTAAAGCTA TGAAATACAAATGGGGGA
U09607	39 T C ---	---	GAGGCCCTATGAGGGTCTCTACTTCAGGAACACCCCATTC/GACATTGCATTTGGGGGGCTCCCG TGGCCTGTAGAATAGCCTGTGGCCTTTGCAATTTGTTAAGTTCAAGACAGATGGGCATATGTGTGAG TGGGGCTCTCTGAGTCTCTGGCCCAAGCAAGCAAGCAACCAATTTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82 T C ---	---	GAGCAGAAGGCAAGAGCGGCAAGATGAGTTTGAGCGTTGTATCCAAAGGCTCATCTGGAGCCTC GGGAAAGTCTGGTCC[T/C]ACATCTGCCCGCCCTTCCAGCCCTTCCCGCCCTCTCTTGTCTTCTTC ATTCATTCAACAAAATTTGGC
U10694	20 C G ---	---	GTACATGAGGCCCATTT[C/G]GCTCTGTGTTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCTCTGGTTCCTTGTCTATTGGGTGATTTGGAGATTTATCCTT GCTCCCTTTTGGAAATGTTCAAAATGTTCTTTAATGGTCAGTTTAAATGAACCTTACCATCGAAGTTAA TGAATGACAGTA
U13877b	162 T C ---	---	AAAAAGGACTCTGGTTCAAATCCAGGTTCCATTTTGTCTATCTTTGTGACCTTGACAAAGTTGTTAAC CTCTTTGTTTCAAGAAATTTCTCCATGGAGTAACAATATCTAGTTGGGAGGATAGTGAAGTTACATGT AAAGCACAGAGGAACACAGCCAAAGAGATTC/TACCGTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTTACCTTCAGCA
U15555	187 T C ---	---	TTTCTGCCACTTTCACTGGTTTAAATAGCCAGCCAGTCATATAATAGTAGGAATCAGTCAAGCAA AAATGCTTTTGAAGAAATTAATAAGCAATGCTGAACATCAGGAATTTAGATATCCGTACAGAGAGT TCCAGTAAATTTTATGAGTCCACGACCCCTTTTCTAAGCAGTCTGGTCCATG[T/C]TGGTCTCATAC CTCATATGCAGGATTCATTCA
U17077	122 T C ---	---	TCCAAATATTGGTCCCAAAAGCAGCTTCCAAACGTTTGCCATCTGGATGACAAACGGAAGATCCACT AAAAAGTCCACGGGATTAAACAGAACGCTTTCAGACTGAGCGATGACACACACATTC/TGTTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTCTTTTCTCTGGGAAAACAACTGTCTCTTGG AATTA
U18543	58 T C ---	---	GCACATGCAGAAATAGACTCAGCCTATGTCCTGATTCAGCTGGGTAGTCTAGAACTTT/CJAGAAG CTCCATCTTTTAAATGTTTTTATTTGTTATGTCCCTCCCGCTCCCACTAAATTTAGAGCTTTAAA AGATGCACTGCCCAATAGGACACAGGATGGTGTAGCTGAAGTTTGTAGCAATTAGGCACCTTCC AAGGCTTTAGTAGAGAGGCC

U25975b	164	C A ---	---	---	TCACGTGCTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCTTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGCTGCGATAACCTGAATGAAGAAGCAATGACTATTCTCTG AAGACAACCAAGAGAAAAATTGCAAAAAGAC/C/AAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25975a	143	C G ---	---	---	TCACGTGCTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCTTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGCTGCGATAACCTGAATGAAGAAGCAATGACTATTCTCTG AAGACAAC/C/GAAGAGAAAAATTGCAAAAAGACAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25997	61	A G ---	---	---	CAGGGAGAGGTTATTCAACAACCTCACCAACTAGTATCATTTTAGGGGTGTTGACACACCA/A/GJTT TTGAGTGTACTGTGCTGGTTTGATTTTTTAAAGTAGTCTCTATTTCTATCCCCCTTAAAGAAAAATT GCATGAAACTAGGCTTCTGTAATCAATATCCCAACATTCTGCAATGGCAGCATTCGCCACCAACAAAA TCC
U28413	29	C T ---	---	---	ATTCTGACAGCTAAATTAGCCCTAAATG/C/JGGGTAATAATTTTCCTCATGTTTAAATGAGGTT AATATTTGCATAAAATCCTAAACAGACTTCTGTATAGTTTATTTAGTCAAAATGTTCCTTGATCC CAGATGTTGTGGCCTGGAAAGCCCTCATTGCTACAGTACAAGTAACACACAGTCGTTGTACCTCAGTT G
U30884c	89	A G ---	---	---	TAGGGGTAGCATTTAAGATTCAAGAGTCATTAGCAGTGATGATTTGGACCTGCCGTATAATCTGTT CTTCTATTTCCACGTTAGCCA/A/GJTTGTTCTTGATGAATCTATATGAGTCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGATATCTGATGGCTTGAACCTTGCCCCACAGTTGAACACAAAGT GCTGTCA
U30884a	34	A G ---	---	---	TAGGGGTAGCATTTAAGATTCAAGAGTCATTAGC/A/GJTGATGATTTTGGGACCTGCCGTATAATCT GTTCTTCTATTTCCACGTTAGCCAATTGTTCTTGATGAATCTATATGAGTCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGATATCTGATGGCTTGAACCTTGCCCCACAGTTGAACACAAAGT GCTGTCA
U31216b	78	A G ---	---	---	GGGACAGCATATGTGGCACCCGCTCTCTGTGCACGTGAAGACCATGAGACGGCTGCAACCAACA GCCGTATCA/A/GJCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGACCAAGAGCCCTTTACAACGTAGAGGAGGAGGATGCCAAGCCGATTGCTTTAGCCCGCC TGGTAGCCCTTCCAT
U31216a	70	G A ---	---	---	GGGACAGCATATGTGGCACCCGCTCTCTGTGCACGTGAAGACCATGAGACGGCTGCAACCAACA GCC/GJATCATCAACCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGACCAAGAGCCCTTTACAACGTAGAGGAGGAGGATGCCAAGCCGATTGCTTTAGCCCGCC TGGTAGCCCTTCCAT

U31416c	76 GA ---			AGTTGCCAGCTCCCATGTACACAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAC[G/A]CCACAAATCTGGTGCCTCTCTCTGCTTACAAATGTCTAGGTCCCACTGCCTGCT GGAAGAAACACACTCCTTTGCTTAGCCACAGTTCTCCATTCACCTTGACCCCTGCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68 CT ---			AGTTGCCAGCTCCCATGTACACAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC [C/T]TCTCACGCCACAAATCTGGTGCCTCTCTCTGCTTACAAATGTCTAGGTCCCACTGCCTGCTG GAAAGAAACACACTCCTTTGCTTAGCCACAGTTCTCCATTCACCTTGACCCCTGCCCAOCTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78 CT ---			ACGGGTACACAGAGAACTTGAGTCTAGCCATGAGGGCTTATGCTCCCACTCACATTGTTCTCTCC AGACCGCAGG[C/T]TCCCCAGCCTCAGGTTGCTGGAGCTGTCACATGACTGCATCCTGCTGCCAGG GCTGCAAAGCAAGGCTTCTGCTTCTATCTGGGGACGCTGCTCGAGAGAGGCGGAGAGGCCGCGAAGC ATGCCAGGTGTC
U37690	54 AG ---			GACCACGCTGAAACCCACCCACCCGCTGTGCTGACCATGGGGCCTGAGCGTCTT[A/G]CCCCGAATTC ACGAGGCTGAGGCATCCGGGAGCTGGCGTAATGCCTGGCCGACGTGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGGCTTT
V00540	39 TC ---			TGAAACCGTTTCAACATGGAATGATCTGTATTGACTAAT[C/A]CACCAGTCCACACTTCTATGACT TCTGCCATTTCAAGACTCATTTCTCTATACCACCGCATGAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAAAGGAAACATCATGTTTACCTGTGCAGGCACTAGTCTTTACAGATGACCATGCTGAT A
X15943	106 AT ---			TCAAGAAGTGACTGCCCTTGTATGATGGATGGGAAGATGAATGACTGGTTTTACTGGGTGTAA AACCACCTGAGCCTCTCTGAGACCATGTGGTTTTAAA[A/T]ATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTTCAGTAGCTAAGACCCCTAGAATTTGGATTCTCTGTTTTTTCATGTCTCTCCTT GTAAACCCTGAGATCATCAG
X52011b	148 CT ---			AGGAAGATCCCACCGACCCCTTCTGGCCTAATCCTTAGATTAGGTCACATTACATTAAACATTTAGGA ACCCAGACCGAAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAAAAGTTGCGAAAATGCG AAATCTGTTGTGCA[C/T]GCTCAAATGAAAACGCCCTTCGGCTTTGGGCTTTATTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT
X52011a	118 A/C ---			AGGAAGATCCCACCGACCCCTTCTGGCCTAATCCTTTAGATTAGGTCACATTACATTAAACATTTAGGA ACCCAGACCGAAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAAA[A/C]GTTGCGAAAAT GCGAAATCTGTTGTGACGCTCAATGAAAACGCCCTTCGGCTTTGGGCTTTATTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT

X54741	24 A G ---	---	CAGGCCACCTGCTTCTCTCCAC/GJTGACAGCTTCTGAGTCAACCCCTCTGTCCAGCCAGCTCCT GCACAAATGGAATCCCCAGGGCTCCAGGCTGGGCTTCCAGGCTTGCAATAGCAAGGCCAG GGCACAGCTGGAGACGATCTTGCTGGCAGGGCTGGCTTGTCCACAGCCCCAACCTGGCCCCCTTCTCC AGCAAGCAGTGC
X54869	99 A G ---	---	AAGCATTGCGTTTACAGTGCATCAGATACATTTATATTTCTTAAATAGAAATATTATGATTGCAT AAATCTGAAATGAATATGTTATTTGCTCT/GJATACAAAAATCTAAATCAATTAATTGAAATAG GATGCACACAATTACTAAAGTACAGACATCCTAGCATTTGTGCGGGCTCATTTTGTCTCAACATGGTA GCCGTGCTGTGACACCTCCAGAACGCGAGTGTGCGCCCGTTCTGCTGGACCCCGGGAACTCTC CTGCCGGAAGCCGACGGCAGGATGGCCCAACTTCCCTGCCCCACTTGACTTCACCAATCCCT TCCTGGAGACT/GJAACTCTGGTCTCAGGAGCGAAGGACTGTGAACCTTGTGGCTGAAGAGCCAGA GAAATGTGAAGAAATGTGACAAAGCCTTTAAGCGTTGTACACTTGATTGTATATAAGATAA/TGJT CATACTGGAGAAACTCCAGAAAGTGTGACAAATGTGACAAATTTAATTAATTCATACCTTA TTGCACAGGAAAGCATTTATCTTGAGAAAAATTTGTATAAAGAAATGGAAGAGTCATTAATATCTGCT CATATCTTAACATCAGCGAGTT
X66924	147 G A ---	---	CTCAACCCATAACCTCAACACATCT/GJATCTCTCCACCCACATCCCACACATCCACCTCCATCC CCAAACCATCTCATGCCAACTACAGCCCAACCCAGCCAGACTAATCCAGGCCATCCCCAA CTCATCTCATCCCCAACTGCAGCCCCAAACCCAAACCCAGGGCATCCCCAAACCCATCCCCAAGCC AAACTCAACACCATCC
X78932	62 T G ---	---	ACCCCAACTCAAGTCCAGGCCCATCTTCTGCCCCGCTTGTGGCCCATCCAGTCCAGG CGCTGGAGCAAGTCTCAGCTACTTCTCTG/CJCACTTTGAAAGACCCCTCCCACTCCTGGCCTCA CATTTCTGTGTGATCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCCCTAGAAAG ACCCCAACTCAAGTCCAGGCCCATCTTCTCTGCCCCGCTTGTGGCCCATCCAGTCC AGGGGCTGGAGCAAGTCTCAGCTACTTCTCTGCACTTTGAAAGACCCCTCCCACTCCTGGCCTCA CATTTCTGTGTGATCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCCCTAGAAAG GGCAACCCAGAGTGACACAAAGTCCAGAGGGAGGGCGCCGCTCGCGGTGTCGGTGTCTTTT CAGCCCGGAGAGGTCTGACCTGGGGCTTCTCAAGCCTCACTGGCCACGCTCCCGCCGCTCT CTTTTCTCCCAAGC/GJAAACCAATGCGCCCTTCACTCGCGTGGCGGAGGCCCGGGGCTT CTTTCAGAGC
X80197b	99 G C ---	---	ACCACAGCCATGGTCTAAGGACATGGATCGGGTGGCCCCCAGACAGTGTGACAGGGGACCCCTCTGCC CACTCTGGGCTTTTCAGATACTCTGACCAAAAGCCTGCTTTAAACCGCAAGATGGGGCT/GJGGG ATGCGCAGGAGGAGCCATCGGGTACTACGCAGCAACACTCACAACCTGTCCAGGCTGAGATAAATCCC GGGA
X80197a	28 A G ---	---	
X85106	150 G A ---	---	
X87160	128 T G ---	---	

[illegible]

1282	130	C T	---			GTGCGATCACCACCTACAGTCTAAATTCAGATGTTTTTCATTACCCCTAAAAGAAATCTTTGTACCCCAATTA GCAATTTATTCCTCAITTCCTGCCCTCACCCCGAGGCCCTACTCTTTATCGCTATAGATTTGGCQ/C/TJACT TGACATATCATACACATGGAGCCATACATATGTGTGCCCTTCATGATTGGCTTCTTTCACTGAGAATA ATGTTTCAAGGT
6810	68	C T	---			AGTATCAGACATCTTAATATATTAGATATACACAATAATAAATCACTCCCTACCTTGAAAACTTT A/C/TJAGAAGCATTTTTAATTTTACAACACAAAGCTCAACGAACCTACAATAAGTCTAGTAGTCTG TTTACGTGCCAAGGATAAGGCTGAACAATAAATTAACCCCTTTAAAATGICTATGAAACAAAGTACAA TTTTCTTTTGTGTTCTGCAGAGCAATGACCACCTAAGAAATATTTTTAAAGGC
6817	118	A C	---			CCAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTTGCTTTTGTAAATCCAGTTAAGACCA TCAGCATATACAACATCATCACTAAGCTCAACAATGTAGCTGCAGGGTAAC/A/CJTGTGGATACCCCTG TGTGCTCTACTGGCCTCCAAAGGCATTGAGGGGATCATCAAGATGTTGGACACCTTGTGTTCAAATC TTGGTTCAGGTGGCGCTGTGCAGATCGGCTTTTGGTTGGTTGCTTAG
6819b	212	C	---			CCATTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAACACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACAGCAGGAAGCCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTCTGCTATTTTGCCTTAGCAAA CAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCA
6819a	166	G T	---			CCATTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAACACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACAGCAGGAAGCCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTTGTJCATATACAAAATTTCTGCTATTTTGCCTTAGC AAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCA
681xx	39	A G	---			CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATTJAGTTATACTATGGCACCATTGGGACA CAGATTATATATGTCAGACACCCAGCAATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCTATGGT TTAACAAGAAATGAACGTCTAGG
6972b	149	G T	---			AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAAACTATTGATTATGCG CACAAATTCAGAGTJGTCCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCCTGGTTAGTCTTGGGA GAGTGTATGTGTCAGGAAT
6972a	122	A G	---			AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAAAGTAAJGJCTATTGATTA TTGCCACAATTTTCAGAGCCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCCTGGTTAGTCTTGGGA GAGTGTATGTGTCAGGAAT

7598k	210 A C ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTTCTTGAGGATGCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCCT CAATGCAG[AC]
7598j	208 A T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTTCTTGAGGATGCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCCT CAATGC[AT]GA
7598i	192 G T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTTCTTGAGGATGCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598h	144 C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTTCTTGAGGATGCCTTTTA ATATTTGATCC[CT]ATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598g	142 C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTTCTTGAGGATGCCTTTTA ATATTTGAT[CT]CCATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598f	120 A G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTTCTTG[AG]GGATGCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598e	83 C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGCCAAAGGAACTCA ATGAAATAAGCCGCTAA[CT]CAGATTTTACCTTGGAGAAATGAAAATTTCTTGAGGATGCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598d	77 C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGCCAAAGGAACTCA ATGAAATAAGC[CT]GCTAACAGATTTTACCTTGGAGAAATGAAAATTTCTTGAGGATGCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA

7598c	56 A G ---	---	AAAGGTAAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCA[A/G]AGGAAC TCAATGAAATAAGCCGCTAACCGATTTTACCTTGGAGAAATGAAAATTAATTTCTTGAGGATGCCCTT TTAATATTGATCCCATTAATGTGAGAGATTTTCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---	---	AAAGGTAAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACAC[C/G]CCAAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCGATTTTACCTTGGAGAAATGAAAATTAATTTCTTGAGGATGCCCTT TTAATATTGATCCCATTAATGTGAGAGATTTTCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---	---	AAAGGTAAATCAAAGTCCCTCTATAAATT[A/G]TGATTTACAAAAGACACCCAAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCGATTTTACCTTGGAGAAATGAAAATTAATTTCTTGAGGATGCCCTT TTAATATTGATCCCATTAATGTGAGAGATTTTCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTCTCTATTACAGACATCTGCCAGCTCTCTCTGTA ATACTTTAAATGAATGGGTGATGCTCTATCTCTCAAGGTCCCAATA[A/T]CCTTGAGGTTTCT
7998b	94 A C ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTCTCTATTACAGACATCTGCCAGCTCTCTCTGTA ATACTTTAAATGAATGGGTGATGCTCTCTCTCAAGGTCCCAATAAACCCTTGAGGTTTCT
7998a	75 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTCTCTATTACAGACATCTGCCAGCTCTCTCTGTA ATACTTT[A/T]ATGAATGGGTGATGCTCTCTCTCAAGGTCCCAATAAACCCTTGAGGTTTCT
8071	119 A G ---	---	AAATACAGAAATTTATTAGAAACTGTTTAAAGTAGAAAAAACCCTGTCAAGAAAGACCAGGTGG AAAATGGGTTCCCAATAAAATGGAATTTTAGGGCAACAAAGCTAAAAGGCC[A/G]CAAAAAGAGA AATAGCACTGTCATTTGAACAATGGCTAGTTACTTGCAATTTTGGCATTGTTAATCACTGAATC TGGGTTTCTCTGTAATTCACACAGAGCATGCACACACATTTTATCAT
8467b	93 C T ---	---	AAGGCTTCTCTAAACATCAGTCTACGGAGAAACTGGGAAATCCTGGATATTTGGCTTATCACTT TGACGCAAAATCCACTTTGCTGTA[A/C]TGGTCAATCCGAACCTCCCTCAGAGAGCAAGCAAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAGGAAAAATTACTG
8467a	70 A G ---	---	AAGGCTTCTCTAAACATCAGTCTACGGAGAAACTGGGAAATCCTGGATATTTGGCTTATCACTT TG[A/G]CGCAAAATCCACTTTGCTGTAACGGTCAATCCGAACCTCCCTCAGAGAGCAAGCAAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAGGAAAAATTACTG
8498	84 C T ---	---	AGGTTTCAGGGTTGGTTTAAATCAGGCTGCACACCTTTCAATCAATCTGACATCTCTATGTCA AACTGGCTTCAGCTAG[C/T]AATACTTCATTAAATCGAAAAGAAAAATTTGCTTTAAGGAAAAAA AATCCAGTTTAAAGAACAAATTAACATTAGCTTTAAATAAAGGAGGCTAATGTTTTCATGTTGCT TTATACATCTCTCTCAATACAGAACCAAGGATGTAATTTCTCTAACTCAG

WI-18562	29 G A ---	---	CTAAGGAAAAATTTAATGATGGAAATATC[G/A]ACAAATATTCAACATCATTTAAAAACAAAGTAG CTTCTCTTATTTACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATCTTACATT TAGCATTAAATCAGAAACGA
WI-18618	51 A C ---	---	ATAGCAGACTTTTAAATCAATGCCAGAGACAAAGTGAGGCCGAGCTAAGAAC[A/C]CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCTTTCGATGCAAAAGTATAATTGTAAACCCACAGTGCTCGCACAGTTC AC
WI-18683	22 C T ---	---	TAAGCTGTTCAGGACTGGACTC[G/T]GGTCCCTTTATTGAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAAATAAATTTCTCTCCCAAAGCCTGCGCTGCAGT
WI-18520	75 G A ---	---	GACTTTGGTGATTTAATTGCTTTTCCCTTAAATATGAGAAATAGGTGTAATTTCTCCTTTTGTCTTTT ACTACA[G/A]CCGGAGTGGTAAATACTACTACTGCCAACAAACACGGGCATCCACTCTGTCTTCAA TGCCCTCTCCGTGAGAC
WI-18563	94 A G ---	---	AAATAAGTTTTATTGGCACACAGCCAAAGCCACTGGATGACACATTGTCCACGGCTCATCTTGCAA TACAATAGCAGGGTCACTAATGTGAC[A/G]GACATGGTGGCTCACAAAGCCAAAGATATT
WI-18582b	69 T A ---	---	GTCTATTTCAAATTTAGCTAGACCCATTTCATCTGTTTAAATGGCTACATTGTTTTCATTGTGAGAC [T/A]GTGCCATAATTTAATCAGTGCCATATTGAAAGACATTTGGATCGTTTCCCAG
WI-18723f	94 G A ---	---	AACTTTATTTGATCTGACGATCAGCGATTAGTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGTAAACAGGTACATAGGTAAACCAA[G/A]TATATAGCTTATTTGGTGAATCTTCATCCT
WI-18723e	71 T C ---	---	AACTTTATTTGATCTGACGATCAGCGATTAGTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGT[C/A]AACAGGTACATAGGTAAACCAAAGTATAGTCTCATCCACATTGACTGTCTGTAGATTTTGAAG
WI-18723c	96 A G ---	---	AACTTTATTTGATCTGACGATCAGCGATTAGTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGTAAACAGGTACATAGGTAAACCAAAGTATAGTCTCATCCACATTGACTGTCTGTAGATTTTGAAG
WI-18619	44 G A ---	---	TTTATTACAATAATTTAGGTGGCACAATAACTAACAGCTTCTGA[G/A]ACAGGAGGTAAACATTCTCA TAGACTTTGCAACTCAGCCAGAAAGTAAACTCGAAATA
WI-18715	76 G A ---	---	TTATTCACAAAAAGTGATATTGACAGGGTCTGGGGCTGTACATGGCAGGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAAGGGAGCCTCCAGGTGGAAGGGTATTTTTTAATAAAAAATAA TGGAGCTACAACCCACCCCG
WI-18535	107 G A ---	---	GTAAATAAGTTTTATTGGCACAGCCAGCTCGTTTCATTCATATGCCATTGACATCTGCTGTGCCCT ACACAGCAGGGTGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCCAAC CTTCTGGTCCCGGTG
D17525	107 C T ---	---	AGAGTGGTCAGAACACAGGCCGAATCCAGGCTCTATCACTTACTAGTTTTCAGTTCTGGCAGGTGAC TTTCATCTCTTCGAACTTCAGTTCTTCATAGATGGAAG[C/T]GCTATACCTTACCTACCTCGTAAAA GTCTGATGAGGAAAAAGATTAACTAATAGATGCATAGCACTTAAACAGAGTGCATAGCATACACTGTTT TCAATAAATGCACCTTAGCAGAGGTGATGTGTCTACCCAGGCAGACGAAG

DWU-133c	313	A G ---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGCTCATGACITTTTTTATGTGTTACCATCCT TTAATAGATCTCATACACCAGAAATCAGATCATGAATGACTGACAGAATAATTTTGTGGCAGTCCT GATTTAAAACCTAAGACTGGCTTGGTTAAATGAATATGTTTCAGTTTTTGAATTTTAAATAGTAACTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236	T C ---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGCTCATGACITTTTTTATGTGTTACCATCCT TTAATAGATCTCATACACCAGAAATCAGATCATGAATGACTGACAGAATAATTTTGTGGCAGTCCT GATTTAAAACCTAAGACTGGCTTGGTTAAATGAATATGTTTCAGTTTTTGAATTTTAAATAGTAACTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199	C T ---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGCTCATGACITTTTTTATGTGTTACCATCCT TTAATAGATCTCATACACCAGAAATCAGATCATGAATGACTGACAGAATAATTTTGTGGCAGTCCT GATTTAAAACCTAAGACTGGCTTGGTTAAATGAATATGTTTCAGTTTTTGAATTTTAAATAGTAA[C/T TTCCAAATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102	C T ---	---	ATGAGATCCTTTAAATCCTTCCATGAACGTTTTTGTGGTGGCCCTCCTACGTCAAAACATGAAGTG TGTTTCCTTCAGTGCACTGGGAAGATTCTAC[C/T]GACCAACAGTTCCTCAGCTCCATTCGCC CCTCATTTATCCCTCAACCCCGCCACAGGTGTTTATACAGCTCAGCTTTTGTCTTTCTGAGGAG AAACAAATAAGACCATAAAGGGAAAGGATTTCATGTGGAATATAAAGAT
DWU-387	169	G T ---	---	GTGTATAAATGCAACTGTTGATTTCCTCAACATGGCTCACAATTTCTATCCCAAATCTTTTCTGAA GATGAAGAGTTTGTGTTTAAACCTGCACTGCCAACAAAGTTCACTCATATATAAAGCATATTATTTTA CTCTTTGAGGTGAATATAATTATATTACAATG[G/T]AAAAGCTTCTTTAATACTAAGTATTTTCA GGTCTCACCAGATATCAAAAGTAAACACAAATGAAGTGTCAATTATCAA
DWU-447b	172	--- --	---	ATTTTAGTGTCTTTGCGTTAAAAATCATTGCAAAAGTATTCTGAACGTGCAAGCTGCCCAGTCAGAT GGGCTGTTGCCATTTAAAATCACTGTAATTAATTAGTTTGTATTAGAGCACAAAGCTTAGCTAATCAA CCATTATTTTCAATTTTGTGTTCTAAGAGGATTGANAATCAGTTTAGTTTAAATGCTTTCTGTTAG GCCTTTCTTTCTTACAATGAAGAGATGATTCTTCTAGTTTATGGTTA
DWU-447	85	A G ---	---	ATTTTAGTGTCTTTGCGTTAAAAATCATTGCAAAAGTATTCTGAACGTGCAAGCTGCCCAGTCAGAT GGGCTGTTGCCATTTAA/GJATCACTGTAATTAATTAGTTTGTATTAGAGCACAAAGCTTAGCTAAT CAACCATATTATTTTCAATTTTGTGTTCTAAGAGGATTGANAATCAGTTTAGTTTAAATGCTTTCTG TTAGGCTTTCTTTCTTACAATGAAGAGATGATTCTTCTAGTTTATGGTTA
DWU-476	63	C G ---	---	GTAAAATTCAGTTTTTTCCAGTTCCTTTTGTGCTGCTTCTCAATTAGCGTTTAAAGTGAG[C/G]AT AAATCAACTGTCCATCAGGTGAGGTGTGCTCCATACCAGGGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGAGATTTTTT

DWU-505	67	A T	---			TCATACTAGGCGAGTATCTCCTCTAGCTAGTGCCCATACAGAAAATTCACCATACAAAAATTA[ATJTGCAATATTTATGTTTAAAGCACAGGTGTACCGAAAGTGTGAAAGTCTGAATTTATGGTT CTATGCATGCATTTTGCCTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTTGAAGATGGAT TAACITTTGACITTTGAGCTTTAAACTTTTAA
DWU-512	131	A G	---			AAATCCAGGCAITTCGAATCTGTTTTCATGATTATAGAGGTTTACACAAAGTGCCACTTATTA AGAGCTTCCACAGTGAAGATGGAGAGGTGAACCTTGCTTTGAATATCCAGATGTGTTTGGTC[A/G] TGCGTATGGGAGTGAGCAGGTATGTGTTGCTTTTGCTTGCACTGAAATTTAAATTTGCTATCAAGAGC AACTATGAACGGTTTTTATTCAGATGCTCCAGAGTGAAGATGCCGAG
DWU-525	97	A C	---			AACTGCATATAGATAATTATCCAGGATGTGGCTCATCTTTTCAGCTTGTTCTATACTGTTTGT ATATACAGTTTTTGTAAACCATATGATTGA/CJAAGAAGAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAAATAACATATCTTGCTTTTCAAAATATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTAATCTCTAAATCTAGTCTCTGATTTC
DWU-59	94	C T	---			CATTCTTTGTAAAGGTAATGGACTCACAAGGGGGAAGAACATGCTGAGATGGAAGTCTACCGG CCCTTTCTTTGTGAACGTACATTGGC/CJTGAGCCGTGTTGAGTCCAGGTGGCAGACTCGTTTGTG GTAGTTGTTTAACTTCAAGTGGTTTACTTCTGATAGCCGGTGATTTTCCCTCTAGCAGACATG CCACACCGGTAAGAGCTCTGAGTCTTAGTGTTAAGC
EST11	68	C	---			CTTGATCATGGGTGGAATTTTGTTATCTGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAAG CAGCAGGTGCCGAGGCTGGATCAGAAAAAAGGCA
WI-19856b	63	C T	---			CACACTGGCATCTAGGCTTGGCTGCATTGCAGAAGGAGAGCCAGGTCCTCCCTCTGGAGAA[C/T]G CTGGTTCCCGAGCCACACCCGCTTGCACCACACAGGCTGTTGAGGCAGGAGGTGGGTAAAGCGT AGCTGTAGACCCAAAGCAACCAAGCCCTGGACCCCTGGGAGAGGAGCAGTCTTAGAACATGGAA AAGTGTGGTCATCCCATCATTAGACAAGACACATCCTACATAATAAAAAAGT
WI-18014	40	A G	---			TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAAJ/GJGAATGAAAGTGCACCATCAGAGT GTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTTAACAGAGATTTCTCAAGGGCAAGTGGCTTCT A
WI-18036b	97	T A	---			TTCCAATGTAAGAGTCAAGTACCAAGTTAACTTCTAGAAAATACAAAGAGAACATGATAAAATCTG ATCACAGTGGAAAAATTTAATTTCTTTCATAA[T/A]CTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27	T C	---			TTCCAATGTAAGAGTCAAGTACCAAGT[C/J]AAACTTCTAGAAAATACAAAGAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTAATTTCTTTCATAATCTGACAGGTCAAGTAAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72	C T	---			TGTAAGGTGACTTCTATAAGCTTCTAACTGTCAAACTTTCAATTTACTGAGATTTATTCAGGCCAAT GTGTC/TGTTGGGTCTGAGATTGATTATCAGCTGGGTAAAGTTAACCTGTCTCTGTTTCA

WI-18063	105	G A	---				AGGCTTTAAACTGATAACAAATTTGCCTTTAATCACATACAAAAAAGCTGCACTTTTCATTCCTTCCTTC CCATGTTTTCTGATTTTGATGTAAGCTTAAATTTGTGTAJTCCTTTAAACAATATACGTAGCTGCA
WI-18078	86	A T	---			---	AGTTGAAAGATCAGAGAGGTTAGTTGGTGAGTAGCTGAACCTCAGATTCAAAACCTGGTCCAGTG TTGTTTTTTCAGCATCAGATGTCCACTAGCCAAAGTTGATCTCTGCAGTATCTACATGTGGT
WI-18091	90	T C	---			---	CCAAAGCTCACTCAGTATTTAATCATCTGCTAAATTCATCCTTTGTTAATTCATCAGACACTGTGGT TTTCATCTCTAGAAAGTTTGACTTTCGCGGCTTTTATACCTTCATATCTCAACTTGTTAAGC
WI-18119	38	T C	---			---	GCAATCTGTAAACAGTTTTGGTAGTGGTATTACAGAGGAJTCJTGTAAAAATGGATTGGAGTACTTTAC CACTAATTCATCTGCTCTGAAATAGTTCACTAACCAAACTACTGACAAACAGTTTAATTTTGGTTCTT
WI-18142	66	T G	---			---	TTCAAAGATAATTACAAATTTGGAAGGGGACCAATAATTCACATTTTAAATCGAAAAATAATCTATATACJ TJGJCCCAATAAACTCACAGTAAATAAGCTTCAAAAAGCCTTAAGACACCAAAAAGAGGAAAA
WI-18178	68	T C	---			---	GCATAGGTTGAGGGGTGTACAAGAGGAGAACCCAGATTTCAGTCCATGCTGGAGGTAGTCTGGGG GTJCGCGGGATGGACACACAGACACATAGATCTGGCATCTGATAGCAGGGGCATACAG
WI-18244	35	G T	---			---	TCATCTGAAAACCTTGCTGTAGCCAGCATGGGTGJGGGAGGTGATTATGGCTGGGGAAGATG GGCACTACCCGACAGCAGCATCTAGCACCAAGTGCAGGGAGCTTGAGGTGGCAGAGGGCTTT
WI-18245	115	G A	---			---	ACAGATGTCAGTTGTTGAAATGGCCCATTAAGTATGGGGCTTTCTTGTAAAAAGTCATTCCAAA AGGCTTGGCAAGAGTTTGCTATACAACGGAGGGACAGAGAAACATGAJGJCTGGGGAGTAGGCTCT GACAGAAGGTGGGCTGTC
WI-18261	26	G A	---			---	GATTTGAAGGGATTGCTTTATTTAAAGJGJTGAAAAAGCGTGATAGAGGAACTGTTTAAAGATAAACAA CTTATAAATACTCCCAATTTGTAAGGTGAAAGATTG
WI-18268	88	C T	---			---	TAGGAGGAAAAAGGAGGTGGGCTGCCTGGGGCCCTCAAGACATGAGAAACGGGTGGTGGCTTCCAAGC TTCCTTACTTCCCCATAGATCTJCCGTGACAATGTCTGCAGAAAGCCCTCCAACCTGGAAC
WI-18299f	107	C A	---			---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAACCTGGTTTGCCAAATTTTTT ATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAAATTCJAJTTTTGCCAAATTAATTGACATATCTG CAG
WI-18299e	101	A G	---			---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAACCTGGTTTGCCAAATTTTTT ATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAAATTCJTTTTGCCAAATTAATTGACATATCTG CAG
WI-18299d	77	G A	---			---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAACCTGGTTTGCCAAATTTTTT ATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAAATTCJTTTTGCCAAATTAATTGACATATCTG CAG
WI-18299c	67	T G	---			---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAACCTGGTTTGCCAAATTTTTT TJGIATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAAATTCJTTTTGCCAAATTAATTGACATATCTG CAG

EST5	93 A ---			CTGGTGGGAGGAAACAAATTGTGGTATATTCATACAATGGAACAACTCTTCAGAAATAGAAAGGAA CAAACCACTGAATCACACAACATGGACAAATCTCAAATCATTATGCTGATGGAAGAAACCAATTCATCA TAAGAATACACAGTACAT
EST6	48 C ---			TTAGCTACTTTTCAGAATTGAAGGAGAAAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGCTCT GAACA/AAAGCTTTCTTTCTTTTGCAACAAGACAAGCAAGCCACATTTTGCAATTAGACAGAT
EST8	158 A ---			GGACAGGACCTCTATTCCCGCTGGTCAGCAGCGGCTGATGGACTGAGGCCCGCCAGGGATCTGGGOC CTCTTCTAGGGGGCTCTCCAGGACCCAGAGCTGTTCTGCTTTGAGTTTCCCTAGAGCTGTGGGGCA GATAGCTGTTCTGAGTTGCAAGCACGATGGAGATTTGGACACTGTGTGCTTTGGTGGGT
WI-18740c	104 G T ---			TCCTCATTGTTGGGGATGATGAGAAGAAATGATTTGGGAAAATTAAAGTAACAACGACCTAGAAAAGT GAGAACAACTCATTTACCATCATGTATCCAGTAGTG/G/ATAATTTCATTTTGATGGCTTCTATTTT TGGCCA
WI-18740b	96 C G ---			TCCTCATTGTTGGGGATGATGAGAAGAAATGATTTGGGAAAATTAAAGTAACAACGACCTAGAAAAGT GAGAACAACTCATTTACCATCATGTATC/G/AGTAGTGATAATTTCATTTTGATGGCTTCTATTTT TGGCCA
WI-18985a	105 C T ---			CCAAAGTCTCCTGTTCCGCTCATAAAGAAGTTTTTGGGATGGGAGAGAATCCAGACCATCTTGGGGCA GCCAGGCCCTTGCCCTTCATTTTACAGAGGTAGCACAA/C/TTGATTCCAACACAAAACCCCTTCCOC TTTTAAATGATTCTGTTCTAATGCCATAGATCAAGGCTCAGAAACCAATTGTGTTTCTCTTT TGAAGCAATGACAAGCACCTTACTTTCACGGTGGTTTTGTTTTCTTAT
WI-18746	114 G A ---			GCCAGCAGCTGAAGTCTCTTTCTCTCTCGGCTGGAAGAATCAAGATACCTTTGCGTGGATCA AGCTTGCTACTTGACCGTTTTTATATTCTTTTGTAATATTCTTG/A/TCCACATTTCTACTTCAGCT TTGGATGGTTACCG
WI-19112	212 G A ---			CCGTGTTACACACACACAATGGCAAGCATAAGTCGCTGGTTACGGCCAGGGGAATATGCCAAGG GACCCCTTAATGGAACACAGATCAGTAGTGCTATCTCATGACACCACAAAGAACCGACGACAAA TCTTTGCGAGATTTCTTCTAGTGGCTTAGAACATGGCTTTAAGAAACACGGTGATATCTTTGAG GGTGACAAGGC/G/A/TCTCTTCAAACAGTTCCATACCAACTGCTTTGCTCTAG
WI-19092	232 A C ---			TGGTGGCTGGCTAGCTAGTTTCTACAGAACATAATTTGCCCTCTATAGAAGGCTATTCTTAGATCATGT CTCAATGGAACACACTCTTCTTCTTAGCCTTACTTGAATCTTGCTATAATAAGTAGAGCAACACAG ATTGAAAGCTTCTGATCAACGGTCCGAAATTTTCATCTTGAATGCTTTGTTATTAAGTGAATTTTC TTTTAAGCTAACAAAGATCATAATTTTTC/A/C/ATGATTAGCCGTTGAAC
WI-19057i	175 G A ---			CCCATTTATTATAGCCAGTGATGTCTCAAAGAGTAGAGGCGTCTACTGGTCTTTCAACTCCTTCA GTCTTCTGACGGCGGACTTTACCGTGACAGGGAGTGGTATTGTACGTCCAGGCAACCGACGCACTG TCTTCATGCGAGGAACCAAGTGCCAGATCCCCACAGCTC/G/A/TCTCTTCATCTTGGTTTGCCACA

WI-20103	168	C T ---	---			TGGGACTTCCAACCTCAGAGGATGTGGGAATCCAGCTCAAATGATACAGGATAAACTGGGATGGGCT AGGATGGACAGGCTGTGGATATGGGAGTCAATGGGTCAAAGTCTTATCCAGATGGCTCCAGGTACAG TGGGCTTCTGGGCTGGAGCTGGGTCTCCCA[C/T]TTCATTCTGCTCAAAGCTTCTTGAAGGAGC TGGTTGACTTCAACTTGTAGAGCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111	G A ---	---			GCCTTACCCATTTTGCACATATACATATGCACCACCTTTCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAATCTTGTAGGACAAGAAATGGA[G/A]TTGAATAAGTACCCCCCAA CATATACAAGAAAGTTAGCATACTTACCCCGTTTTCTACTACATCAGAGGCAAAATAAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGGG
WI-19911b	116	A G ---	---			TGGTTACAAACCTAAGCCATATACAAATTAGGAACACATTTAGATGCTCTTTTGAAGAAGCGT TTTAGTCTTTTAAACTGAGTTTAAAAAAATAACAATGCAATTTT[A/G]ACACTGTTTTTGAAG ACTTAAAGTGCAGCAATA
WI-20613c	165	A G ---	---			GTCTCAAGGGGGAGAAACCTGGTTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAATAATGGCATGGGAGGAGGAGTTAGAAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAGTTGGAA[G/A]AAAGGGAGTTTCCACGCAGCCAGTGGTGAGC TGC
WI-20613b	156	A C ---	---			GTCTCAAGGGGGAGAAACCTGGTTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAATAATGGCATGGGAGGAGGAGTTAGAAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATA[G/C]AGTTGGAAAAAGGGAGTTTCCACGCAGCCAGTGGTGAGC TGC
WI-19984	47	A G ---	---			CAGTAAAGAGTGATTCAAGTTGCAGTAATACACTGACAGGTAAATA[G/G]TATAACATTAGAAAA GCAAAATTCITTTAACTTAAGGACAGACTGAACCATCAGGTATGGGTCTGAGATCAAGTAAATACAGG TAGGCAAGAGTTTTCACACACTGGAAATGAAGGCAGTTTCCAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135	T C ---	---			GCCAGTTGGAATATGGCCTATACGAACCAAGAGTGTATACAAATGGAAGTGGTCATCAGGCAATA ATTGTTTCTTGGAACTCTGCACCGACTGCCATGCTCTGTGGGACTTACACATTCAAGTTTGACAGI T/C]TGA AAAACCAACTGGAGCTGCTTTCCAAAGATGTTCTGTCTTCAATAGGAATCCATG TTATTTCTTCTTGGCTTAAGCTCTTATATCTTCAATGACCTAAGCTGA
WI-18846a	49	G A ---	---			GAGTGCCATACCTTCTCCAGGCTCTGCCCCAAGAGCAGGAGTGCTG[A/J]AAAGCTGGGAGCGT GGGCTCAGCAGGCTGTACCTCCATCCCGTAAGACCTCCTTCCCTCCTCAGCAGGCCAAACATG GCCAGACTCCTT
WI-18959	123	G A ---	---			AGCAGTGGCCTTATGCATCCCAACCAACCGCTCTTGACCAGGCTGCTCCCTTGTGGCAGCAACGGC ACAGCTAATTTCTACTACAGTGTCTTTAAGTAAAAATGGTCGAGAAAGAGGCACCG[A/J]GGAAGCCG TCCTGGCGCTGGCAGTCCGTGGGACGGGATGGTTCTGGCTGTTGAGATTCTCAAAGGAGCGAGCAT GTCGTGGACACACACAGACTATTTTAGATTCTTTTGGCCTTTTGAACC

WI-20146	31 T C ---				TGAGTCTTCTGTAATTCATTGAGCAGTTAGCTG/CATTTGAGATAAAGTCAAAATGCCAAACACTAG CTCTGTATTATCCCATCATTTACTGGTAAAGCCTCATTTGAATGTGTGAATTCATTAACAGGC
WI-18922	74 G A ---			---	TAGGAATTGGTTTCACGCCTGAGGCAATTAGACACTTTGGAAGATGGCATAACCTGTCTCACCTGGAC TTAAGC/G/ATCTGGCTCTAAATTCACAGTCTCTTTCTCTCACTGTATCCAGGTTCCCTCCAGAG GAGCACCAAGTTCTC
WI-18763b	53 A G ---			---	TTCTGTGTGTGGGGTCAACCGTACAATGGTGGGAATGACGATGATGTGA/G/ATTTAGAAATG TACCATAATTTTGTAAATTTATTAATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA TGTTTTTGCCAA
WI-18763a	38 A G ---			---	TTCTGTGTGTGGGGTCAACCGTACAATGGTGGGA/G/ATGACGATGATGTGAATATTTAGAAATG TACCATAATTTTGTAAATTTATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA TGTTTTTGCCAA
WI-18771b	75 G A ---			---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAGAAAGATGTTGGG AACAGAA/G/A/AAATAAACTGAGTTTAAAGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18771a	57 A G ---			---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAG/G/ATGATGTT GGGAACAGAGAAATAAACTGAGTTTAAAGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18820	70 T C ---			---	GGGAAAAATTTGAGACGCAATACCAATACTTAGGATTTTGGTCTGGTGTGATGAAATTTCTGAG GCC/C/ATGATTAAATCTTTCAATTTGATTGTGATTTCTTTAGGTATATTGCGCTAAGTGAAACTT GTCA
WI-18742b	51 C T ---			---	ACAAAGTCTGTAGCCCCCTCACCTTTCTGTTTCACTTTTGCCAAATGTA/C/ATCGGGTTTGTTTT TCTTGATTATTTAAACGGTTGTGGTTTCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGA GTTTTACC
WI-18882	94 C T ---			---	GTGTGTCCAAAAATGGGGTCTGCTCTGCTACCTTGACCCCTTCCCTTCTCTGCTTCTCTCTCATCA TCATTTCCCAACAAACATCCTCTGCCA/C/TAACAAACAAACGTAAGTTTTCATTTGGGCAAAAAATTGA GC
WI-19970b	167 G A ---			---	TATAAGCCCGAGTCAACAGGACGGCCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCTGCCAAC GGCCCCCGGAGTGCAGTCCAGCGGGGAGGAGGCTGCCGTTCTGCCAGTTCTCTCACTGCGGGGACC AGCAAAAGGCCCTTCTCACTGGTTGGTCAAG/G/ATAGTACCTTGGCCTGGTGCATCCACAGAGGA TGTTGTCAAACCCAGAAATCTTTAAACGACTGACCTTCTTTAAAAACAGA
WI-19970a	126 T C ---			---	TATAAGCCCGAGTCAACAGGACGGCCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCTGCCAAC GGCCCCCGGAGTGCAGTCCAGCGGGGAGGAGGCTGCCGTTCTGCCAGTTCTCTCACTGCGGGG ACCAGAAAGGCCCTTCTCACTGGTTGGTCAAGGTAGTACCTTGGCCTGGTGCATCCACAGAGGAT GTTGTTCAAACCCAGAAATCTTTAAACGACTGACCTTCTTTAAAAACAGA

WI-19067d	202 T G ---	---	TATTGCTGCTTGCTCACTGCCTGACATTACGGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTC ACATTCCCTGCTGCTCCAGAGACTGCCTCCGCCATCCACAGATGATGGATCTTCAGTGGTTCTC TTGGGCTCTAGGCTCTGGAGAAATGTTGTAGGGGTTTATTTTTTAATAGTGTTCATAAGAAAT/ GIACATAGTATTCTTCTCTCAAGACGTGGGGGAAATTATCTCATTATC
WI-19067c	153 G C ---	---	TATTGCTGCTTGCTCACTGCCTGACATTACGGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTC ACATTCCCTGCTGCTCCAGAGACTGCCTCCGCCATCCACAGATGATGGATCTTCAGTGGTTCTC TTGGGCTCTAGGCTCTG/CJAGAAATGTTGTAGGGGTTTATTTTTTAATAGTGTTCATAAGAA ATACATAGTATTCTTCTCTCAAGACGTGGGGGAAATTATCTCATTATC
WI-19067b	151 T C ---	---	TATTGCTGCTTGCTCACTGCCTGACATTACGGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTC ACATTCCCTGCTGCTCCAGAGACTGCCTCCGCCATCCACAGATGATGGATCTTCAGTGGTTCTC TTGGGCTCTAGGCTCTG/CJGAGAAATGTTGTAGGGGTTTATTTTTTAATAGTGTTCATAAGAA ATACATAGTATTCTTCTCTCAAGACGTGGGGGAAATTATCTCATTATC
WI-19067a	57 C G ---	---	TATTGCTGCTTGCTCACTGCCTGACATTACGGGCAGAGGCAAGGCTGCTGCAGCCTCC/CJCTGGCTG TGCACATCCCTGCTGCTCCAGAGACTGCCTCCGCCATCCACAGATGATGGATCTTCAGTGGTT CTCTGGGCTCTAGGCTCTGGAGAAATGTTGTAGGGGTTTATTTTTTAATAGTGTTCATAAGAA ATACATAGTATTCTTCTCTCAAGACGTGGGGGAAATTATCTCATTATC
WI-19106	247 T C ---	---	TAAATCCAGCCCTACCTTGTAGTATTTAGGAGACAGTCTCAAGCACTAAAAGTGGCTAATTC AATTATGGGATAGTGGCCAAATAGCACATCTCCACGTTAAAGACAGTGGATCATGAAAAGT GCTGTTTGTCTTTGAGAAAGAAATATTTGTTGAGCGCAGAGTAAATAAAGGCTCTTCATGTGGC GTATTGGCCATAGCCTATAATTGGTTAGAACCTCCTATTATTTAA/T/CJGG
WI-18944	147 A G ---	---	CAAGGCAAAATATCAGGAGCTTTTTACACACCTACTAAAAAGTTATTATGTAGCTGAAACAAA AATGCCAGAGGATAATATTGATTCTCACATCTTTAACTTAGTATTTACCTAGCATTTCAAACCC AAATGGCTAGAAC/A/GJGTTTAATTAATTTACAAATATAAAGTTCTACAGTTAATTATGTGCATA TTAAACAATGGCCTGGTTCAATTTCTTCTTCTTAAATAATTTAAGTTTT
WI-18952	232 G A ---	---	CCCATCCCTGTGAAGGAGTAGGCCACTTTAAGTGAAGGATTGGATGATTGTTCATAATACATAAA GTTCTCTGTAATTACAACATAATTTATGCCCTCTCTCACAGTCAAAGGAACTGGGTGGTTGGT TTTTGTTGCTTTTATAGATTATTGTCCCATGTGGGATGAGTTTTAAATGCCACAAGACATAATTTA AAATAAATAAACCTTTGGGAAAGGTGA/G/AJACAGTAGCCCCATCACAT
WI-18932d	177 C/T ---	---	CACACCTCATGTAGCCTCACGAACTGGAATAAGCCTTCGAAAAGAAATTGCTCTGAAGCTTGTA TCTGATATCAGCACTGGATTGTAGAACTTTGTGCTGATTGTGACCTGTATTCAAGTTAACTGTTCCC CTTGGTATTTGTTTAATACCCTGTACATATCTTTGAGTTCAA/CJCTTTAGTACGTGTGGCTTGGTCA CTTCGTGGCTGAGGTAAGAACGTGCTTTGTGGAAGACAAAGTCTGTGGCTTG

WI-19042	193 A C ---	---	TTTGTCAGTGTGCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATG GATAAGGGAATAATAGGCCACAGAGGTGAACCTTTGTGCTTCAAGGACATTTGGTGAGAGTCCACACAG ACACAAATTTATACCTCGACAGAACTTCAGCATTTGTAATATGTAATAACTCTAACC[A/C]GGCTG TGTTAGATTGATTAACTATCTCTTTGGACTTCTGAAGAGACCACCTCAAT
WI-18984	208 A C ---	---	ATTGGCCCTGTACAGTTTGCCTATTATAAATTCATTAAAACTACAGGTGTGAATGGTTAAAA TGTAGGCCCTCAGTTCAATTTTCAGTTATTTCTGAGTGTGCAGACGTATTTTCGACGTGATTAAT GTAACCTATTAAATGAATCAGAAGCAGTAGACAGATGTTGGTGCATACAAATATTGTGATGCATT TATCTT[A/C]ATAAAATGCTAAATGTCAATTTATCACTGGCATGTTTGAAT
WI-18851	90 T A ---	---	GCCTCAATTGGCGATTGATTCAAGTGGCCACAATGTAAACAGGGTGGTAGTTGTACTCATTTTGAAT ATACCTTTTCCCTATTGTATTCTT[A/G]ATAATAGGATCCTGGAAATGAGACCTGGTGGAA
WI-18821b	76 T C ---	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC ACAGAGGCT[C/G]GGGGTAGCCATTGTGCAGTCATGGCCCGGGGAACTTGCCAACTTCGTGTGTCAG GTGCTGTGT
WI-18821a	69 C T ---	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC A[C/T]AGAGGCTGGGGTAGCCATTGTGCAGTCATGGCCCGGGGAACTTGCCAACTTCGTGTGTCAG GTGCTGTGT
WI-19021a	20 C G ---	---	ACTCCTCTGCTGCTGCCAT[C/G]ACTGTCTTTTGAACACAGGAAAGTCACAGAGTTTAAAGAGAA GCAAATTAACATCCTGAATCGGGAACAAAGGGTTTATCTAATAAAGTCTCTTCCATCACGTTG CTACCTACCCACACTCCCTCTGATTTGCTGAGGACGTGGCATCTACTACGTACGTGGCATAAC ACATCGTGTGAGCCCATGTATGCTGGGGTAGAGCAAGTAGCCCTCCCTGTGTC
WI-18908	70 G C ---	---	TGGAATTCCTTTCATCTGGAACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAAGGGTCAGTA TGG[G/C]TTAGGGAACAACTCCATCCTTGAGTCAAAAAATCTCAATCTTCCCTATCTTTGCCACCC TCATGCTGTGTGACT
WI-19037b	155 A G ---	---	CACGGTTCTCTGCATCGTTACCAGAGCGCCTTCTGGTCTAGCCACGCCCTGTATGACCGCGCAATA TCCCCAAAGCTTTTGGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCATTTCTGGAGAGGGTGC CCCTCCCTTACGAACAC[A/G]AAACCCAGCCACATGACTAGCAGCTGAGCTCTGCAGGGACCA GTGCAGGCACTGGGGGTGGAAGTGTGTGACACAGTGAATGGGAGGTGG
WI-19037a	47 C A ---	---	CACGGTTCTCTGCATCGTTACCAGAGCGCCTTCTGGTCTAGCCACG[C/A]CCTGTATGACCGCGCAA ATATCCCCAAAGCTTTTGGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCATTTCTGGAGAGGG GTCCCTCCCTTACGAACACAAAAACAGCCACATGACTAGCAGCTGAGCTCTGCAGGGACCA GTGCAGGCACTGGGGGTGGAAGTGTGTGACACAGTGAATGGGAGGTGG
WI-19064	66 T C ---	---	TTGAGGAGGTGGGTGAATGCTCTCTGGCAGGGATTTGTGACACTGCATGCTGGGCTGTGTTCTCT/ CJCGGGCTCTCTGGACCTTGACCGTGGATACAGGCCCATGTGCCATGGTATTTGGGTCTGGAGGG TGGGTGAATAAAGGC

WI-18972a	112 A G ---	---	---	AGGCTGTGGCTTATGTACCCACAGAGGGTCTCTGAGAAGTCTGGCTGCCTGGGATGCCCTGCC CCCTCTGGAAGCTCTGCAGAGTACTGGCTGGGAGAGAG/GJTGCTTGTGGCATGGAGCC TCATTGCAAGTTGTTCTTGAACACCTGAGGCTTCTGTGGCCACAGGCACCTACGGCTTCTCTCTCC AGATGTGCTTTGCCCTGAGCACAGACAGTCAAGTGAATGCTCTTTGGCCA
WI-19016b	184 C A ---	---	---	GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCACCTGTTTAAATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGATTAACGAAGTTCAAGATTAGAAATACATCTGTGTC CTGAAAACCTTAGATACATAGCCGACTGTATACAGAGGTTTCATCAAC/AJCTCAACACTATTGAC TTTTGGGGCTGGATAGTCTCTGTGTGGGGTTTGTCTGTGCACTGTAG
WI-19016a	161 C T ---	---	---	GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCACCTGTTTAAATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGATTAACGAAGTTCAAGATTAGAAATACATCTGTGTC CTGAAAACCTTAGATACATAGCCGAG/CJ/TJGTATACAGAGGTTTCATCTCAACCTCAACACTATTGAC TTTTGGGGCTGGATAGTCTCTGTGTGGGGTTTGTCTGTGCACTGTAG
WI-20096	21 T C ---	---	---	GGTTTGGGGCATTTATTTCT/CJGATAGAGACTGGCACAAAGCTTTGGGCTAAGGACACCCGCCOOC ACCCTCATCTAGAACAAATCTCTCGCCAGACTTG
WI-19591b	156 C A ---	---	---	TGGGGCAATTTTAAACAAACAGGCAAAATATACATATACCTGAATTAAGGTAACCTCAAGCCATG AGTATAAGATTAAAGCAGTTACTTTATTTTGAACAAGGAGTGGCATAAGCAACTCAGTGTGCCCC CTTAGGGTGGGAGCTCTCC/CJ/ACTACCACCTCCCAAGGATCATTTTGGGAGAAAAA GTGCTTCTATCTGGTAGTGTGTATCTAGGGATTGCACCTTCTTACACGG
WI-19591a	45 T A ---	---	---	TGGGGCAATTTTAAACAAACAGGCAAAATATACATATACCTGAATTAAGGTAACCTCAAGC CATGATATAAGATTAAAGCAGTTACTTTATTTTGAACAAGGAGTGGCATAAGCAACTCAGTGTGT GCCCCTAGGGTGGGAGCTCTCCCCCTACCCTCCCAAGGATCATTTTGGGAGAAAAA GTGCTTCTATCTGGTAGTGTGTATCTAGGGATTGCACCTTCTTACACGG
WI-20310	125 G A ---	---	---	TCTCCAGCTCTGTCTCTTGTCTTGAAGGTTCTGTGTTACGGCCCCCTCCAGGCATGGTTCTTCAT TTAGGTAGGAACAAAAGGCCAAAAGAACATACAGCCAGCTCTCTAGAGGCTCCA/G/JTCAGAA CTGGACCTTTAACTACAAAGGAATCTTGGATGAATTTTTCGGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGCACTCAGGCCATCTTCTCCCAATGTCTCCCCGGGG
WI-20560	224 G A ---	---	---	CTCTCCCCAAGGAGCCTTGGCCTTGACGCCCTTACAGAGGGATGGAAGTCACAGACAATGAGT GGAGCCTCATGCCCTCCCATGAGGAAGCCCTTAGTATTGCTGACATCTGCCCTTATCTGTCTCTCT CCCCAGTGTCTACACTTGGGCAAGCAGAGTGTGGCAGACCCAGCCTTGAGAGCTCTTGTAGACC GGAAGGAAGGGCGGTCTT/GJ/AGGTGATGGCTTCTGGCTCTCTGGCTT
WI-19359a	39 T C ---	---	---	GACGTGGACAAAGGAGGTTTAAATGAATACTTGTGTTTGT/CJCATGTTCAAAAAAGAGATTAAAT ATTTTGTGACTGCATCTGTGAATGAAGACACTCAAAAGCCATGTTTCCAACTTAGGTTAATAATAA GGCTATTTGTCCACCCACTCTCTGGGCATTGCTGCAATATCTGGGCTCAAGTGGGAGGCCACGTG GGAACAAGGCCCTCAGAAAAACAAGGACATGACGCTCTCCCTGAGCCAGTTCTCT

WI-19766b	93 A G ---	---	TGGCTCAATGACTGGTACATTGGAGAAAGCTGTGCAGGAGCATCCTTTCTGTGGTGGGAGGGAGGAGATGAACCATAGGAGCCAAAGTC/GJGACAAACAGAAAGGCACACCAAGCCTGAAACCCCTC
WI-19766a	31 G A ---	---	CGGACACAGCAGAGTTACCAGCTAGGGATGTCCTGGAGTTTCTGACCCATGAGAGGCCCCCTCACCTCTTACCCCTCCTCTACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126 C G ---	---	TGGCTCAATGACTGGTACATTGGAGAAAGCT/GJGACAGAGCATCCTTTCTGTGGTGGGAGGGCAGGAGATGAACCATAGGAGCCAAAGTCAGACAAAGAAAGGCACACCAAGCCTGAAACCCCTC
WI-20512c	59 T G ---	---	CGGACACAGCAGAGTTACCAGCTAGGGATGTCCTGGAGTTTCTGACCCATGAGAGGCCCCCTCACCTCTTACCCCTCCTCTACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-19599	230 C G ---	---	CTTCTCTGTTTGGCTTGCATTTGTGCGATTGGAAAAACCACTTGAAGAAGGGACTTTCTCTGCAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGA/C/GJAAAGC
WI-19599	230 C G ---	---	TAGAAAGGAAGTGAATTCCTTTGAATATGGAATTTAGGGCGGGCGTGGTGGGCTCACGCCCTTATTAATCCAGGCACGTTGGGAGGGCCCAACGCGGGTGGGATCACCTGA
WI-20679	82 T C ---	---	CTTCTCTGTTTGGCTTGCATTTGTGCGATTGGAAAAACCACTTGAAGAAGGGACTTT/GJTCCTGCAAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGACAAAGC
WI-19909a	29 T C ---	---	TAGAAAGGAAGTGAATTCCTTTGAATATGGAATTTAGGGCGGGCGTGGTGGGCTCACGCCCTTATTAATCCAGGCACGTTGGGAGGGCCCAACGCGGGTGGGATCACCTGA
WI-20341	221 G C ---	---	GGGCTTAAATCCCTCTGTTGGGACTGGTCTCCAGTTTACAGCAAAGGATCGCACCCCTTTTCCATAACCCCTTCTACATTGGAAAGAGCACACCTTGTATACAGAATGGCTCCGTGAAGTCTTTTAAACG
WI-20341	221 G C ---	---	GACAAAGGTAAATCACAGCTAACAAACGTGATGTTGGCTCACAGTAAACCAACACCTCTTTTTCAGAACAGAGAGCGTTAAAGTAAAGGGCA/C/GJTTCCAAGAGTAACACTGCTA
WI-20679	82 T C ---	---	TGTTTGAATAAAAAATTTCCATGGTCTTAATTGAAGTGTATGTTACTTTCTTTTGAATATCCTTTTTCATTAAAAATAATTCCTAAACCACTCTATGTGTTCAACCTCTGTTTAAACATAAGATATGGGT
WI-19909a	29 T C ---	---	TTTTGGAAAGGCCACAAAGTCACAGCTCCATGAAGTGGGCGAATGGTCTTTTGGAAAGCTCTCAGGGTGTCTTCTCCAGAAA
WI-20341	221 G C ---	---	CCAGAAATAAAGCCTGAATATCTCTTTCT/CJTTAAAAATAAATTTTCTCTTTGCTCTTCCAAAGTAAATCTTAAATGAACCTGTCTAGTCTATTTTAACTAGGCAATTAACACTACCTAGGCGGGTTTTTTCCTTATACCTTGTCTGACTGGAATCAACTAA
WI-20341	221 G C ---	---	TTGAGAGGCTGAGAGAGGCTGTTGAGACATTGTAATAAGTCTTAGGGGCATGAGACATTAGGAAGGCCACAAATATGAGTAATGAATGAGAGGCTGATGAGAGCTACTGCTCCATTTGTTAGCAGGAGGCAGGAAAGTGATCTGGGGTCTCTGGCAGCAAAAGCGTGGTAAATTTGGGTGACGTCATGC
WI-20341	221 G C ---	---	ATCCCCATGCATTGGTTTTC/JATGCTCCAGTGAGCTGTGGGCAAGTCT

WI-20113	60	T C	---			TTCTGGTACATGGTAAAGTCTCAGTATTACTAGTGAATGAGCAAGACCTGAAATACGTGTCJGGA AACAGTAAAAGCAAAATACCACACAATTAGGAGGAATATTTTCAGACATAGGATATTTAAACAT CACTCAAACTACTGGAGCATGATTCAGCAATAAATCTATCCATAAACCCAGGTAGATAAATGTCACA GCITTAATAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATCCGTAAT
WI-20895	107	G C	---			TGATGGCAAGTACAAAGGCTCTGAAAGAACACAGAGTAACAAGAGCGCGCAGTGCGAGGTGGC CACTTCCACCAGGAGCAACACTTGACTTCATTAAGGCAAJG/CJCTTTACTCTGTACTTTTCCCTC CCACATAGTTTAAACCAATAGAAAGGCATTCCTTCTCACACTACTGCTCTCTAAGGTCCTAGGAA TATAACTGGTACTATAGGCAACAGATGCA
WI-20721	72	T C	---			CCTGCAATCACAAAAGTGGAACTAGTTGATATTTTGAATCATACITTGATTTAACCACTTTCAGAAA TTCTATTCJAAACACTAGCAACTTCCTTTTATCAGA
WI-19415c	161	A G	---			CTGGATTTAATATTTCTGGCCTAATAACCAATGTAATCAATAAAATTTGGTCAATATCTCACCTC ATTTCTGCTAACATGTTTTGCAAGATCCCTAAGTAAGGTATTGACACTGAGACTAGTCCGGCAA GTCATGAGACCCCTTAGCTGATCTCATJGJAAGTCCACCTCATGAAGGAGATGATTCACATCTCAA GCTAAGGTATAAAGTGTGGACATACAAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103	C T	---			GCTGCTACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTAGCAGTGGGCCATGCACCTCTG GCGGTGATGAAGAGACTGTTGGTCATGGCGGTGACJTGCTCTTCCAGGCTCATATGGATGTCCT CGAGTTGCACAGGGAAGTCTCTGCTTGTAGAAGCTTCTCC
WI-19348b	98	A	---			GCTGCTACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTAGCAGTGGGCCATGCACCTCTG GCGGTGATGAAGAGACTGTTGGTCATGGCJGJAAGTACGTCCTCTCCAGGCTCATATGGATGTCCT CGAGTTGCACAGGGAAGTCTCTGCTTGTAGAAGCTTCTCC
WI-19635	98	A T	---			ATTAGTTGTTGGCCACATTCAAAGCCATCCACACAAGCTTCTGTAGGCCATTGTAACACAATG TTAAAGGTACAGTAAAATACAGTATTATJATCTTATTGTAGCACGGCTGTGAGGCTCAT GTTGAATGAAGCATCCTTAGGCAGCAAGTGAAGTGCATGCAGATATGTGTCTGAAAGAACTTTGCCTT T
WI-19641a	46	A G	---			TCAAATTTTCAAAAACATGTTCCATGTTTATTGTGATAAGCACTAGJAGJTATTATAGTCTCATGTT TTAAATTTATGAATAACGTCGTGATTCATTTGATTTTGTATTTACAGAAGATGTCAGGGCTATCTCATTC AGTTATTAATAAATGGATCAGAGTAGTAAGTCAAGAATAAGTGACATAATGTGGTTTAAATTTTAAAA AATCTCAGAAATGAGTATTTTAAATTTTAAATTCATCCACCCACCTTG
WI-19642b	52	C A	---			ATATAGAGTACCATCCATGGTTTCAAGCATGGCCTGGACACATTATCCCCCTCJAJGGGTAAACCAG GACTATTGCATGAGCATTCITTAATACGTATTTTGTATGGACACAAGTTTTCATGCTATTA
WI-19673b	180	C T	---			TCTGCCATGATCACATTGTATGAAGAACATGATGGTCACTAGTAGGTAACCTTCTGTGTCATTGCCT TACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGATCACCAGTGAATCTAAATAGT GAAAAGGCAATGATGTCTCAGTATCACTGTGAAAACATTTTTCJCTCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACAGTCAAAAAACACAGCCC

WI-19673a	35	G A ---	---		TCTGCCATGATCACATTGTGATGAAGAACATGATG[G/A]TCACTAGTAGGTAACTTTCTGTGTCAATTG CCTTACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGCAATCAACCACTGTAATCTAAAT AGTGAAGAGGCAATGATGCTCAGTATCACTGTGAAACATTTTCCCTTGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGTCAAAAACACAGCCCC
WI-19724	35	A G ---	---		TTTATTGGGAACAAAGGATTGTAATTTGGGTAA[G/A]GCTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAAAACAGAGATTGTTGGTTTTTCCTT
WI-19307	196	T C ---	---		TCCTCCTCCCCAACTAGATGGTATTGATCACTCTGCCACAAATGGTACCCCCCTCAGCAAGAACTG CAAGCCCTTCTTGGATTTGCCCTCATGAGAAATGGTGGCTTGGATGGAGGTGACATTCCTTGTCTGT GGTGAACCTGCAAGAGGAAACCAAGCAATGATTTCCATAGAGGCTTTAAAGAGACCCG[T/C]TGG AAATGGGCCATGGTCTAATTTGGTGTGAAATAAACTAACCTCTTTGGCTG
WI-19269	85	A T ---	---		CTTCCCTCATCCCTCTCCACACACCATCCCGGAACAAGTGCTCCAGGATTCCTGCCCACTGGC CATTTTGGAGTGTCC[AT/TT]GGGTAGCAATGTGGAACACCAAGGCTTTGTGGAGAAATGG AGGGGTTGAGGAGTCCAGGAGGGCTTATTTGAGGGCTTTGCCACTTGTCTCATAGGCGAGCTCG ATCTCTCATCATCTGGACAGGTGGAAGCGAATTTCCCGGGCGTAGGCA
WI-19946	122	C T ---	---		CAATGGACTGAATGAGTGGTGGTGGGTGGGGGCGACACACACCTTCAATACACGTCAAGGTG CTTCCAGTTT TAGAAACAGAAATCTGCATCTCAGCCTGAGACGCACAGAGAGGT[C/T]CTTCCCTG ACCCAGACGCACTCAGGAGCCAGGTCTGGTTTCAAACTGCATTTAACTGCGCCAGAGAGTTCAAC CGTAGGCATCTTTAATAAACTAACCTCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141	G A ---	---		CACAGCATGGTGAATAGCATCAGATTGAATGAAAGTTTGTAAATGCAACCAATAAATAATATA ATAAATATACATCAAGTAACCTTACAGCACACATTTTGGGCCAAGTTTGGATCTGTCTGGACCT CAATGT[G/A]CTCTCGGAGAAGCAGCCACGTTAGCAGCAGATACCTTACAGCTTGTCTACTCAA GTGATGGCCCAACAGAAGCTTCTGAACTCCTCTGGGGAGGTAGCTGACAAG
WI-19076	40	G A ---	---		TTGGTTGGATACTTGTGGAAAAAAGCAGTTTAAAT[G/A]GTATTCAAAATACCTTTTAAAAA GTATTCTAGCACAAAGATTTTCTGTAACTAGATTATGTTGTAACATTTTCTTAAATCTTGTAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATTCCTATTCCTATCTGCTCCTGAAACCACTGCAGA AAGGCATTTGAAAGCTGTTCTTTAAGATATGGGATTCTTTTATTCTT
WI-20218	26	T C ---	---		CCACACACTCTGGTTTTATAAAGCTA[T/C]JAGGACAGAGCAGAGATGGAACCTGAAACACAGGTAG AAAATAACATAAATTTGAGGGGAACAGTGGGATGCAGAAAGAATGACAACAGCCACATGTGCCCCA GTCAAATACTTTTAGTCCCTGCAGCAGAAAGATGCCAACCAAGTCTCTATAGTGGCTGGGATCCTGCC ATGGATGCAGGAGAAAAA
WI-20295g	154	T G ---	---		CAACCTTTTGACAAGGGGACGTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATTCATAATTG GGAATTCTCTTTTAAATATCTCAGGCTTGTATTTGGGAGGGCTGGGCTCTACCCCTTCTCTTCCCA TCCAGTCTATTGCCAGAT/GCCAGAGAAAGCGCGGGAAGCCAGCTCTCCAGCATAGCCACTGTGG GTCCGCTTCACCTTCTGTCTGACTCTCTCATGCTGGGACTTGTCTTCGGGG

WI-19066e	147 GC ---	---	---	TGACAAGGGAGAGAGGAAATTCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCATTAAACCCATGAACCTTCAGCTGATC[G/A]TCTTAGCCAGTCCAATCTCTACGAGGAAC CATATGTTCTTG[C/G]CTTGGTCACCTGTAGCTGAATTACTTCTCCATATTCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCTTCACTAGTTCTTTTAA
WI-19066c	100 GA ---	---	---	TGACAAGGGAGAGAGGAAATCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCATTAAACCCATGAACCTTCAGCTGATC[G/A]TCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATAATGTTCTTGCGTTGGTCACCTGTAGCTGAATTACTTCTCCATATTCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCTTCACTAGTTCTTTTAA
WI-19066b	87 CT ---	---	---	TGACAAGGGAGAGAGGAAATCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCATTAAACCCATGA[C/T]CTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATAATGTTCTTGCGTTGGTCACCTGTAGCTGAATTACTTCTCCATATTCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCTTCACTAGTTCTTTTAA
WI-19066a	72 CT ---	---	---	TGACAAGGGAGAGAGGAAATCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGC[C/T]TTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATAATGTTCTTGCGTTGGTCACCTGTAGCTGAATTACTTCTCCATATTCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCTTCACTAGTTCTTTTAA
WI-20660	105 GC ---	---	---	TTTACAGCGAGTTTTCCCGTCAATAAGTATGAATCAATAGATTAGGTGAAAGAAAATGTG TGCTAAATAAATCTCCCTTTTGAATGATATTTGT[G/C]TTAAAGGGAAGCATTAAATATTA CAGACATAATTACAAGGTTCTGAACATGAGTGATCCACTACTGTTTCTGTACAAGATAGAACAAA AAGCTATCCACCCGCCCCCAAAAATACTGTTTAAACAACACTATGTTTAAAGA
WI-18768	120 CT ---	---	---	CTGCTGCCAGCTTCTCTTGGCGCTGCTCCAGATGGGGTCTCCTGGCAGCCTCCCTCAGTCTTCC TCCACCGCGCTCTTCTTCCAGCCTGCCTGCATGTCACCGCTGG[C/T]TTCGGCTCCATCGCC TTGAAAGCTCTGAA
WI-19087	37 AG ---	---	---	TTCCCCAGGGTTCTGTATTGCAGCTAAGCTCAAATG[T/G]TATTAACTTCTAGTTGCTCTTGTG GTCTTCTTCCAATGATGCTTACTACAGAAAGCAAATCAGACACAATTAGAGAAGCCTTTTCCATAAA GTGTAATTTAATGGCTGCAAAACCGGCAACCTGTAACCTGCCCTTTTAAATGGCATGACAAGGTGTGC AGTGGCCCATCCAGCATGTGTGTCTCTATCTTGCATCTACCTGCTCC
WI-18790	49 AT ---	---	---	GAAAGCCAGAGATTAGCCCCGCAATCCGCGATCTGTCAACAGGACAGAA[T/G]GATGGACAAGGGA TGAGCTTTACAAAGATGATGCACITTTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACA CAGTGATTTGGGAATGCCT
WI-18987	35 GA ---	---	---	AGGAGGCTGTTCCAGGAGTCTGCCACAGCCTC[G/A]GTGGCCCAAGCCAGACACTCACCCACCTT CCCCAGTGGCCCGTGGATCCTGGTCTAGGCTGGACAGGATTCAGAAAGACACCCAGGCTGCACA GAAAGAGCCAGATGGACCTGAGTGTGGTGCACAGCCCCCTACACTCAAGGCTGAGAGGCTCAGGAA AGTCA

WI-19236	54	G A ---	---	TACACAGAGGGTGCACCTTGGAAGGCTGAGGGTTGGGTGGAGGGGAAAGG[G/A]GATGGAGAC CTGCTCCCCAGCTCTTCTGTACGCGGTTTACATGGGAACAGGGTTAAACATCTGTGTAGGGGAGGT CACCTTACCCCTTTTCATAGGGGAAGAGTGCACACTCTCTGGCTATCTCAGGGGAATGGGAAAG AATCTTTCAAGGGCAAGAACTCGTGGGAGGATGCTGTGTATGTAATACT
WI-19144	222	G C ---	---	GTGCCAGTCTTCCAGAAAGCAAGGACTGCCCTTCATTACGCTTCTGACCTCCAGCCCTTCTAAGG CTCAGCCCCACGGGACTCTGGTGGCTGCCAGCTTGTAGCTATCTATCTATATTCATTTCATAGCCAA ACAGGAGACCCCTTTGCAGGACTTGCACAGGGAGGCTGTAGCCAGGAAACCTCTCTTCCCTGGT CTGGCTCTGCTGGAGCG[G/C]TGGGAACCAACACCTTCAGTCTGGTG
WI-19139b	110	C A ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACAGAGGGTAGAC GGCAGATGCCTGACAGAGAGTGGTTGGCAGACAACACACTAG[C/A]ATTTACGGGTGTGGGCAC ATGGTGTGGCACCCTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGAAGCCACCGTCTCTCTTTGG GGGGCCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-19139a	66	C T ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACAGAGGGTAGA[C C/T]GGCAGATGCCTGACAGAGAGTGGTTGGCAGACAACACACTAGCATTTTACGGGTGTGGGCAC ATGGTGTGGCACCCTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGAAGCCACCGTCTCTCTTTGG GGGGCCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-18910	112	T C ---	---	GGCTGGGACCTTTAGGAAAGTGAATGCAGGTGAGAAGAACCTAAACATGAAGGAAAGGGTGCCT CATCCAGCAACCTGTCTTGTGGGTGATGATCACTGTGCTGTG[C/G]GGCTCATGGCAGAGCAT CAGTGCACGGTTTAGG
WI-19235	173	A G ---	---	TTACAGGAGGTGGAGTTCGTGCTAGCTCTCTGCTGTGATGTGGAAGCTTCTGATATTTGAAGAAACA CGAATGTCTCTGTAGCTTCTCTTCACTGCCCCAGTATTGCTCTGTATTTATCAGCGATGCCCTCTGT CACTCATGCCCTTGCCTAATTTGTTCAACAATGGTGGAA[G/G]CTTTCATGTAATATGATCAGGACCCACC TCCAGTTCTTCTGAAAGTGTGACAGTGTCCAGCCGGTTCTGACGACTA
WI-19222	179	C T ---	---	CGTTTTCCCTAACTACCCAGTTTAGTTGGGATGATTGATTTCTGTTGTGTGATCCCATTTCTAA CTTGGAAATTGTAGCCCTCTATGTTTTCTGTTAGGTGAGTGTGGTTTTTCCOCCACCAGGAAGT GGCAGCATCCCTCCTTCTCCOCTAAAGGACTCTGCGGAAC[C/T]TTTCACACCTCTTTCTCAGGGAC GGGGCAGGTGTGTGTGTACACTGACGTGTCCAGAAGCAGCATT
WI-19117	134	A G ---	---	AAATAATGCAACGCGAGGAGGAGAAAGAAATGCACCTAAGACAAGAACATTCCTCATAGAACATTG ATCTGTTTTACAGGAACAACCTTGCCTTGAATTTACACAGTGAGACTGTACATAATTGCATGAA A[A/G]TAGCTATTTTTCTCTAAGACATTTTTCATTTCATGAATATTTCAAGTTTTTCATACTGTACA CATTCTTAAACACATGATACCAGCAGCAACTGAAATGAATGCCGGAATTTG

WI-19134c	263 C T ---	---	CTCCTGTTGCTGACCTGACAGGGTGACACAGCCCTTTACACTCTGCTCCTCTATCTTCTCGGTAGA TGCCCTGGGTAGGGCTGAGTACTGAATGGTCTTCCATCCCCAGCAAGGGGTGAGCCAGGCTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGACAGGTGGCTAGAGCCAGCTGCACTATCCTTTTCAGAGCAC TTATCCACTTGGCTCCTCCCTACCCCTCGGCACCCCTGGGTGGAAAGGG
WI-19134a	162 T C ---	---	CTCCTGTTGCTGACCTGACAGGGTGACACAGCCCTTTACACTCTGCTCCTCTATCTTCTCGGTAGA TGCCCTGGGTAGGGCTGAGTACTGAATGGTCTTCCATCCCCAGCAAGGGGTGAGCCAGGCTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGACAGGTGGCTAGAGCCAGCTGCACTATCCTTTTCAGAG CACTTCATCCACTTGGCTCCTCCTACCCCTCGGCACCCCTGGGTGGAA
WI-19224	112 C T ---	---	GGTTTACCAGTCTTCCAGGGAACTCCGATGAAGTGTCCAACAAAATGAGCGAGTGAACCAAGA AGAGGATGACATTAGATCCAGGAGATACACAGAGGAGATAATCTCTCAGGATGCCTGTGAAGA AAGATCCCTGGATCCAGGATGATTATAGGACAAGTTGTTTATATATCCAGAGCCAGGAGCAAGACTTCC AGGGAACCTCATTCAAGGAGGTGAAAATGATGGATGACTCCTCCAGATGAAAA
WI-19201	179 T C ---	---	GCAGCTCCTAAGGAOCCACTGGCCATTAGCTCTTGTCTTGTGATGGCATCTCTTCCACCTTGTCTCTC CTTTGCTCCTCTGTGTAGTGGCAGGTATGACAACTCATCCAGTGGAAACACAGAGCCCTCACACTGCC CTTCCGCCCCCACCACACTTTGCCCTGAGGTGCACCGAAGGACCTCTGTTGGGGGATAAAATCAAAAAA GTGTGATGTGCTGCTCAGAGGTGACACTCCATGTCTGCTCTGGCCTCAA
WI-19034	45 T C ---	---	GAATGGCTCCACTCAGAGCTACCCCGGTGATGAGGATAGGGGAATCTTCTTCTTATACATTAAAG GCAACAGCAGTTAGTAAAGGTTTACAGTGTCTGCTGTTGAAAGTGCAATATAAAATTTTGTG CTAGCCCATGATCAATCGACTCTATTGTTTGTATATACACTTCAGCATTTAAGTCTGTGCAATTGAC ATTTGCTACTTATAAACTTAGTCCCTAAGTCTCTTATGCTGTGCTATATA
WI-19102	25 C G ---	---	TGTTCTGAGTCACGCTGAGGAGAGCTGCTTCACTCAGGAGTTCATGCTGAGATGATGAGTTCATCA TGCGACGTATATTTTCCCTTGGAAACAGAATGAAGCAGAGGAAACTCTTAATACTTAAATCGTTCT TGATTAGTATCGTGAGTTTGAAGAGCTAGAACTCCTGTAAAGTTTGAAGTCAAGGGAGAGGATAT AGTGGATGAGTGTGAGCATCGGGCTTGCAGTCCCATAGAACAGAAATGGG
WI-18548b	65 A G ---	---	AAAGGAGGGAGAACTCTTTTACATAAATGCCTTGCATCCTCCAGTCCCTCACTGGGGGAATV GIAAAAGCATCTNCAAGTCTTTGTCCAACTTTGGCTGC
WI-18548a	62 G A ---	---	AAAGGAGGGAGAACTCTTTTACATAAATGCCTTGCATCCTCCAGTCCCTCACTGGGGGAG/AJA AAAAAAGCATCTNCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97 T C ---	---	GGCAGCAGCTTTTAAATTTGAACACTTTCTCTTGAGGACACACCTTCAGTACAGTTAACAAATGGT TACACCTGAAATCTGCTGAGAGCAGAGCTTTCJAAGATCCAAATTGCAAGGGCCACTGCTGGCTCA CTTCTCTACA
WI-18501	121 C T ---	---	CAGAGGGGAAAAGTTTATTGAGTCAGCCACAGAGGAACAGAGAAACAGACACAAAGGAGGTTCTGTGT GCATGGAGGAAATCAGGGCGCGNACAGCTGAACCTGCGCAGGACAGAGGGCGCTCTGGACAGCA GGCATGCCACAAACATTCA

WI-18017	87	C A ---	---	ACAAAGAAAATGAAATAGGTTGCGAAACCTTATCTGCATGTACAAAGTAATCCCGTAGATAA GGAGAGGCAACCCNGGAACA/C/AJACTGCTGGATAAAATCGTTCAATTAATATCTCTTTGCAT CAGAGCTGGTGGAAATCAT
WI-18148b	101	A G ---	---	TATTCGGTTCCTCGATAACCTCTCTTTGGGACTATGAGATCATCACCAGATGTGAAACGAAAGCA GTGATTTCAGAAACCNCGATTCTGAATATCCC/AJGTTGGCGCATATGCAAGGAAGATGA
WI-18254	64	T C ---	---	TATACGGATCATGTATTTGTGTGACCACTACACAGTCAATTTGTAGAGCAGTTAAATCAC/T/C JGCCAAATTCCTCTTGCTTCCTGTAGTCAGTCTCTCCCAACCCAGGNACTTGGCAACCTGTTT TCCGTTCCCTAGACATTT
WI-18265b	117	C A ---	---	CAATGGTGGACTGAGTGATAAAACGCATATTGAGAACAAAGACGGCCTTCTGGCCNCTCTGCGTCC AAGGCTGTAAAGGTCTCAGGATTGCTGCTAAGTGAGCCATGAACCTGGCTG/C/AJGTTTTCAACCTTTTC CTTGGGTGGTTCTTCAG
WI-18295	40	C T ---	---	ACCACACATTTGTTGAGAGCCTATTGTGGAGAACAAACAG/C/TJTTGGGAAGTAAAGGTTGATTACT TCCTCTCCAAGGATGATATGTTTAATGAATTCCTTTNCCCTAGCTTCATCTTCATAATGCCAAA
WI-18459b	64	T C ---	---	GGGCAAGAGACAGAGATTTAATTGAATAAAACTCCAGGCTGTGACACGGGTGGGAGACACAAAT/ CJAGTAATTAAACAACATAATATTTANATGACAGTGCAATTAATTAACTCCTGGTAAGCCAGAG GGGAGGAGGGCGTCTTCA
WI-22585	56	A G ---	---	TTTATTTAAATTTGCATCTGAGATAATAAAATTTATCTGACAAGTGAACAATG/AJG/CAGAAAGC AGCAGTGAAGTTTCGGAGAGGCGAGGTATCCTTCATTTTGGCAGAGCTGTATATAGATTGA
WI-21155	36	A G ---	---	GGGCTGTGGAGTAACAGAACTTGATGGAAAATTTGGC/AJGJCTGTGTAGAATGATTTCTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88	G A ---	---	GCCTTTGCTCTTTGCTGCTCAGAGGCCTCAGATGGATACGCAACCTTCTTTTGAACCTTTTAT TTTCCTGGCAGGAAGAAGA/GA/JGGATCCAGCAGTGAGATCAGGCAGGTTCTGTGTTGCACAGACAG GGAACAGGC
WI-19888a	98	C T ---	---	GGCAGGATCAACCCATAACAGAGAAATAACTCCTTATTGGAACAAGGTTTTTATTTGATATGATG AAATATTTTGGAACTAGAAAGTAGCAGTGA/C/TJGGACAACGTTGTAAAGATATTAAATGCCACT GAACTGTTCAITTTAAATGGTAATTTCAITGTTATGTGATTTTCCACCTCAATTAAAGAATGGAACATGT CTTATAATTGTAATACATGAGANCATATTTATGTTGGAAGTGAACACAAG
WI-21485	82	C T ---	---	TGAGACCATCCTCCTCAACAAAGATCAGTCAGTTTCAGCACTAATTTTCCACACTGAAGTCTACG CAATTTTCATGCAGA/C/TJGTGCACACAGTACAGTGCACAAATCCAGAGGGCAACACATTTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125	T C ---	---	TCAGAATTGCTTTCCACTGCCCAACCAACAAAGAAATTTAATGAATGCNCTTACAATTGAGATGACTT GAAGTTAAAGAAAGGTACCTTCTTGGAGGTTGCATGACAGGATTAGTCTCTCTGTTT/CJCTTGGT GCAAGTTTGAACACAGTATTATGATACCATTCATGATCAGAGCACTGTTTCCCTGTCAGATCCCCACTAG

WI- 20561b	94 T C ---			CGTTGCTTATTAAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTATTG TACTTCAGATGAAAAATCCTTACATGTC[G]GGAATCAATGTCTTTTAAATTTTCAGATAAAGAAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20561a	25 A G ---			CGTTGCTTATTAAAGATGGCTGTTT[G]GTAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTAT TTGTACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTTAAATTTTCAGATAAAGAAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20116e	69 T A ---			GCCTTCATTTTCTGCACCCACCCCTGTCACCCAGTTATGTTGGCCTTCAATATATGGCGTTAGAACAT AAT/AJATAAATCTATATCATATATTTATACACACAAACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGCTCTCCCATGCCACTTAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20116c	59 T A ---			GCCTTCATTTTCTGCACCCACCCCTGTCACCCAGTTATGTTGGCCTTCAATATATGGCGTTAGAA CATATATAAATCTATATCATATATTTATACACACAAACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGCTCTCCCATGCCACTTAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20116a	22 C G ---			GCCTTCATTTTCTGCACCCAC[C]GCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAA CATATATAAATCTATATCATATATTTATACACACAAACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGCTCTCCCATGCCACTTAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20466b	133 G A ---			AAAGATTGCAGTCTCTGGGACACAGTTTGGAAACACTATTTATAAGTTGGCCTTCAATATATCAAAACAG NTCCCAATGGTGAACTGGTATTTCTAAGATGAAAGCTTAATGAACATAATGAAGTGAATAAACGCJ G/AJGTGAACATAATGTTTAAAGTTAGAGCTTGCTCAAGTCAGTACAGCTCTTAAGATAATAAAT ACAGTAACTACTACTTTTATTTCTTGGCTTTATCCCTTTCAGGTTGATT
WI-21444	39 A G ---			CTGGGACGCAAGTAACTATTTAAAGAAATCTCTCAAC[A]G/AGTTCTTTTATGGGGTATTTCA GTTGTTAACAAAGTTAAATCTTATTGGAACATAATCTTTGTATTTTTCGAGGAAGAAGAAATCT ATAAGATTGACTTACTACTTGTGACTGGTTTTCGAGGCTTACTGGGG
WI- 21034b	148 T C ---			AGAAATGGACAATGATGCAGATGATTGTGAGCATTTTGTAGATAAAGTGGTGTAGAGGATACAG CATAAATTTAATTTGAACATGCTTATCTAGCTAACCTAATCTGTTCTGTAGAAATCTGGTCTATGG GAGATTGGATAGAT[C]GCTTAACCTATCTCAATTTTAAGTAATGTGAGCAA
WI- 22091c	205 G A ---			GGCGTATTGTGATGCAATGTCCAAACCAGTCAAGCTATCATTTGAATCCAAATATTTCCAGTAGAG ACATGCAGAGCAATGTCAATGTAAACATACAGCATATTACCTCCCCCTTAAGTGACTCATAATTTTC ATTACTGTGTGTAGCTTTTAAAGGTTTAAATGTGTAGCATTAAAGTGGTATTACTTGAGGGCA ACA[G/A]AATTACGGCTTAACAACACACTAAATCATGAGGCTCAGGGATTG

WI- 21805a	45 A T ---	---	CAACTGCTCTGAGGCTTTCACTAGCTGATTTATAATCCTATATTATJAAAAAAAATCTATAGTCTG CAGTCTTTGACATACTTCTCAAGGGTGGATATGTGGTGAATGCAGACTCCATCAATATGTGGT TTGTTGCTTTTGTAGCTTAAGTCTGTTTAGNAAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTCATAAAATTCGAACAGTTGAAGGCTGTTTGTAAATTGCTG
WI- 21778b	155 T C ---	---	AAAAATCCATAATTATTGAACCCCAAGTTACAGAGAAAGTTCGTAACCTTTTATTGAATTATTGAC TCTGCCCGGCTGCTGCTGCTGCTTCAACTCCAGTCTGTCATGCCCCCTGTAGGTGGGGTCCCCAG GTCTGGGCTTCTGAGGCTCTCJGGTAGAAGGAGGGCAGGTGGT
WI-20907	241 A C ---	---	TGAGTCAGTGGTCAGATGGGGCAGTTGCGCTCAGCTGCAGTCCCTGACTCCGGAAACACTGTGCTCT CAATGATCTAGAGCTCATCTTGGGCGTACATGAGGGCAGTTGTTCTAGTACCCATTTAGCC ATGGCTCTCAAGCCAAATTCACACTGGGAAACACACCCCTACAAGATGCCTATCCATTTGAGTTC ATACAGGTTTGTAGTAGTAGTAACATAAAAAACATTTTAA/CJAAATTATCTA
WI- 21449b	222 C T ---	---	AACAGCAGCAGTCACCTTCCAAAATGCAAAAAAATTACAATTTTGAATAAAAAATTATAATGTTTA TAATGCGGGTCAGAAAGANTGAAGGTACACAGAAATCAACGACACTGGAGCGGCTGGAG AAGCCAAAGCCCACTGTGTCAGGGTCCAAAGCTGACAAGAGTCCCAACCTGAGAGGCTCTCCACACCC AATCATACCCCTCAGCTTCCCA/CJTTGACAGAGCCAGTCTCTGGGTTAG
WI- 21558a	157 G A ---	---	GCTTACAAGGAAGCCTGTGGACAGGCGAGNTGGTGGAAACCGACTCCAGCCTGGAACCTGCCCTC CCATCCCCCTTAGCGCTTCTGGCCTTCCGGCTGATTTCTTCGACAGCAGTTCTGGCCAGGGCAAGG AGCTGTGGTGGGGGCGAGTATG/AJAGCCAGGACTCCCTTCCACAGATGAGGCCCTAGGGCTGCAA AAGGGCCCGTGAAGAGAGATGTGGTCAAGGCTTTATGGGCTCTCCACC
WI- 22187b	178 G A ---	---	TTTGCTGTGAATCCATGAGAGCCGGAAGCATGTTGGGCGCTGGCTAGCAGAGCTCATGGNGACCA GTCCTGGGCGCTGACCAATGGGTGATTACATTTAAAAACCAAA/CJCAAAAAACAAAAATACCAAGA ACAGATCAGTTGCCATGGACATCAGTAATCTATTGGTAATGGTG/AJAAATTTTCATGAAAAATTTCC CCTAAACCATAACAAAAACTGTCTCTCTACCCCAAAAGTCTGGAGGAAAG
WI- 22187a	110 C A ---	---	TTTGCTGTGAATCCATGAGAGCCGGAAGCATGTTGGGCGCTGGCTAGCAGAGCTCATGGNGACCA GTCCTGGGCGCTGACCAATGGGTGATTACATTTAAAAACCAAA/CJCAAAAAACAAAAATACCA AGAACAGATCAGTTGCCATGGACATCAGTAATCTATTGGTAATGGTGAAATTTTCATGAAAAATTTCC CCTAAACCATAACAAAAACTGTCTCTCTACCCCAAAAGTCTGGAGGAAAG
WI- 21609b	146 G A ---	---	TCATGAATATGCAGCTCCATAATCTTCTCCCTTGTAACAACGTGCAGTCCGTTACAGCTGTAAA AACAGCCCCAACCCAAAGACATCACAAGAGGCAAGAGCTGGCAGTGAGAAGGGAGCCTGTAAAG GATGTTCAAAG/G/AJAGGGTCCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

WI- 21609a	42 C T ---	---	TCATGAATATGAGCGCTCCATAATCTTCTCCCTTGTAAACAAAC/CTGTGCAGTCGCTTACAAAGCTGT AAAACAAAGCCCAACCAAGACATCACAAGAGGCAAGCAGTGGCAGTGAGAGGGAGCCTGTGA AAGGATGTTTCAAGAGGGTCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI- 22512a	104 T G ---	---	ACATTCCGAGCCAGTTTTTCCATATTGCTCCACTGCCTAAATCCCTTGGTGCCTCCCTAGGGCTTCA GGGTAAGCCCTGACATCATGGTCTTTTGTGATCTGTG/ACCTCACCCATGTCTCCACCTNAGTTCC CACATTTCCCCACGCTTAAGGGCAGGCAGCTACACTTGACTGCA
WI- 21028b	139 A G ---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGTCCCTTTTAAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCTGTGATTGAGCAATCTAGGGGATATGTACAGGGG TTTC/A/GTGCAGTGTACAGAACACACAGGGAGTTTCACAAATTTTTTATACAAATGCTTGGGAAT CTACGG
WI- 21028a	121 A C ---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGTCCCTTTTAAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCTGTGATTGAGCAATCTAGGGG/A/CJTATGTGACAG GGGTTTCATGCACTGGTACAGAACACACAGGGAGTTTCACAAATTTTTTATACAAATGCTTGGGAATC TACGG
WI- 18829d	58 A G ---	---	ACAACATGCTGTTTACAGGGGGGAAAAATCCTAGGNAATAACTTATGTGTACTTCTTG/A/GJTTC TCATACAAGACAAAGCACAAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI- 18829b	35 T A ---	---	ACAACATGCTGTTTACAGGGGGGAAAAATCCTAGG/A/ATAACTTATGTGTACTTCTTGATTTC TCATACAAGACAAAGCACAAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI-20964	87 G A ---	---	AGCCAACTCAAGGCCAAAAAATTTCTTAATATAGTTATTATGCGAGGGGAGGGGAAGCAAGGA GCACAGGTAGTCCACAGAATA/G/A/GACACAAAGAAACCTCAAGCTGTGAGGTCAAATTTGTAAATTA AAGAATACTAAGATTAGATGAACACACACTCAGAAATACTCTAGGAGAGCTGAAAAAGAAAGGAAC AGATGTTAACAAAAACAAATTAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI- 20059a	59 T A ---	---	CTCTGAACATAAGGGCCGTGAAGGCATGATTGGTTTTGGCACACAGAGTGGATAACCAAT/AJACAT TGGCTGGAATGAGGTGGTCAGGAAATAAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA GTTCTGGAGAAAGTTAAAGTGTAATAATTACAAAGACTGACATGCAACTCTTACCTTACATTATT CATCTACAGACTATTTCTCCCTTAGGAGATGAGGAGTATGGCCCTTAGGT
WI- 22130b	165 C T ---	---	TGTTTTGAGGGCTGTAGCAGACTACATAATGAGCGGTGAAGCGGCTGCCCTCCCTCTCTCTGACAC CAGCAAGGGGGAGGCCACCATCACCGGCCCTGCCCATCATGCAATCAATGATTACTAGCAGCTAGGAA GCCAAGGGAANAGGACCCCGCGCTTGCTTCTGTTTAAATCCAGGTTAAGCTATACACCGTTTAA ATACATGTCGGAGGTTACATGGTCTCATGCAAGTCCCTCTGTGATGGGAATGAC

WI-21661	117	G C ---				GCCTAGTCTCCACCCCTTTAAATGTACTGTAGGTACAAAATAAACATTATACACATATAAGATCAGT CTTTCCAACTTTAGAATGTATAAATAAGAAATGACATTTTAAATAAAAATA[G/C]TTTAGTCACAGTC ACACAAAACACTACCTTCTAAGGAAAACGTCCAGTGAAGCCGTTAAATTTGTGCTTTTCAGCTATGAAG GA
WI-21980a	25	T C ---				TCAGTTAAACACATTTCATCAAGGA[G/C]AGATTAAATTAATGTGAGGTGAGCATAAAAGGGAGATTA TAAACCAGAAAATGTGTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTTATTAATTTTCAT GGGTGAAGCCCTCGGATAAAG
WI-21636	71	A G ---				TGCTTGATTAAATGTGGTGTTCACATTATCCTATTTCACAGATGGAACAGAAAATACCAGCTTTTTT AAI[G]TAGCAATATCTATTATAATAAATTTGAAATAACACCATATAATATCACTAAGGA AGTAATCTAATTGTGTTGATTTGCAGAGGGGAGAAAACATTACCTCTAGAGCTGAGGCTATTGTGC TCATGCAAACTCCAATCTGAAGGTGGTAGAAACTAGGAAGGGACAGGGATTTC
WI-22457a	112	G A ---				TTGCTATAATTTCCTTAAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAATCACTCATTAGA CAACAGTAAACATACTGGACACGGTTTCAGGCATGAAGGATACA[G/A]CAGTTAATTAACTAAAG GAACAGAGTCCCTGCATTCCTGAAGCATAGGATGGGAAACAGTAATGCAGATTAACTACCTGGGGCC AAAACCACTGAACCTCACCCAGCTGAAAACACTGAAGGATACCTGGGTAAAGGA
WI-21524b	97	C T ---				GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATAGCCTGATGTACGACCTTCGCGTCATCTTAT AATGGTTAATAACAGCATTCCTGTCTACCC[G/C]TGATGATGCTTCTCTCGCAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAGAAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCAGGGGATG
WI-21524a	35	A C ---				GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAAT[AC]GCCTGATGTACGACCTTCGCGTCATACT TATAATGGTTAATAACAGCATTCCTGTACCCCGATGATGCTTCTCTCGCAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAGAAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCAGGGGATG
WI-22652a	32	G T ---				TTACCTTCCAAAACCCAGGCCACTTTGGAGAAAAG[G/T]AAGAGAATGCTATTAAATCAATAAGCCAAAGAC AATAGGGACTACCTGGGTAGACCAAGATGGGCAGTCACCATACACCATCATTCCTGCCACAGAACCC TTTGACATGCTGCCCTCCCTACTCCGCACCTCACCTGTCTAATTTGGACCTGAAGCTTCAGCATCCCTT CTTTAGGG
WI-21703d	197	A G ---				CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGCAGGGCTC TGCAATCCCTTTCTCAGCACAGCACCATCTTCACCCCTCTGGGAAAGCAGCATTGGAGCCTACACCA CTTGCTTTTCTCACCAGGGTAAGAAATGCAGTATTTCAGAGGGGAGTGAGTCTGGGA[A/G]G TGGGCAGAGCAGACTAGGGGCAAGGACTTAAGGGAACCTTTGGGGGAAGAG

WI- 21703c	134	A G ---	---	CAACAGGCTCATGGAACAGAGCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGCAGGGCTC TGCATCCCTTTCTCAGACAGCACCATTTCACCTCTCTGGGAAAGCAGCATTTGAGCCTACACQ A/GCTTGTGCTTTTCTCACCAGGTAAGAAATGCAGGTATTTGCAGAGGGAGTGAGTCTGGGAAAG TGGCAGAGCAGCAGCTAGGGCAAGGACTTAAGGGAACCTTGTGGGGGAAGAG
WI- 22663c	139	G A ---	---	CCCTTGTGAGTCTGTGCTCGGCTTCTCACTGCAGTGGCAGGTGACCGGCGCTCGCTAATCTTATTC CCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCAGCTGGTGCACTTACAG GC/GA/GAAGAGCTTCTCATTTGCTGAGGGCTTTTCCGTGAATCCGTGTGAATGTGGGT
WI- 22663b	55	C T ---	---	CCCTTGTGAGTCTGTGCTCGGCTTCTCACTGCAGTGGCAGGTGACCGGCGCTC/GCTAATCTTA TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCAGCTGGTGCACTTAC AGGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCCGTGAATCCGTGTGAATGTGGGT
WI- 22663a	38	C T ---	---	CCCTTGTGAGTCTGTGCTCGGCTTCTCACTGCAGTGGCAGGTGACCGGCGCTCGCTAATCTTA TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCAGCTGGTGCACTTAC AGGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCCGTGAATCCGTGTGAATGTGGGT
WI-22668	99	A G ---	---	TCTTTTATCTGCTGCTGCTGAGTATTTCTGGGAATCTACAAAGATTTGAGGGAGCCCTTGGGATT CCAACTAACAAATTAGTTTCTGTAATATTGA/GTCTAGTCCATTTAGATTGTGTAATGATCTAA ATGNGTAACCATTTAATATCAAAAGTATAACAGCATTTAAGTCAGCTTTTGAAGAAACTTTTATT
WI- 22631a	52	T C ---	---	AAGATATAGTGGCAGGACAAGATTGGTCACGAAATCCCTGGCTTCAGTCTGAT/CJAGCACCATTTT CAAGTTTATAGGCAAGGTATTTAACCTCTCAGGCTCATTTTCTCTTTTGTAAATTTGTGATAATGGACC TATGTACCATCATAGGGTACTTGGACAAATCAACTGAAATTTT
WI-20258	157	G T ---	---	AATCCACACTTTCACGGAGGGGAACAGCCTGCCATGTCTCCAGGCTCACAGCAGCGGGGCTAC TCTGCTGGTGGTTTGGTGGCAGGTGGAGATGGTGAACGGCAATTGGAACCGTAAGGCATGACAACG GGAGCCCGCGGGGTGTTTCA/GTJCGCGTTGACGAGGTGCATGGCTGGCAGCGGGCTCTACAGA AGGAGGGAGCGCAATTCACAGCCTCTTGACGTAGTTTCCGGGGAAGTACC
WI-22714	212	C A ---	---	ACTACACATATGCTGATTTTCAACAGTAAAAATAACATTTTACATTTGTAGAGAAAATCTAGGGTCT ACTAAATATCTAGTACTTGTTCACCTCTCTGCTAATCTGACAGGAGTGTGTGGGAAACGAAAGT CTGAAAGGATTCAAAGGGGCTAGGATTTGCCACAGATCCTGTAAAGGAAAGGATGAGGTGAGCTT ACCAACCCCA/C/ATGAGTAGGGGGCAAAACATCCTTAACAAGTAGTTGCT
WI- 22734a	44	G A ---	---	TGGGGCTACTTTAGATGGGATGGCGTCAGGGTCTGGGAAGGCCTG/ATCTTTAGAAGACATTACCCA AATGATGAGAGGCCAGCTGTCGAAGCCATAGTTTGGATGGCGAGACTTTTCGGGCAGAGGAAAT AGCAAGTGCAAGGGCCTGAGGGAGAAATGAACCTTGGGCTTGTCTACAGGGTGAAGGGCGGCGGT NTGGCTGAGGTTTAGTGGATG

WI-22724	117 A G ---	---		TGATATGATGCTGAGATTGCTCCAAATATGCCTAGGAAGGGAAGTGTATTAGAGATATAGGA CAAATCAAGATTGTCAAATGTATAGTAAGTGTAAAGCTTGCTAAGGGT[A/G]GTTATTCTATTTT TGGGATATGTTGGGAATT
WI-22750	48 G A ---	---		TGTAACCTGTGTTTTCCTGAAAGTTGAGGGAAAGCTGAGGCAGCTAA[T/G/A]GGCTCATACAAAGGT TTGGAAGACCCATTCTGACTACCTAAAGGAGAGTCAGCATTCTGACCACTCTGACTGTGCT
WI-22775a	60 A G ---	---		TGCTGTTTCTTTAGTTTCATGACGTTTATCACAATGTGCTACTGTTTCCATTGTTTACATC[A/G]TAGTA GGAAGGGGAAATAAATCCCTAAGGGCAGCAATAATTTCTGCTTTGAATCCCTTCATTGAGGCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAAGTGGGATGAGGTATGAGGTGTTGGGAGCCAGGAAAGGAAG GGT
WI-22808	143 C T ---	---		CTTTAGCTAATGAAACTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCAAGTCCTGAGGGAG CCTAGTCTCTCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGCGTTTAGCAACCAGGA GGATGAAGA[C/T]AGCAAACTGATTAAAGAGAGTAGGTATAAGAAACCAAGGAGAGTGGGTCCAAAT ATC
WI-21016	207 G A ---	---		TCTCTGCTGCTTGAGCCCTCATCCCCACCCCTCCAAGCCCTCATGCCACACACCGTGTCCCACATT CCCCATCCTCCCTGCTGCTCCCATCTCAAGTCCAAATCCAAGGCCAGAGCCCTGGCAGCTTTTCTG GGAGACAGCATGAAAGGAGGGAGTGGAGATGGCAGAGATGGGTGGAGCCAGTGGCTGTGGGTC CT[G/A]TTGGCTGGTGTATGGGGGCCAATCTGAGGCCAGAGTTCA
WI-21031	31 C T ---	---		TTGAAACACTGACCTGACCTGACATGGG[C/T]CTCTGGTCCCCATTTGTCTCCACGGTGGCACA TCTTCATCTTTGTTATATATCTGCAGGAACACCTCAGTCTCTTCAGCAGCCGAGAAACACACACA
WI-21314	122 A T ---	---		CCATATCCAGTCTCTTTGAAGCTTTCTATTGACTTTTAGGGTTGAGTTATATATATCTTATCACTAT GACTTTCAATTTGATTTTATTTATTTGTTCTCCATTTCTGTCAAACCTTT[C/A/T]TTTGTATTATAA ACTGTTTCTAAACTTCACCTTAATCTCTATCTGTATTNCTTGTAGTCCCTGAACCTTCTTTAGAGG
WI-21186	95 G A ---	---		AGCGAGCATCAGAAATCACCTAGAGGGTTGACTAAACAGACTCTGGACCCAAACCCAGAGCTTCT GATTGAGTAGGCTGAGGTGGGCTTAC[G/A]AATTAGTATTGGAAGACCTTCCCTAAGTGTGCAG ATGCTGCTTGTCCCGGGGAACACACTTTGAGAACTATTGTTCTAAATGTTCTCTCTCTTTTAAA GGAGAGACAGGAATCCAGAGAACTGCTAATTTAAGCATATGTTGTAAT
WI-21187a	94 A G ---	---		CCACGATAACTATAAAGCAGAAATTAGCTTTGAAATCAAAATACATATTTAGTAACACACATT CATTTTTATAACACACATAAAGACACC[A/G]GNTCTCAGTAATGCTCTAGTCCAGGGTTCTCAA AGTATGGCTTCAGACAAGCCCCATTTGCATCACCTAGGGGAATTGCTAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAAACTCTGAGGGTGAGACCAAGCAACCTGT

WI-21190	39 T C ---	---	TTTTCCCCACATACCAATGCACCTGTTTGATATAAACTATT/CJGTGGGGTAAGCCCTCTTTGGAGAC CAGTGACATAGACATGATCCCATTTATTTAACAATAATATTATAATCTGTACTATTACTGC TTTAGTTATCTAGTGTATTGAGAAAGGAGAAGTCAGCATAGTTTATTTCCATGTAATAAAGCTT AACACA
WI-19937d	186 G A ---	---	ACCATGTGCATTATTGGCATAGGAATAGTGACCAAGAAATGCAGCANCTAAACTTGAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCAGCTTCATGTTGTCT GTAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTGTTCCCTCAGCAAGTC[G/A]TCCAAAACCTTC CAAAAGAAGCAGTCATTGAAAATGCTGACTTATGCATTGCGCTCAGGAAGAA
WI-19937c	185 C T ---	---	ACCATGTGCATTATTGGCATAGGAATAGTGACCAAGAAATGCAGCANCTAAACTTGAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCAGCTTCATGTTGTCT GTAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTGTTCCCTCAGCAAGTC[G]GTCCAAAACCTTC CAAAAGAAGCAGTCATTGAAAATGCTGACTTATGCATTGCGCTCAGGAAGAA
WI-2117b	227 C T ---	---	GAAAACGGGGTGCTAAACAAGAAAAGTCTCAGATCCCACTGAAAATCTGTTTCAGTTTTACAGGCTC TCTCCAGAAAATGCATATGTACCAATTTGCATGTACAAATTCAGAGCCTTCAAATACATTCCTGGGG TCCAATCAGACATCTCAGGTTTCAGACTCCTAGCTCCCAATATTCACAGTTCTGAAGANTTAGCAGT CCTCTCATTTCTACAGTCTGTTTCTTCTACTGAACTGTTGGTGGGAG
WI-21122a	42 C T ---	---	TCACITTTGATCATAATCCCTGTAAAAGCTAAAGTTATTCA[C/T]TAACAGGAAGTCTGTTTTTCC TTATTCAAATGTCACAAGCTGACGCTTACTGTACATATTGCTAGCAGGAGACAACTGGAAATACT AAACAAATACTGGAATTCACATTACAGACAGACGAAACCAACATGGGATGGCACACATAACTTCCT TTGTAGGTTTCACAGAGAGCCTATTTGTGGGTGCT
WI-21254	53 A G ---	---	CAGTTTGGTACAGGAAGGGCCCATGAATGTGGCGGGAACATTTCACAGGAG[A/G]CAAGGAGAAG CTGTTCTCTGG
WI-21054	23 G T ---	---	AAGGAAACTGCGATGGGTACAAAT[G/T]TCCAATTCATACTTAACAAGGTGGGGAACGGGTCAATTCT TGGCCTGCTCCAGAACAAAGGGCGAGTCTATGCACTCTG
WI-21059b	181 T C ---	---	GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGGTGAA CTACAGCTGCCAGCATTTCTGGGCTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTGAAA AATCCTGGGGAAGAGACATACTTCACTGAAGTCATTTCTATTC[T/C]ATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT
WI-21059a	63 C T ---	---	GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGG[C/T] GAACTACAGCTGCCAGCATTTCTGGGCTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTG AAAAATCCTGGGAAGAGACATACTTCACTGAAGTCATTTCTATTCATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT

WI-20442			37 T C ---			TCCACGTGAAGGAAAGAAAAAANGGGGGGGCTT/CJTAAGGTGGCACAATTTTAAGAAAAT ACCATCCATTTTTCTCAGTCTAATCTGAATCCATATAATCAAACAAAAGTGCAAGTGATGAGACGAA CA
WI-21235			43 T C ---			GTGACAAAGAGTGAAGCAAGGGACAAAGGGCGACGAGGGCAGTC/T/CJCTCGGGCCGATGTTCCAGGG CAAGCTACGTA
WI- 22012a			57 T C ---			ATCAGAACTGCAATCTGCACATGAAAAACCTGGGGGAATGCCTACATCTGGAATT/T/CJCATTA ATCAACGTTAAATTTTGTCCGACCAGTCTTCATTGCTGATCACATTTTGATAATGACAGATCCAACAT GAAACTCTGAAGCAATGAATATTACCTGTGCTTTTCATGCAAAATTAGGGACCAAACTCAAAGG TTTCATCCATGCTGGGACACAGATCTAAGGAATTGTACAGGGATCTCT
WI- 21149a			167 G A ---			AGGACCTGCTCACAAGTTCCCTCACCCCCCAGCTTTTGGCAAAGATAGTTGACTAAATAOCCACT AAATAGTGGCTTTTTTTTTTAAACAATGACCTTATTTATCTTTAACTTAACAGTCTTATATA CAGACCTGCCAACTGGAAGCTTTTACAC/G/AJTGCTTCAGAATGCGGCAGTATTGCACAATGGTT TGGGCGAGTTCTGTGTTAAACATGGGATGGAAOCCCAGGCTCTAOCTG
WI- 21376b			188 A G ---			GGTGCAACTTGGAAATAATGGTTTAAAAACAGGATAAGCATTAAAGAAAAACACTTTTCAATGTGTC TTCCATTTGATGAATTTGTTTTCTCTCTTTATCCCCGCAAGTGGAGTTTCATGCTCGGTGAAACCA GACAGTGAATCTGTTCCAGCCCCAAATCTGCAGCATTAGGGATGAGTTCTC/A/G]GAAGTGATTTCT GAACTGAGCAGCACTCATGTCTGCATGGGGAACCTCTGGGAGAGAAGGCOCT
WI- 21382d			125 C G ---			CCATTGCAGTCCAGAGATGAGAAACTGGACCAGAGGCAATCATGAACAGAACGGGAGTCAAGAGA AGGGTTTCTAAGATGGAGAAGTGGGGGGGGTTGGATCCAGTGGGATNNGCTTCCQ/CJGAGGTT GCAOCCCAAGGAAGTCTCTGGAAGCAGCACCACTGCTGATGGGGAGCAGAAGAGCTGCCATCCTC AGTCAGGTCOCGAGTCAGGGTCCGAGGAGAGCTGCTGCTCCATAGTCTGCGAC
WI- 21437a			201 G A ---			TCCCTGAGGTTGGAGTCTAGCATAGTCCCTCCCTCAAAGAGGGACAAGGGGTCAAGGGCAGAGC AAAAATCCAGTCTGCTCAACCACGGAGACTGCCCTTTGGGATGGAAGTTTCTGGAGCTCCCTCCATT CTATTCTGTGGGCGAGGAACATGCCAGGGCTGCTGGTAAATGGCAGGGGTCAOCTTTACCAAGGGC/G /A]CAGGCATAGTGTGGCCOCTGNCTGCCCTGGGGGCCACOCTGGGAACAGT
WI- 21202b			156 A C ---			C AAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTATTTCTGTATAAGCTAAATATGTTGATCT GTTTTATGAACATGATTTTATAAAAATGGTCACAATATATTTTAACTTAAGTTAACTGATTTATTGAGGG AGGAGGAGAGAGTTGACCA/A/C]GTCTACATGCATAGACAGTCTAAAAGCGTATCTCAAAACATG A
WI- 21202a			61 T C ---			C AAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTATTTCTGTATAAGCTAAATATGTTGATG TCTGTTTTATGAACATGATTTTATAAAAATGGTCACAATATATTTTAACTTAAGTTAACTGATTTATTGA GGGAGGAGGAGAGATTGACCAAGTCTACATGCATAGACAGTCTCTAAAAGCGTATCTCAAAACATG A

WI- 21627b	153 A G ---	---	GCATGAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCAATTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAAA[A/G]TCCAAAGTCATCTAATAATTAAACCATATTTACATAAATTTGTAGG GACAGTATACTAATACTACATAAATAAGGGTTTAAAAATGTTGCTTA
WI- 21627a	106 A G ---	---	GCATGAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCA/GTATTGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATAATTAAACCATATTTACATAAATTTGTAGG GACAGTATACTAATACTACATAAATAAGGGTTTAAAAATGTTGCTTA
WI- 21399a	75 C T ---	---	GGATTGAGTCCCAACTTGATCTCAAAATTCACCTCTTGCAATGTAACAAGCTCAATTCCTCTAAAGTT TCAGTTT[C/T]TTCACCAGTAAGGAAAGGTTGGACCAGACATGTTGGACCGTAATTCCTTGGTAA CTGCCCTCTGCAATTTGCTCTGAGGTTGTGTGCTCCCTAGGACTAGGTAGGATCTCTCTGCTTTCTGCC TTACCTAGGCATAGTGCCCTGATAGCAGGCTGAAGGCCCAATTCATCTTGT
WI- 20323a	68 G A ---	---	CGATGCTGCTAAGATAGGAGGTTAATCTTTACATGGTGGGTCACAGACAGACATCAAT C[G/A]TCTGTTAGCAGCGAGAGACACTTTAAGTTGCCCCAAGAGTACAAATCCCCTCTATGAGAC AGCAGTGTGGCTTCTTAAACAGATAAACCAATCAAAAAGAAAGATTTAGAGGTTTCAGACATT AGGAACAANTGTGGCCAGAGATACCACAGAGCCCTTGAAGGGAAAGGCCCTCACT
WI-21249	155 T C ---	---	TTCTGGCATTCAAATGTACATGTAAATCCAATTAACAGATCAAAATGTTACACTAAGTTTCACT TAGTATCTAAGTATCCAATCACAATGTATCTAAGTTTCACTTTAAGAAACATTATAAAGGTAATT AAACTCTAGGTGTACTT[A/T]CJATGGAACAGTATTTCCNATTTAACTACTGTTCAATTGCCGTA AAGTATGTTGCCCAATTTTCAGCTGTTTAAAGGAATTATAAACATTGAGA
WI-21504	147 C T ---	---	TGACACAGCATCAATTTTCATGAATACTTTGAAAGGGCCATTAGAAAAATAAGAGCCAAATTTGGGTC ATTTGAGAAACATTTTCAGCACAAATACAGTGGGGGCACGGCCGTTCCGGCTCCAGCTGGGTTTCCOC AGATGCAACAAT[C/T]GCGGTTCTGGCTTCTCCACTGTGGGGATGGGGATCGCGCTTCGGAGCTCT CAGGG
WI-21242	115 G A ---	---	CTGCACAGGGGAGACAGCTGCTGGCAGGGACTAATAAACCCCTTCCACCTGGCCATGGTGGTGT CTCTATGGACCGAGGCCCTGAACCGCGGCGAGGGAGGGGCAGAGAAC[G/A]CACTAGCTTGGGGGTG GGCACCAGCTTCAGACCCCTT
WI- 21475c	181 A G ---	---	TAGCCCTTCTGCCAACATCTGGCAATNTGAGCTGGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGCTCCAAACCCAGGCTTCTCACTTGTCTACTAAGCACAG CAGTCTGAAGCTTGGGACTGGGCAAGTGCCTTTTGGAGAAAGGCA[A/G]AAAAAGCCACAGCAAC ACTTAGGAGCAAGAACCTTCCCGTTCTCCACCCCTATTTCCTCCCTGAAG

WI- 21475b	117 A T ---	---	TAGCCCTCTGCCAACATCTGGCAATNTGAGGCTGGGTGGACGTTGCCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTC/A/TCTTGCTTACTAAGCA CAGCAGTCTGAAGCTTGGACCTGGCAGTGCCTTTGGAGAAAGGCAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCTTCCCGTTCTCCACCCTATTCTCTCCCTGAAAG
WI- 20893d	207 A G ---	---	TGTTTGTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCGTTGTCAGGCTTGTGCAGGG CTGTCTTCGGCGTTTAAAGTCTACTGAGGAATACAATCATTTGTCAGTAAAGTTTCATCCCGCACTCC AGGTCAGGCCAAACCTTTCGGTGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGCAGT TTC/A/GIACATAACATTGGTAGAGTAAACAACAAACCCACAAGCCTAAATG
WI- 20893c	179 T C ---	---	TGTTTGTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCGTTGTCAGGCTTGTGCAGGG CTGTCTTCGGCGTTTAAAGTCTACTGAGGAATACAATCATTTGTCAGTAAAGTTTCATCCCGCACTCC AGGTCAGGCCAAACCTTTCGGTGACCTGGGNAACCTGCCAT/CJTTCCTCTCTTTTACAATGC AGTTTCAACATAACATTGGTAGAGTAAACAACAAACCCACAAGCCTAAATG
WI- 19941c	71 C G ---	---	GAGCTCAAGGGAAGACCCCTTACCAGATAGGGACTAACTGGAGGGTGGAAAGGAAACAAGGTGAAA GGTATC/GGGTCTGTTGAGACAAAGCAGGGGGCCCTGAGAACACAGAGCAAGGTGGTGTGGAG GGAGCAGCAGGGTGCAGGAAGGGAGATGGGGGACATTTCCATTCCAGTGCATGCCCTTTAAAT AAACTGGGTACAGGAGCATTTGGAAGGAGAACCAAGGACAGAAAGCAAGCGG
WI- 21552b	166 C A ---	---	TGGTACATGGACAGATGTATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAAATGCGATCTCCTCACCTCAAGCATTTATCCATAGTTTACAAGAA TCCAAGTACTCTTGATTATTTAAATGTAC/AJAATTAATTTATTTGAATTTAGTTACCCC ATTGTCTATCAAAATTCATCTTATTCATCTTTGTAACTATTTATTTGTA
WI- 21552a	66 G A ---	---	TGGGTACATGGACAGATGTATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG /AJTAATAATTACTTCAGAGTAAATGCGATCTCCTCACCTCAAGCATTTATCCATAGTTTACAAG AATCCAAGTACTCTTGATTATTTAAATGTACAATTAATTTATTTGAATTTAGTTACCCCA TTGTGCTATCAAAATTCATCTTATTCATCTTTGTAACTATTTATTTGTA
WI-21512	54 C G ---	---	TCCTCGTACTTCATGCTCCCTCCCTGCCCCAGAACCTTACAAAATATTTCTGT/C/GITAGAGGGA AAGAGCTGGTGCCTCTGGAGGCAAGTCCAGGTCCGGGAAAGGCACTGCTGCTGTGATCTGTC TCAGTGATGGGAGGTCTCCACTCGCCCCACAGGACGCTCGGGGCCAGAGATGAGAAATGCTGTAA TCCAGTACAGGGGCTGGTCTGGGGGTCCCAACAGCTCTCTTTGGGGG
WI- 21513b	192 G A ---	---	CACATAGTTTCTCAAGAGAGGATGAACCTGAAACTCTCTAAGGCAGGCAAGCAACTTCCATT ATTCTTAGTTTAGACCAGAACTTTAAATTTTATATTTCTCTTTTAACTGTCAAAATACACCAATA CTTAGAGGAAATATTCACAGTATACCAAAACATTTTAAAGATAAGAGGCAAGTGTAA/G/AJAGTAG TATTCTCTACATACCACAGTACAAATGATGCCCTTCTGTCAGGTTTAGGAAC

WI-21514b	133	C T ---	---	---	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTCTAGGACTGGTGTGATGAGCTGACAAGCATAGAGGCAAGTATCTCAACATTACAAACCCCAATCTTCAAGGAAAGGAGCACATTACCATGGAGCJCTACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAAATAAATGAGGANTTTAAGGCTCAGATGGGTTAAGGGTGAATTTGTCAAGGGTCATAAGGAACT
WI-21514a	100	A G ---	---	---	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTCTAGGACTGGTGTGATGAGCTGACAAGCATAGAGGCAAGTATCTCAACATTACAAACCCCA[AG]TCTTCAAGGAAAGGAGCACATTACCATGGAGGCCACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAAATAAATGAGGANTTTAAGGCTCAGATGGGTTAAGGGTGAATTTGTCAAGGGTCATAAGGAACT
WI-22020	27	C G ---	---	---	ATGAACATGTTGCAGTGGGATGAATTC/GTATCATGATGCTAAGTGAATAAGCCAGACACAAAAAATCCAAATGTATCATCTACCTGTATGAGGGTACTT
WI-19576a	113	A G ---	---	---	TTATCGGTTCTTAATACAGTACAATCCTTTTGTGAAACAAAAGTCACACTGGCAATGATTATTACAGATCCAAATAGACTCAGGCTTCAGACATAAAAAATTTAACATTCTA/GTCTAGTTCAGTGATTAGTCACAGAAATTAACATCTGCCAGATGTACACAATTTGGTAAAAACTACAGCTTCTCTCCACGGGA
WI-21695a	141	A C ---	---	---	G ATACACAGGCCACAATTGCAGGATGGAAGGCAAGTGGGCACTTGGAAAGTGACTACACATGGCAATAAGCAGCCTATCTCTTACCAACCCAGAGTTCTTGGGGCATGTGATGGTGGCAGACCCCTTTCCAAAGGGAATA/CJCTACTACCTAAGCCTACACTGTACTGTGAGAGTCAATGTGTGAAACAAGGCCACAGGCAGTGGGAGGAAATGTGATGACTTCACTGTGTTCAGANTTCTAAGGCCACAGCAT
WI-21574a	235	C T ---	---	---	AAACCCAGAAATTTAGGTACTTTTGTATTATGAGGAACTCACTATACTAGGAAGCAACTTATGAGTGTGTAATATTGATCTAGCAGCAACTTCCACTGATCCTGGCAGGTGACAGCTCTCAGTGAACAGCGCTCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTTGTGAATGTCCCTCAGAGTCACTAGGGAGCCATTGGGCAGGCCAGGCAACTTACTGCCCTACTTCCJCTGTGTGTCAGGTGGGA
WI-21644c	151	T A ---	---	---	TGACTGCCAAGATTTAGGCCCAACTTAGGAGCAAGGTCACCTTAACCTTTCAGGAAGTCTTGGGTGTGACCCACTGCATAAATGGATTTTACCATANATTTAACAGACTCAAAGTGATACATACAAGCTTGTTCATAAATAAGGGA/TJTTCAATCAAGATCCATGGAAATGATGCAGTTAACATGTGTCTCAGCTTGCCCTACTGACCACCTTCTCTTCTAAATATGGCAACAGCACAGCAAGTC
WI-21614b	55	G A ---	---	---	TGCTTTAACCTCAAAAGTCCAAATAAACATATAGACATTTTGANTATAGCTATC[G/A]TTTTAAACAACCTCATATGATCACTGTGCAATTTTCAGTCACCTAAATACGGAACCATGACTATTAATAAACAATTTACTGTGTGGGTTTGTGGGACTGAACATTAACCATACGTGTATTCTAAGGTACTAGGGAGTTGGAAACAGCTACTACGGGTCAATGGTATTTTGGGCAGTTGGCTGTGTGTGGG
WI-21615b	151	C T ---	---	---	GACCGAGAAAACTGCAAGGCATATGATGTTTGTGGAAGTATACATGACTATTTCAAGCTTATAGAGAAGTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTCATACATATTAAGATAAGGATGGACTCTTCACTGAGTATTATTC/JAGGACACAATCGACGGATGTAATCTATTTTGANTTATACCATAGGCCCTATTCTATATTGGCCAAAGGGAAGGTAGGATGGGTACTGTGTGGAACGGA

WI-21981	61 T A ---	---			TGTCATCTCATTCTGGAGAATCATAGATGTGGCAGAAATACATATTTCTTGAAGAAAAAAATTTAAGTCTCCCTTATGGGTACTGTGATTTCAATAGGGTGTGGGATAAGTACATGACAACATGCATGGGATAGA CACTCTGTTCTCTACAGATCCGTCTTTGGGAATTACAGGAACATAAAAGGATATAATGGATGGGTT ATTACTTTTACATGTGGACAATCTAGTTGTAGGCGTTTAAAGTTAAATTGG
WI-21660	120 C T ---	---			TOCCAACCTAGCCTCTCAGTATTTAGATGAGGATAGAACAGATACGGTGTAAACACGCCCTCTCCACTGCTT TACTGTGTGTACCAAGAGGAGCAAGCAGCTCACCCAAAGCCTAACCTGGCCJC/TJTGCTCTTTTTCAG GCTTCTCAGGATGCCACAGCACATACCTGGGGAACCTGGGATGCAGGAGAGCCAGGGTCTGTCTTC AGGAGGGTCCACAGC
WI-19105c	211 C T ---	---			TGGAAGTAGCCCTTCTGGACAGAAAGAATATTTGTGGTCCATGTGGTTGAGTCTGTTAAGAAGGA CACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTCTT GTCTGATAGTTTCCAGGGCTGGCCACAGAGGTGAGGCGAGAATNTGGGGTCCCAGTGGATCTCCCC ACAACTTC/C/TTCAGGGGCGAGGATTTCCACCCAGGGCCCGGCTGCCCCG
WI-19105a	33 T C ---	---			TGGAAGTAGCCCTTCTGGACAGAAAGAATATTT/CJGTGGTCCATGTGGTTGAGTCTGTTAAGAA GGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTC CTTGCTGTAGGTTTCCAGGGCTGGCCACAGAGGTGAGGCGAGAATNTGGGGTCCCAGTGGATCTC CCACAACTTCTCTCCAGGGCGAGGATTTCCACCCAGGGCCCGGCTGCCCCG
WI-21760c	81 C A ---	---			CAACCTTAGTCACTCTACTGATGCAATGATTTGGAGGTGTCTTCTAGCTTTACAATAAGNGGAGG GACCTCTGACTGCA/C/A/CCTCTGTCTCAGTTTCAGGGCA
WI-21760a	35 A G ---	---			CAAACTTAGTCACTCTACTGATGCAATGATTTGG/A/GJGGTGTCTTCTAGCTTTACAATAAGNGG AGGGACCTCTGACTGCACCTCTGTCTCAGTTTCAGGGCA
WI-21569b	198 T C ---	---			TCTGCCATATTGTTCCAGCACCACTATTACTGTTATTTCTCTTTGAGGAAAACCAGGNATTAAG AAATCTGGTTTGAATTTCCATGATGCCTAACTCTATGGTTAAAAATCCTTTTCTTACCAAAAAGGA ACTTCTTAATCACCAGAGAAACAGAGGGAAGACTGAGATATGTTGCAGAAATTTATCTCTACT/C/J AGAGACAATTCATAGTTCATAATCTTTCAGGGTGTGCTTTACTTGGGGGGC
WI-20934a	72 T G ---	---			CCACATGCAACATAGTCTTCATTCTTAAAAAGTACATAGTAAAGGTATGAAAAACATTTGTATTCA GAGAA/T/GJCTAAGACAAATGGTCAATATTTCAAATGGCCTGGCACTAGTGGTAATCCAGCAGAG AAACAGCATGAGAAAAGGCCGGGAGACAGTAATAAATACGTGCCATTTGCAATGAGTTACCCAATC AAGCCCTTTTACCTCCTTAAGATGGCAGATTAGAAGACCCTNTTCCCCAGGAGA
WI-21561	55 T T G ---	---			TTTCCATTTTATCAGCCGGGCCATCAGAACATAGCATCTATACCTTCGAACCTT/GJCCCTCTTAAC CTCTCCAGGCAAGAAAGGAAAGTGCATCATTTGAATTCCTCAGAAATGGTGGGATCTCAAGACTT TTTAGAAAGTGCTTATTAAAGTATAAGAGGCTTGAATATAATGATGATAAATGGTAGCCCTTTCTGGA AATAATTTTGTGTAATCTGTTTAAAAAGATTTTGGATGCATTGTCCCCA

WI-21961c	200 T G ---	---	AGCTTTGCTTGAAAATTTGGTACTACTACCTTTGCAATCTCTTTATTATTATTATTACTTTATTTTCCGTAAGTTATTGGGTACAGGAGTATTTGGTTATAAAGTCTTTAGTGGGATTTGTGATTTGGTGACCCATTACCAAGGAGTATACACTGCACCATCTCGTCTTTTATCCCTCGCCCCCT/GJC
WI-21961b	73 G A ---	---	TCCACTTTTCCCCTCAAGTCCCAAAGTCCATTGTATCATCTTATGCG AGCTTTGCTTGAAAATTTGGTACTACTACCTTTGCAATCTCTTTATTATTATTATTACTTTATTTTCC[G/A]TAAAGTTATTGGGTACAGGAGTATTTGGTTATAAAGTCTTTAGTGGGATTTGTGTGATTTGGTGACCCATTACCAAGGAGTATACACTGCACCATCTCGTCTTTTATCCCTCGCCCCCTC
WI-21956	26 T G ---	---	TCCCCTTTTCCCCTCAAGTCCCAAAGTCCATTGTATCATCTTATGCG CCACTTGGGTCTCTTTCAAGTGAAT[G/T]TCCCTTCGTTCTTAAAGCCCTTTTAAATGAACCTCCATTCCTGTCTGAAACTTGCTTAGTCTGTTTCTGCTTCATGCCCTCAGTCGAATCTTCTTCTGAGCGCGCAAGGACTGAAGTTGCTGTGACCTGTAGGGTTGACGCGGTAACCTCAGGGTAACCTCTATCTTCCACCGGTAACAGAGGGTTACATTATGGGGTCCAGGTT
WI-21966	148 G A ---	---	CAACATACATTATGGGTGCCTTTATTTAAGAAATGTTTACTGAGAATCTGTACTGTAAACAATATTTTTGTAGAAGCATGAGTGAGTGTTGTGTGTGCGCGCGCGGACGGCATGGCACTGAGGGGATTGCAATGGG[G/A]AACAGGATAAAAGGTATAAAACTTGGTCCGAAATCTTTGCTTATTAACTTGGCCCTGCTCCTCACAAATGTTTCTACACTTAATTCATAAAGAGAGGTAGA
WI-21930c	146 G C ---	---	TATACTGGTTTTGGTTACATGGATGAATGTCTAATGGTGAAGTCTGAGATTTAGTGTAACCATCACTGAGTAGTGATACATTGACCAACTTGAGGCTTTTATCCCTTACCCTACCTCCACCCCTCCCCATTTGAGTCT[G/C]CATAGTCCATTATACACTCTGTATGCCTTTGCATACCCATAGCTTAACCTCCC
WI-21139a	165 T C ---	---	GCTCTAGTGAAGAAATTCAGGACGCGGTCTTCAGAGCAGAGGGCTTGGTTCAAGTCCCTGTTCTGCGCATTAACCTGACATGACCTTGAGCAAGCCACTTAATTTCTCTGCTCTCTCTGTGAAATGGGTACAA
WI-20317b	217 G T ---	---	TGTGGGTCAGCAGTAAAGGAACTAATACAT[G/C]GTACAGCACTTCAGCACAAAGCCCTGGGACACAGCACTGCATGGAATACACAGGTAAACATTTTAAACAGTGGGACAAAATTTAAGTACGTGGCCAGCTGTTGGTTGCTTGTGGTCATTAAAGACAATGTTAAGANTCAGGAGTACTTAAGTGTAGTGGTTACA
WI-22082e	179 G A ---	---	AATTTGTTCTCTTCAGTTTTTTCATTAAAGTAAATCTAATAGATGATATACATATTACTGCAGATAAAACCATCATCAGAAA[G/T]TATTAAATTAATGTCATAATTTGAGGCTACTCT CAGGACTTGGTTTGTCTCCCACTGCACATAAATGTCCTTTTTTGTGAGTTATGGTTGTGTGCGTTTTTCCCTTTTGCAATAAGAAATATGTCCATTATAGTCCAGAGGCTCTTGCTTTATCCGGATGACGGAGGTACACGGGGCTCCGCTCAGTCCCGCGGAAAGGAGTAT[G/A]CTGAACTGGGACGAGTCTACTCTCCCCCACAGGAGCCACGATTTCAAATCCTCTTTGTGCAACCTCT

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WI-22082b	67 C T ---	---		CAGGACTTGGTTGCTGTCCTCCAACTGCACATAAATGTCCTTTTGTGTTGAGTTATTTGGTTGTGTC[C /T]GTTTTCCTTTTGCATAAGAATAATGTCCATTTAGTCCAGAGGCTCTTGCTTTATCCGGATGACGG AGGGTACACGGGGCTCGCTCAGTCCCGCCGAAGGACGTATTCGCTGAAGTGGGACGAGTCTACTC CTCCCCACAGGAGGCCACGATTCAAATCCTCTTTGTGCAACCTCT
WI-20993	139 A G ---	---		AACACAAACTCCATGCTTTCAAGATTCCACACCCAGATACTAAGACATATTAATAATTACAGCAAT TAAACAGTGTAGTTTGGTACAATAACACATATAGCAATGATACAAATTAGGGGAAAAACCCCTGG GCTTCTA/G]TAACAAGTGAGTATACATTAAAGACAGTATTGCAGAATGGCTTCAGGATTAAATTTGA TTAATTTAGAGAGAGGCTATTTCAAGGCTCTCCTAGCTCATCCACACATCACC
WI-21723b	125 A G ---	---		AAGCGATTTTATTAAATTGATTGGACATACTGTAGGTCAAAATAATATTTCTGAAGATAACAATTA TGGACTTTAAAGCTCGACATAAAATTAGTAGCTTCAAAAGGGTAGTCATATTTCCCAIA/G]CAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-21723a	82 G A ---	---		AAGCGATTTTATTAAATTGATTGGACATACTGTAGGTCAAAATAATATTTCTGAAGATAACAATTA TGGACTTTAAAGCTC[G]ACATAAAATTAGTAGCTTCAAAAGGGTAGTCATATTTCCCAACAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-22132	99 T G ---	---		CAACAGATGCTTGAGCCAAAAAGCAACATAGGCAGAAATACAATTGAGAATATCTTCATGTTTC AACCTTTAATCTGACTTGCCTTTTACTATCCTT[G]G]CCCCATTTCTCTAATCTCTTTTGCCTTACAA TATATTACCTTCTAGGTATCACCTCATCTATAGGAATGCCTTCTAGTTTAAATGCTGCCCCCAACA ATACTAACCCATTGAAGGATACTATGGAACCTTTAAATGGGACAGTGGG
WI-21006a	106 A G ---	---		TGACAGATCACACCACATTTGTTTGTAACTTTTCTCCTTCAAGAGTCACCTTAGCTTAAGCCAGAA GATTCTCTTAAAGAACACATACACACATGTGCACACAC[G]AGAGGGCAAGTACAAAAATGTAACC CCACCAAAGTGCATGTGAATGAAAGTGCAAAAAGGCTTCATTTGCAAACTCTGAGGATCATCTCT CTGCTTCAGGAAAATAAACAGAAAGGTCCTAACTGCCCTAGGCCT
WI-21761b	138 C G ---	---		CTGAGGCCCTGCTCTAACTTCATNTGACGGAGCGAGTTTCTGCTTGGAAATAACTGAAAAGATTTCAT TTTCTCTTTGTGTACAAAGGATTCAAAATATTTACATCTTCTCTGCCAGTTAAACGTGCCGTGG CTC[G]CAATACACACCAAGCCAAAGCGTAACCTTGGCTCAGGAAGGCTGGGAGGAAGTGCCAG ATGGTA
WI-21079c	166 G A ---	---		AATGAAAATGCCACCCAGAGTTAACAGCTTGCCATGCATGCACTGTGTGCGCAAAATCAAGTTGT TTTAATACCAGTGTGCAGCTTTGATTCTCCATGAAATTAAGCTGTGTGCTCACTTGTTTACATAA CTCAGGGCACCCCTGAAATATCTGCTAGTGGG[G]A]AATTTACAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGCAAT

WI-21079a	50	G A ---	---	AATGAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGTG/AJCGCAAAATCAAGT TGTTTAAATACCAGTGTGCAGCTTGATTOCTCATGAAATTAAGCTGTGTGCTCAGCTTGTTTACA TAACTCAGGCCACCCTGAAATATCTGCTAGTGGGAATTTACAAACCCACTGACCCTCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGGCAAT
WI-22129a	45	T G ---	---	TCGTAGATTTAGCCATGCCATATATTTAACTTTTAAAGGAAAAGT/GJTTATATAACAGTCATTGCT TGGTAGAATCCAGTCTGTCAATAAGTTAGCTTAACAGTTAACATTGAAGCTTATACCTTATATTTA AATGTTTAGCAATCTCTACTACATTTTCAAATATAAATAATTTGGTTGCAAAATCCAGNAAGGGCA TTAACCAACATGGGACTGATCTGGGGCTTCCACCTGACTAAGGTTTTA
WI-21941	79	A G ---	---	TGGAGTTAAGTGGGGCTCTGCTATTTCCCCCAAGAGGACTCGGAAGATGTTGATCCAGGGCAGAGT GAGGGCAGAC/AJGGATGAGGCTCTTGTAAAGTCCAACAGACGCTCAGAGATGCTGGGAGGCT GGGACTGCCAGGTTGGGAGCCTCACCCAGAGAGCCTCACTGCAATTGACCCACACCCACCCTCACC CAGCACACAGGCACACGCGAGGGCACACGACACAGNTGCACCTCACACGC
WI-18916b	42	C T ---	---	AATGGCATCCTGTGATACCAACATCTTCAGCAGCTCAGC/AJGJCTCAGCCGGCTTCCCACCTTCTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCACTACTGCACTGGACACAGCCTCACCC AATGCCACCTTCATA
WI-18916a	35	G C ---	---	AATGGCATCCTGTGATACCAACATCTTCAGCAGCTCAGC/AJGJCTCAGCCGGCTTCCCACCTTCTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCACTACTGCACTGGACACAGCCTCACCC AATGCCACCTTCATA
WI-19828c	200	A G ---	---	TTCCCTTCTCCCCAAGAAGTGGGCAGAAAGCTTTGTTAACCTCCTTTACAGATGAAGAAAAACAA GATCAGAGGTGCTAAGTGTGTAGCCTAGTGCCAGGNCCTCTGGCCCCAATCTGGGTTCTCCCCAAG CCCATGCTTCTCCACTTCTCACAATCTTTACTTCTCCTCTGACCCCTCACCACCCACCAAAAT/A/G JCTTTTAACTCTGGAAAAGAACCCAGCTGCACACTGGGCACACTTGACCT
WI-21863b	47	C T ---	---	CACAAGTCTGTACAACCTTAGGGACACAGCCCTGGCCCTGCCCCTG/AGCTGCATGCCACCCCTC ATATCCACCCCATCCCCAGCCTCTCTGCCCGACACCCCGAGGCTCCCTGCTCTGTTGAAGTATTTT CTCCAAGGCAGGAATGAGTCTTGATCCAACCCACAGCATCT
WI-19860	51	C G ---	---	TTGACCTAAAGCCTAGCATAAAATTAGCTAAGTAGAATGTTTCCAAAGATG/C/GJCTGCATCAGTAT CTCCCATCCACATAATTTCTGTGTTGATTTGCCATTACCCCATAAAATGGTGGGATCTACCTCCCCT CCTTGCAAAATTGAGCTGGNCCCTCTGATCCTGCTAAGGATCTGAAGCC
WI-19889b	80	C T ---	---	ACCCAGCTCCTCTTACCCTCTGGCTTTTCAAGTGGCTTTGGCTAATGGCCANTGAACCTGCAGGGCAAG AGGAGTGAGGGG/C/TJACAGCATTTATTTCCCTCTTCACTCCCTGTAGCTTTGGTAGTGGCTGTAT TTCTCTACTGATAGTTCCTTGCCACACAGTCGTAACCTATTCG

WI-19891c	172	C G	---			TGTTGGTCTGAGAAATTCACAGCTTACTACAAGGAAGCTGAGAATTCGTTGGTGGCCCCCTCCCCCCCCG ACTCCTCTGTCTCTGGGAAACGTGGCTTTGNCCTCCAGACACGTCGTGATGCCAGCTCTCCTCAGCGG AGCTCCGATCCCTCAATTTGCCATCTGTCTGACTC/C/GJGCTCTCCCGGGCGTGGGGCGTCTGTGT CAGGCAGCGGGGGGAGGAAGGAAGGAGATCCAGGCTGTCTG
WI-20155a	81	C T	---			GCACCTGTAGGGGTGTAGCTTCCATGGTTCTCCAGCACGGGTGTACATTACCTTAGGCTGACCAT TCCCTTGGGGGGG/C/JGCAAACTGCTTTGAGGAAATNTCCAGGAGGAATAAAC TAGAGACGC ACCTGCTATTTACCATACTATGGAGAAATACAGCTAATGAAGTGGTGACAGAGCTTTGGCCGTGTGA GTGCCCCAGGGTAAAGTCTCTCTCTGTCAGTCCAGAGCAGAGACTTCTC
WI-20270b	91	T G	---			AGCCATACAATGCATTGCAAAAGAAACAAAGCAGCTGTACAGGAGTGGGGACGCGTCAGTGTACAAT ACATTGATGCCAGGATAAGGAGCA/TGACACAGGATTTATACACGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAGTATATTTCCATCTATATAATACACAGCTGGGTGGGAAGGATGCT GGGTGATCTTGTTCCTCCGACAGAGGCGCTGGGAGGCGAGGNGGGTGGGAA
WI-20270a	53	G A	---			AGCCATACAATGCATTGCAAAAGAAACAAAGCAGCTGTACAGGAGTGGGGACGCG/C/ATCAGTGTAC AATACATTGATGCCAGGATAAGGAGCATACACAGGATTTATACACGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAGTATATTTCCATCTATATAATACACAGCTGGGTGGGAAGGATGCT GGGTGATCTTGTTCCTCCGACAGAGGCGCTGGGAGGCGAGGNGGGTGGGAA
WI-20622	130	T C	---			CCACTTCAATATTTACAAAATGCTACGACGCAAAATATGAAAAGTTCAACACTTCCCTTTGTA ACTTGTGCAATAAATGCAACTTTAACAACATACAAATTTCTCTGTATCTTAAAGTTGAAT/C/] TACTAATTTTATGATGTTACTCATATTTTATTCATATACCTTTAATGACATCATTGCCAAATACATA CATTATTTCTNTAACITTTATTTTACAATAAGCCAACTCTGTCATGGAG
WI-20768b	190	C T	---			TCCACTCAAAACTCCACCCCACTTCCCTGGAGGCGAGGCTAACAGGACCTCCTGCCTGCCTGC TCACGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTTCTGTATATCACCACTTA CAGGAGAGGTC/TATTTCTGGGACCCAGAGNTCAGCACACATCTGCTGGG/C/JCAGGGACTC GTAATTCGCCTTGGTCCAACTCCTTCTATGGGGTTTAGCTGCCCTCATTC
WI-20768a	71	C T	---			TCCACTCAAAACTCCACCCCACTTCCCTGGAGGCGAGGCTAACAGGACCTCCTGCCTGCCTGC TCA/C/JGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTTCTGTATATCACCACT CTACAGGAGAGGCTATTTCTGGGACCCAGAGNTCAGCACACATCTGCTGGGACACAGGACTC GTAATTCGCCTTGGTCCAACTCCTTCTATGGGGTTTAGCTGCCCTCATTC
WI-21909	153	A T	---			TGTTGCTTTGTGCCAGGTACTCTACTGCTTTACATAAAATATCTCATCTGTACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACCTAAAATAAGGATATTTGGTCATCTTTAAAGAAA TGCTTAACATACCAAAG/JATGAGTGGAAATCAATAGATAAAATATTTAAGCTTACAAAGCGTAC GACACTAAAGTAATATAGGATACCACCTAAATTTATATTTCTATGTATGGAAAG

WI-22202	128	A G ---				TGTTGCTTTGGTTGTTGCTTCTGGAACATATTGGAACACTGTTTTTCATAAGCTGTCTCCTGACAGT GGCACAATCCCATCCATCTCAGGCCTTTTAATAAGGTCAATTATGAAATCTGAATTTCTTJA/GJTTAAT ACTCTGGTGCAATTCATCTGCAAAAGCAACTGGCAACCACTCTTGGCGGTGCAGCTCTCGG AGAACATCTAATATTGAGTCTAGTTCTGTGCGGAACCTCTCCAGCTCAC
WI-22189	70	C T ---				CCAAGGATGAAATTTCCACATTTATTNCTTTTATGTGAATAGAAAATGGCAGTGAAGTGTCTCTATG AA/CJT/GAGGCGAGGAATGGCATGGCGTGGCTGCGGTACCAAGCTTGACGTTGTCTTCCAAAGTACAC TATGTGTGGTGAGACAAAGGT
WI-22283	109	T C ---				GGGGAGGCATCATAGAAAAAAACCCCTCAGCCAGAAGTTAGGACATTGTGATTCTCAGCCACTAACGA GCTGTATGACCTTGGTCACTAGGCCCTCTGCAGGCTCTGGTTG/CJTTCATTTGCAAAATAAACCCCA GACCGGGTCATCTTTCAGTTCCCTTCCAGCTCTATTATTTATGATTTGCTCTTAGTCTTTATGAGCCA TGTATGATTTATCAGTCTCCCTGATGCACTCAACTCCAATGATGCAAAAAG
WI-22290a	136	C T ---				GACGTATCTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGTTTTATGGGCCCTCTAAGCAACCG GCCAGTAGTGGGAATGCCACATGCAATGGGTGAGTGGGATCTGGGGGGGTGAGGACCTTGCTTTT [C/JT]TCCAATCTCTGCTTCTTAGCCAGAATTTGCGAGAGCCCTTTNATTTCTCTTCCCTCTATTCC CCTCCTTCCCAATGTGCTAAGTCCCAATTCGAGAGCCCTCCAG
WI-22292	53	A G ---				CCAGTGAAGGGTTACAGCCATAGTGAGGTTCCCCATTTGCTCAGTACCAGA/A/GJTTTGTAGTAC GGTCGTTTAAAAATACTTATCTGACCACAGTGGAAA
WI-22387	186	C T ---				ACCTTGCACACCTGCCATCCGGTGCCATCTCCTGGCTGGCACATCTATACCCACTCTGGCTCTGAAAG GCTTGTCAACCAAAATGGCAGCTGGGCTAAGGCATATTTAAACAAAGGCTCCAAAGGACCCCTT TCACTGGGTCTAGCATCCAGCCTCTCTCTCAGCAAGGCGAGGATTGGTG/CJTCTTGTGTTTTCTG AACAGGGCCAGGGCAGCCAGGCATGCCATCACTGCAGCACTCAACCCT
WI-22395b	127	A G ---				GCCGTTCCAGTATTGATAATAATTTGTGTTTAAATTTCTATACAGAAATGGTCTTTCTTGAATATTTT GTAGGGATGGATGAATTGAAGTGAATTAAGTCAAGATAAAGGGGGCAACTCTTTAATJA/GJAAG GAAATGTTACCAAATCCATAGTGAAGAGTAGAATATGTTCTTTTAGAGTAGNTAGAAAAGTCCCCCAGG CTCCT
WI-22405	90	A C ---				TTTATGGCTCCTGAGTGCCCTTCCAGCTACACTTTACCTTGTATCTATAAAAGTGAATTTAGAGT AAATACATTTGGCTGTAAAGTCG/A/CJGATCAGGTGCTCTCCACCAAAAGCAAAACAAACAACTGCTGA AATGTGGCAAGGTTTCTCAGTG
WI-22419b	67	T C ---				CCCTTCTGGACAGTTTGTCTTATGTGTTTCAGACATCAAGGNTCCCTTCCAGGCACAGCCAGTGCTT /CJCTGGATGGCATCAGCAGGCTCCCTGCCCCGGCCTTGAAGCATGGCTGTGTGCACGAT
WI-21342d	59	T C ---				ATTTTCCCTTTCTGTGTTTCGTATTTCCTTTTGTTCAGTAAATNAGCAATACACTGAIT/CJTGGAA ATCTGCATGATTAAATAACATTAAACAGTTCTAATAACACACCCCATATCAGAGTATAAAGCAAGAG GTTGAAAAATATCCCTAACCGAATGCAAAATTAGGTATCCCTCAAAATTCACATTTCTCCTCCTAGTT T

WI-21763b	154 A G ---	---	CATACCCCTTTAGGTGCCACACATTGATCTTAGTTAACAGTCTTGTAGTCCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACTTCCAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT GCTCTCCACAGCTGATT[AG]CAGACATTGCCTGTGCTTCTACCCACGAGCTGTCTAGTGCACCTT GA
WI-21763a	135 T C ---	---	CATACCCCTTTAGGTGCCACACATTGATCTTAGTTAACAGTCTTGTAGTCCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACTTCCAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT T/C]GCTCTCCACAGCTGATTACAGACATTGCCTGTGCTTCTACCCACGAGCTGTCTAGTGCACCTT GA
WI-22440	64 A C ---	---	CAGTCCATTGAGTCCACAGTCGAGGGTGCAATCTTCTTATCTTGTCTTAAGCCACTTGGGTAA/C] TCCATTCCAGCTCTGCACCTTCTCCAGTTTCTCATGTGCAAGTCCCTGGAGGAGGAGGCTTCTGG AAAT
WI-22449	74 T C ---	---	CAATGAATGTTGTGGCATATGATTTNCCATTGTGTGACAATTTATTAGCTGGCATCCGAATACAGTAC TTCCTTT/C]GAAAAAATACACAATGGGAACCTGACA
WI-21965a	112 A G ---	---	CAGTTCCACCCAGAGGCTTTATTTACGCCACTCAGGACCCCTGGCTTCTGCTCCAAAGCCACTGAACA CAGTCAGGCTCTTCTAAACACTGGCAGGACCTCCCCACAGCC[AG]CCCCACAGGTTCTCTGTT TCCAAAGTCTGATGGATTACAGCAAGACCTTACACATTACCCCACTACCTGCTGGAGAGGAGGTC ATGAGGCAGCCTGTGGTCCAGCTCAGTGTGACACACTGCCAATGTGC
WI-21687c	115 C G ---	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAAATTAACCCAGATGGGTCTACATTTTNTTCAAGTTCA AACCACATGGTTTCTAGTCAGAAAGTCTCATGGACTTCTTCTTAAG[C]GTTGTTCTATGATCAGAC CACCTCTAAATGTGGCTTTTACCATTACAGGCTACAGTTGAATCAGGCAGGAGCAGCTGCTGGAG AG
WI-22374a	149 T C ---	---	AGCTTTTACAACAAAGCGAGGTTTAAAGAGCCTGAGAAGAAATTTACAACATTTGACTATACAGAG TCTTCAATCCAAAACAGTTAATAGTAACCTGGTGGCACATACAACATGCATTGAATACTCTGTAT TATTCAGTAACTAAAT/C]AGGNTCCTGCATCATCTCTTCACA
WI-22250b	132 C T ---	---	ACTTGTCTTCAGGCAGGCAATTTCTGGGATCTAAACTAGAAAATCCTTGAAAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCAGTGTAGTGGTTTATTATGGGGTCTCTGCCTCCTGGCTGTGTTATG[C/T] GGANCCAGGAGTGGAGGAGCCGTTGGAATAGACAGGGGAG
WI-22250a	89 G A ---	---	ACTTGTCTTCAGGCAGGCAATTTCTGGGATCTAAACTAGAAAATCCTTGAAAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCAGTGTAGTGGTTTATTATGGGGTCTCTGCCTCCTGGCTGTGTTATG GGANCCAGGAGTGGAGGAGCCGTTGGAATAGACAGGGGAG
UTR-04932-2b	192 G C ---	---	GCAGCCATCTCTCTCCACACCTCCAGGCCACCCCTGGGGCAGAGACACCTCATGCCACGAGCAG CTACGTGGCCCGAGTACGGACCCGCTGGCCACAGGTTCTCGGCTCTCAGGACGTCOCAGCAAGTGA GCCAGAGGTTTGTCTGGGACTCCACGCCAGGGGATAGGCCACGCCAGAACCTG[C]G/C]AGTGCTTC TTTGACGGGGCCCGCTGCTCAGCTGCTCTCTGGGAGGTGAGGAAGGAGGT

UTR- 04932-2a	149 C T ---			GCAGCCATCTCTCTCCAAACCTCCAGGCCACCCCTGGGGCCAGAGACCTCATGCCAGGACAC CTACGTGGCCCGAGTACGGACCCGCTGGCCCGAGTTCTGGCTCTAGGACGTCCAGCAAGTGGGA GCCAGAGGTTG[C]/TTGGGACTCCAGAGGGGATGAGGCCAGCCAGCCAGAACCTGGAGTGCTTC TTTGACGGGGCCGCGTCTCAGCTGCTCTGGGAGGTGAGGAAGGAGGT
stFIBBb	412 G C ---			GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTCGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACACGGCCCTTGCCACTGTCTCTGGCCCTCTCTCTGATGCCAGG TTTGACCCAGCTCGAGTCTCCCATGTTGTAGTACATTCTCAAGATGCAGCCAGGAGGCTCTCTGA AGGACCATGCTGGTTACGATGGTCTGAGCTTCCTTAGAACCTTCCATGGTT
stFIBBa	341 T C ---			GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTCGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACACGGCCCTTGCCACTGTCTCTGGCCCTCTCTCTGATGCCAGG TTTGACCCAGCTCGAGTCTCCCATGTTGTAGTACATTCTCAAGATGCAGCCAGGAGGCTCTCTGA AGGACCATGCTGGTTACGATGGTCTGAGCTTCCTTAGAACCTTCCATGGTT
stGLV2	61 T C ---			GTCAAGAGGACGCGCTCTCGGAGCTCTCCACCATGGGCTCTGCTGCTCACTAC[C]/CCTC CTCACTCAGGACACAGGTGACGCCCTCCAGGGAAGGGTCTTTGGGAACTCTGGGCTGATCCTTGCTC TCTGCTCTCAGGCTCAGCGGCCAGGCTGACTGACTCACTGGCATGT
stSG1001 7c	70 T C ---			GTTACGGCTCATCTTGAACCTCTGGGTCAAGCGATCTCCACCTCGACCTCCAGGGTCTGGGAT TA[T]/C/JAGGCATGAGCCCGACACCTGGACACAAATACATTATATACTCTAAAGTATAGGATTACT TTAAGAGAAGGAAACTAAAGTATGATGGCTTACTTTCTAATCC
stSG1001 7a	33 G A ---			GTTACGGCTCATCTTGAACCTCTGGGTCAAGC[G]/AJATCCTCCACCTCCAGGCTCCAGGGTCTGG GATTATAGGCATGAGCCCCCAGACCTGGACACAAATACATTATATACTCTAAAGTATAGGATTACT TTAAGAGAAGGAAACTAAAGTATGATGGCTTACTTTCTAATCC
stSG1002 3	63 A T ---			TAATGATAATTAGGGCATCTTCCACACGAAGATGACACAAATTGACCCCAATATCATTTGAGGC[A/T] AACAGTTTGGGCTGTTTTCCAGTAGTATGACAGTGA
stSG1009 6	36 G C ---			GTGAGAAAGATCGTCTTCTCCCTCCCATGAC[C]/GCTTCCCGGGGACCTGTGCGTTTCC ACCCGAGACGGCCTTTGTAGGACCCACTGCCACTCCGCTGTGCGCTGGGTCCGCTCTCTAG GGCTCGAGTGTTTAAG
stSG1011 8	107 C A ---			TAGGCTTAAACCTGGAACTCTACAAGCCAAAAGTCCCTCCCTGCTGAGGGCAGTACCTCCATTGGGC ACAGTCCAGACCCCAAGTCAAGATGCCCATTCCTTGG[C]/AJCTCAGCCCTCAGTTCTCTCATTTCC ACCAAGCGGTGCTTGTGTTGAGTTTCTCCCAAGTGA
stSG1012 0	89 T C ---			TAGTAGGTAAGAAAGCAAGGAGGATGCTTATGCGATGACTGTTTACAGTGGTGTGAGACTATGC CGTGTTCACGAACACTTAAAT[C]/GTTGTGTAATCTGATTTTATCCTCGTCTTACAAATG
stSG1017 8	42 C T ---			TTGAAGCAATATTGTCTAGCACTCTGCTGGACATTAAAGTCCG[C]/TGGGAGGAGAAAGTGAACAGGAA TCGATTCTTTGTCTTTAACTGCCCTTAGTTAGGAGATGTTAAATACTTTGGC

stSG1019 3	136 GA ---	---	---	GGACAATACTACCTAAGGACAAAATACTATTATTAATAAAAAAGTCTCTAGTGTATATTGTGTAA CACATTTCTGGAGCTGGTAGGAATAACCATTTTATTTTCTGTAGTGCCATCTATACAAAACCTTTTAC T[G/A]TTTGAACCTGAGATTTAAGTTGCAAACT
stSG1020 2c	143 GT ---	---	---	AAGCTAACTTAGGTGAATGGTGCCACTCAAAGGCTTTCCGAGGGAAGCTCAGTCTGGCTTGGGAG AGTCAGCCTTGGTCACCTCATACGGGGCTCCAAGCTAAGGCGTCAAGGAAGCAGTCCCACTGCTTCT CGCTGTCA[G/T]CAAGACCACAAGGCAGATGCCACTGCTGCTCTTTCTTGTCTACTTTCT
stSG1020 9b	75 A G ---	---	---	TCTTTTCTCTTTTCACTCTCAGTCACCATGATTCATAATAAACTAATTCCTCTAAGATCCCACTTTAT TTTTA[G/G]CTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1020 9a	34 CT ---	---	---	TCTTTTCTCTTTTCACTCTCAGTCACCATGATT[C/T]AAATAAACTAATTCCTCTAAGATCCCACT TTATTTTAACTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1021 8	29 TC ---	---	---	TACTAGACATGCAAAATGAGAAGATTACA[T/C]GTGAATATTTAAAGAAAGTTATATTTGTTTGACAT AATATGCATTGTACCCGGGCATAATAAAGTTAAAGCCAGTTATTCTGA
stSG1025 2	108 AC ---	---	---	ATAGGTTTCAGGAACAAAATCATTAATGGAAAAATGAGAAGAAATTCCTTTATTTTGGACCAATTTT AGGCACCTAAGAGTTTCTTTTCTCTCTTCCCTTTCCCTTGATCA[C/G]AGTGAAGATATGATAGGGAATTC AGAAATTTCTCTCTTG
EST10915 0	123 AC ---	---	---	CTGTATTAATTAGAAGGCACATTAATGAGGGACGGAAAAATCTACCTGTACACAAAAATCTGTAC TTTAACAGCATCTTCAATAAACCCTTTAAAGGATAATGGTTACGATCATTTTAAAG[C/A]ATTTTAA GAACGAGTTATTGGAC
EST11023 1	166 TA ---	---	---	TTTTTTGTTAAACCAACCCTGAAAGTTCCACATGTGAATATAGATACAAACAGTGAACAAAAT ATGTGGCTCCCATGTACATTGGTTACCTATGTACAAAGTATCTATACACCAGTAAACAGCAGGGC AATTAGTCAATTAAAAAAATAGTACATGTTA[T/A]GTGTAATAAAATTTAAATTTACAAAGGCTTT TCCACTCGTGGATTGATTCTTTTGGAGGGAGTAATCTGG
EST14096 8	71 GC ---	---	---	GGGATGTATATTACAGATAACACAACCTCACAATAATACCATCAGACATTGAAAACTAAGGCCATTCT GTGA[G/C]TTATTTTAAACCTTGGTGTTCACATAATGATCTTAAAAAAAATGAATTACCAAA ACCAAGATTCTCTTCTAAATGAAAAATTAATGCAGGTACAGGATAAATTTAGGGCTATATCTAATC TGAAG
EST22113 6c	125 CA ---	---	---	TGCAAAATTGTAGAAGGCAGCAGGGGCCAACCCCTGGGACCTCATCTCTGTAGATGTGAGGTG CAGGGATGCTTAAGTCTTCTCTGGCAGAGACCCGAGGTGCAGAGATGATTCTTCTCA[C/A]CCCTTC TCTCAGGGTGTGGAG
EST22555 7	60 GA ---	---	---	TCAAGCATGTGTAAAGGCACCTGCCCCCGCCAGACCCCTTTTAACTTCTGCACACTGGAAGGT[G/A]AAA CCTGGGAGAGAGAAGACACTCCCTCCCTAGCTTCTACCTGGGCACCCCTCCAAGATGAGCATTCATC TTGGAGACCAAAATAAAAAAGGACAAAAGACCAAGCCAGGGCTCAGAG

EST22917 6	74 C T ---	---	GTAAACCTTGCAAGCCCATGCTAAATGGAAGCCTGACTACCAGGGGGCTCTTGGGCTCTCAATGCA ATAGAAA[C/TT]GACATGGGGCCCAAAAGACTTCCAGACAAAAGCAGCGAAGGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65 A G ---	---	CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGTAACTTAACCTCAGGCTGTCCTACTCA[A/ G]TGTGGTTGCTAGCCTACTCGCACACAGGAAGCTTGGAAATTTGGAGGCTCCAAAGTCACCTCCCA
EST36745 3	56 A G ---	---	GAGGGGGAACCTTCAAAGAGGATTCCAACAGTGAAGCAGAATCATGGGGCAAAAGTC[A/G]CTATGG GGCCAGACTGAGGTTGGACACACAGCAAGCACTCCAAAGCTGGGCCAATCCCAACCGCTGGTGAAGCCGC ACAGCACGGAGTAGCCAT
STS- R37410c	201 A T ---	---	TGTGACCATACCAACCTATGCAATAAAGAAAAAGAAAAAATCCTCACCTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTTCAGGCTTTTTGAAGTGTGAATAAAAGTTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAATAACAAAATGTGTATCTCCTGAGACACATTTATAAACATTTCTGGTATG T[A/TT]ATTGTGAGTGGTCTCTAGTGGCCAAAT
STS- R37410b	139 G T ---	---	TGTGACCATACCAACCTATGCAATAAAGAAAAAGAAAAAATCCTCACCTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTTCAGGCTTTTTGAAGTGTGAATAAAAGTTTCATAGCATTTTGGGA ATTTAT[G/TT]GTTGAATAAATAACAAAATGTGTATCTCCTGAGACACATTTATAAACATTTCTGGT ATGTATATTGTGAGTGGTCTCTAGTGGCCAAAT
STS- R37410a	48 C T ---	---	TGTGACCATACCAACCTATGCAATAAAGAAAAAGAAAAAATCCTCA[C/TT]TAAAAAACAACAA AAAAACCTTTGCAATGCTATCATTTTTTCAGGCTTTTTGAAGTGTGAATAAAAGTTTCATAGCATTTT GGAATTTATGGTTTGAATAAATAACAAAATGTGTATCTCCTGAGACACATTTATAAACATTTCTGGT ATGTATATTGTGAGTGGTCTCTAGTGGCCAAAT
STS- R42778	74 C T ---	---	TATCGTGGGAAGTTCCAACTCATACTTATGCTGCTTTTCTACTTGCTAATATTGGATGCTTCTTGCCA GGCTC[C/TT]TAAATTGTGCTGTAACTGGGAAGAAACCTTCTCTCCACAACCCCTGAA
UTR- 04350	125 C G ---	---	CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTTCAGCAGCTGTGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGTTTCCCTCCGGGATGGTGAAAATGTTCCGGACCTAGATA[C/G]TGACGA AGGTAGCACGACACTGTGAGTGCACTAA
stSG1026 6	55 T C ---	---	GAAATAAACTAAACTGCAAAAGCAAAATCACGTGTTAATAAGAAATTGTTCTTCTGT[TT/C]GACAGTTG AAGTGGGTGTGAGATGGGCATAGCAATGAACAGTGGGAGCCCAATGAGGTCTCAGAAATGCGGGCAAA CTCCTCTGTGAAAAATGTAT
stSG1028 2	70 T G ---	---	GTATAATTCAGCATAAGCCAAAGCCCTTTTAAAAATAACCAATACTATCATTTTATGAAATCTTTACA AGAT[G/A]AGCACAGTAGTACAATATTTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC
stSG1031 0	128 C A ---	---	CACTTTAGATATGAGGAAAATGGTTTTAATGGACACAAAAGGAGTCAGCACGTTGGAACCAACATAG TTTCATACCACGTTGAAACCATGTGTTTATGATATGCAATAACAGCAAAATAATTTTTCACCT[C/A]TTG TCAATGCCAATGCATTGAAAGGCCACAGAAAATGAGAAAAGGATAACAAACCTTTTGATAAAAAAGTGA AGAAATTTCTGTGTG

[illegible]

siSG1847 b	95 GA ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACACAAATGCTACCCCTAAATGAAAGAAATTT AGAGGTTAAATAAAACAAGTGAGAGACC[G/A]TTTACTTACATCAGTTGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAAATTAACCTTGATCACTGTGCT TCAAACACAACCTG
siSG1847 a	49 CA ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACACAAATGCTACC[C/A]CTAAAATGAAAGA ATTTAGAGGTTAAATAAAACAAGTGAGAGACC[G/T]TACTTACATCAGTTCCGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAAATTAACCTTGATCACTGTGC TTCAACACAACCTG
siSG1897 a	83 AG ---	---	CTTAATGCCCTTCTCTCTCTGACACAGGACACAGATGGGTAACATAGAGGCATGGGAAGTGG AGGAGGACACAGGACTT[G/G]CCCAACCACTTCTCTCCCGTCTCCCAAGATGACT
siSG2022 a	86 TC ---	---	TGCTTTGAGGTTCAAATCTGAGATATCTATGGCAAGTTTATAAAAAGTACATTTGATCAAGGTACAA TTTTAACATTAAATACAT[C/G]ATTCCTAATCTCATCTATTTAACATTAAACACAGGCCCTTTGTGT TGTTATTTTTCTCCCTACAATATTTCTGACTCTGTAGGACAGTGGGCCTCAGTTGGGGGGTTGAC T
siSG2076	104 CG ---	---	AAACGTTGTCCCAAAATTGTTTCAGTTTCAACAAGTATAAATAAGACTTCTGAAAAAAGTTTACA ATTAGTTATAAACACATTAAGAATAATTTTGACATT[C/G]ACATCACAGTGGGCAATTT
siSG2108 c	71 AG ---	---	TTGAGCAACAATGATTTCGCAATTGGCAGCTCCAACCAAAAATGATTGAGGGCTCCACAGAGA GAGC[G/T]AAGGGGAAGACTTTTATAGGACAACTGTAGAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGTCTGA
siSG2108 a	49 TC ---	---	TTGAGCAACAATGATTTCGCAATTGGCAGCTCCAACCAAAAATGATT[C/G]AGGGGCTCCACAG AGAGAGCATAAGGGGAAGACTTTTATAGGACAACTGTAGAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGTCTGA
siSG2141 b	173 AG ---	---	TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTATTTTAAACAAATGACTGCGGTGTAC TGAATCTGACTGTGTGAATAATCTCAGAATGGCAGCACCAGTGGCATGGCGATGGTGCAAGTGGGT GCAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAAG[G/A]AGTTCCCTATTATTATTTAAGGC AGTTTCAGAGCACTGGCATCTTGTGCTCTG
siSG2141 a	113 CT ---	---	TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTATTTTAAACAAATGACTGCGGTGTAC TGAATCTGACTGTGTGAATAATCTCAGAATGGCAGCACCAGTGG[C/T]ATGGCGATGGTGCAAGTG GGTGCAAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAAGTCCCTATTATTATTAAAGGC AGTTTCAGAGCACTGGCATCTTGTGCTCTG

stSG2148	50 A G ---	---	TGGGAACAACCGGCTATAGTCTAGTCAATATTTTATAGACCGTGATTC[AG]AAAGAAACAATAA ATGTGGATTAGAAAGGAACATCCATTACTGTATTTTCGATACCTTGTGATGTTCCACAGACGAGCTC ATCAC
stSG2175	68 C T ---	---	CTCAATGAGGACTCCATCAGCCAGCGGTTTATATGGCAGATGAGCTGTACAAATCTGTTGTGCT [C]TGCCGCGTGACTCAGCTAATGCTACCGGGTTGGAGCGCACACCGAGCCAGCCACCTTTTCCAT ACCTGGCAGAGGGAAGGAGTGAAGGACCA
stSG2189	41 C T ---	---	CAAGTGTGAAAGCTGGGATTTGAGCCTGATATTCACACTA[C]TCTACATTCCTCCAGTATAATA GGAACATCATCGCTAACTTTGAGCAGTCTAGTCTGAGTACTTCGTATAGGTTATCTCAATCCTACTC CAGCTTTGCGAAC
stSG2200	49 T C ---	---	TGTTGATGACCATAGAGGATGCAAGCTCCGGCTGGTTCTGTATGATG[T/C]TTTATATTTATGTAT AATGCTTACCTGATGATACCCAAACATATTACTAGCCTTATAGATGAGGATGGATGGCAGCTTGGCTG GTCAAT
stSG2243	85 G T ---	---	CATTTCTGCCTCTGCTTCCAGTACTACCCGTCAGCAACTGCCTCTGTATATAAATAAGTATCAA GATGGTCAGTAGAAAAG[G/T]AGAGCATCTCTCAGCCCTGGAGACAGTGTGGGAGCTTCAGCT
stSG2257	65 A C ---	---	TCAGTGATTGTAGGAGCTGGCTAAGTCATGCTAACTCTGTGAGGCAGGCTATCAGAAGGGCAG[A/ C]GTGCAGGAACCTCGCCAAGCACTGGGCTGCTCTCAGGCAGAAATTCCTCCT
stSG2306	67 A G ---	---	GTCAATCAGCGTAGAGGTCACTGGTATAAACAACAGTAGCTATATGATATTTGGGAACATTTTACA [A/G]TATGCTCCCATTTGGGTTTCCAACTGATACCAACCATGAGGTGAACACTTTCAGTGTTTCACAG TTCCTCCAGAGA
stSG2334	70 T G ---	---	GAAACTACCCACAGCATCATGTTAAAGAAGAGAGATGAAAGAAAAAATCCCCGCAAAAAACA AAAAAT[G/T]GCAGTGGAGGGGCTGTGGGAGGGTGAATG
stSG2339	63 T C ---	---	AGAGCAGAATGGTGAATCAACAAGACCTCAAATTTGTCTTGAAGTGCAGAAAGTAACTGCTGTCAC[T/C] GTTCTCAGAGTCACCATTAAGGTGACTGTCTATTTCTGGCTGTGCTTCTTCTATTCATCA
stSG2465	76 C T ---	---	CAAGACTAAGAAGCCGACCCGAGTGGTCCCACTCAAAAAAGAGATTTCTGATTTACCTCAAATG CAGAAACCA[C/T]TACAGATTAAAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCCTC ATCTTCAAAGTGTGGGTATGCA
stSG2549	140 T C ---	---	TTGCAGGCTTGATTCACAATAACAAAGTCATGTATAGAGAATGTGAAATGATACTTGAAAAACCAA GATATATAAATATTGAAGTCATTTATGCCCTTTTGTGACTGGGTTAAATATGCAAGCAGCTAAAG GAATAT[T/C]TACACCAACCCACCCCTTTTAACT
stSG2577	123 T G ---	---	AATTGCCAAATGGAAAATTCACAGAGGATTTTAGACCAACTTTGCCCTGTGTCATTCCCAGTTTGGT CCCAATATAGGCCCTTCTGCAAGAAGAGATCAATGCCGAACCCGAACCTGTGAAAGCA[T/G]GAACAATC CCGGCCCAAGATTAATTATT

siSG2577 a	121	C T	---		AATTGCCAAATGGAATAATCCAGAGGATTTTAGACCAACATTTGCCCCTGTTGCATTCGCCAGTTTGGT CCCAATATAGCCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAGC/TTATGAACAATC CCGGCCAGATTAAATTAT
siSG2700	58	G A	---		ATCTCTCGACTGCTTATAGTGGGAAAGGAATCAATTATTAATGAAGTGTCCGGCCCGC/GA/AGTCAC TCAGCGTTTGGGGAAATAAACCACTGGTCCAGAGCAGAGGAAGGCTACTTGAGCCGGACACCA
siSG2724 b	101	T G	---		AAACAAGCTTTGTCATTTCCACTACATTTTGTGTGCTTTATATTAATATTTGCAAAATGCTATAAT TTAATCTATATTCCAATTGCTTGCATAATCAT/GTTTTTTTAACTCCTGGGGTGTGAAAGAAC
siSG2776 a	65	G A	---		GTGGCCGATCTTTACTTTCCAGAAAAGGGGTAAATAAAAACCTGTAGAAAAGTCTCGAATATGC/G/ ATATTGGCCCTTTGGAGTTAGGCCAGGAACCTCAACAAGGGACACTGCTGGCCAACCAAAAA ATATCCACTAAATCCCGAATATAGTAACCCCTGTCTTGTCCGAATG
siSG2791 b	109	G T	---		AAGGAAAGGTGGAGGGAAGGGAAGAAATTAACAATGGTTAGAAAAGAGCAACTAAAGATTATTC TATTATACCTCTGAACGGTAACTAGCAATTTTAAATAATTTG/TGGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
siSG2791 a	100	A G	---		AAGGAAAGGTGGAGGGAAGGGAAGAAATTAACAATGGTTAGAAAAGAGCAACTAAAGATTATTC TATTATACCTCTGAACGGTAACTAGCAATTTTAAATAATTTG/TGGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
siSG2826	85	C T	---		CCGCAATTTCAACACACATTTCTATGAAAACCTAAGGGTGGATCATGTACAAACACAAAAACAAGC TCCCTCCCTCCAAAAACAAC/CT/GAACAAAAATAAAGAAAGAAAAACCCATGAAATGCCAGGTTTA ATTTTTTTCC
siSG2850	88	G A	---		ATGGTGCATTGTAAAGGCAAAATTAATACTTTTCAGGCGGGGCTGGCAAAATTTAATGAGCTGA TGTGTCCCAAGGGAGACGGCC/GA/GGCTCACACATCCCATCAAAATACTCTCCCAT
siSG3031	71	T C	---		ATACTCACGGGGCTGAAGGGCAATGTGAAGAGTGAAGTCAAGTCTCTGGCATTTTCTGTGGTGCAGC AAAT/C/GCCCTTTATTTTAAATGATTCAGACATCTGGGCAGCATAGCT
siSG3058	81	G A	---		GTCCCAACTCCTCTCCTCTTAGAGAAAAAAGTGTGATTACCTCAACTTGAATATGAAACTGTGATTG AAAAAAGTCAAAAC/GA/ITGAAGAAGCATCAAGCCCAAAAGGCAAAACTGGCTGAGGC
siSG3092	94	T G	---		CAGCATCTCCAGAACATTCCTAGAACTGAACCATTTCTGCACTATTGAAAAACAAGCCAAAGTTC CAATCCAAATAATAATGAACGTGC/T/G/GATAAACATTCCTTATGTTCCAGCCCCCTACTTT AGTT
siSG3230	95	A G	---		AAGAAGTACTTTGGTAGCTATTTAAATAAGAGGGGGTGGGAATGAATGTGAGATACGAGCACCTG CATCTTTTAGTCAATTGTGAGTGGAGT/C/G/GTGGGGTGTGAAGTGTCTGAAGTGAAGTAG
siSG3245	160	G C	---		ACATCTCATACCCAGTAAGATGCAAGAAAGGAATATCTGAGCAAGACGCCCTGCTCCAGGGGCC CAGGTATGTAGAGGCCAGTGGGGTGGCCACTTGGTGTCTTACCAACCCCTGCCATCCAGTCTG GCCCCAGTACCTACCTGGGAGGTG/C/TGTACTTGGCTTAAGTACTTCATGCTTAT

stSG3265	42	T C ---			AGGTGAATGAGTTACTAAATGTAGCATTATTTATAAGGAATTCGCAATTGTGAATAGTTTCTCAG TTTTCAATATGAAAGATGATGATTTTCAAGCCACATTCAGTGTATGTTTCTTAATAACACAATCGAC AGGACTGTCTGTTTCAGTACATGAGGACAGCTTTTTCAGGGCAATGGGATTTCTTGATAATGCTAA ATCTGTCTTGTGAGCTGAATTCITGGGCTTATGTGGCAGTGTGGTAAAA
stSG3269 b	141	C T ---			TGTACTACTGTGTCATCCTATCCATTCCTTCCCTGAGCCTGGACTGCTCTTCCAAGGGAGACTAGG AGTGAAGGGAGGAGTCTCCCAAAGTTACCCCTTTAAGCTTGTAAATAGCTCCATAGCCATGCTAAA GCATGA[CT]TGTAGATCCCAAGTCCCTGACACATTTTCTTCTAAGAACT
stSG3269 a	24	A G ---			TGTACTACTGTGTCATCCTATCC[AG]TTCCTTCCCTGAGCCTGGACTGCTCTTCCAAGGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAAGTTACCCCTTTAAGCTTGTAAATAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCAAGTCCCTGACACATTTTCTTCTAAGAACT
stSG3284	130	C T ---			TTAACCTCAAGAACTTTCAGTTACAGGAAGATTATCTAATATTAATGACTAAATTACAAAAAGC ATAAAATGTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCCCA[CT] TCCCTAACCTTTTGTAAATGCTGTAAATGGGACATTTGTTTGTATCTACCC
stSG3292	99	A T ---			GTCTCAAGTGAATCTGTAATACATTTTAAAGTCTGACTTCAATCGGTACATGAGGCTTAGACATA CACATCATTTGGACAAGTGACTTAAATATCTAA[AT]TACAAATCAAAATAGCATTTTCTTAACCTCAA TAAATGTCATATCTTTAGCTCTCACT[CA]CCAGTGTATCCATTTTCCCCAGCGGTAGAGCTTTCTG TTTCTGTAGATTGCCTGTCCTGGACATTTGATATAAATGGAGTTGCTGTATCATGTTCCGACTTCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATGCGTCACTGCTTCACTTCCCTTTAA GATCCGCGAGTATTATTTCTAAATTTGAACTTGTTTGTGGAAATAAAAAATCTGAGGACCACCTCAGAG GG[CT]ATAAGGGGAACCTCTTTTGTCTTAGTTCATAGGACTTTCT
stSG3323	26	C A ---			CAAGACTGTAAAGACGTAGGCTTGTGAGAGTGAAGGAGGATGCTGAACTTGCCAGGACTCAGG CTTCAGCTTCACATCCCGAGGAAGGAATGACATTTCCAACTGTCACTTTGTAGC[GT]CTGGGT CAAAGTCTAAGAGGACAAATAAATAGAGACT
stSG3369	69	C T ---			TCTTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCAG[AG]CTCACTGTAGCCTGGACCTCC TGGGTTCAAGTGATCCTTCCACTCAGCCAACTGAGTAGCTGGCTGCAGGACAAGTCACCATGCCTA CCTAAGTTTTGTAGAGACAG
stSG3398	125	G T ---			GTAAAGACAAGGTTTTGCTATGTTGACCAGGCTGGTCTTGAACCTCTTGGCTTCAAGCGACCGTACCA CCTTGGCCTCCCAAGTTGCTGATATTACAGGTGAGCCACTGCCCGCCGACTTTTAACTGAAT GTTGAAATCATTTCTGCTCTTTGCTGGGTAACACTGAT[AT]CAAGTTGCTTTAACCTTTGTGAAACCA TTTCCCTATCTGTACAAATGGACAACAGAACTTTTCCCTTCTCTC
stSG3416 a	43	A G ---			GTTTATGTTAAAGATTAGGAAAGCTGTGGATGTGAGGGGTGAGGTGATGTGATGGAGGCGCTCACAGA ATGAGTGGCAGAGAGGGCCCC[TA]GAAATAGCTTACTCTGTCTTCTATC
stSG3424	173	T A ---			
stSG3436	88	T A ---			

stSG3463	103	C T	---			GATACAGAAGATAGTGGTATGGATGGATAGTATGAAGGACAAAATAATACAAAATATATTTATTG AAATAAACAAAAATGCATACACAGCTCAATGGGTCA[C/T]JGGAAACAAACTTGCTTGACTATATTA CTGA
stSG3491	71	G A	---			CAAGATACCTCATTGTCTCTAAGTAGTGCAGTGTGGCAAATATTTCTCACGAACAAGGACGATTTG AAGA[G/A]GTGGAAATCTGTGCAAGGAGTACTTTACCTCCAAATAGCCTGCAATTTAGCAGTCTGA ACAACTCTCTAATCTTTACTGGCACCTGTGGATTTCTATTAAACTCATTTATACTATTTTCTGTGATG ACAGAAAATAAGTTAAC
stSG3523	33	C T	---			TAGCCATCTTACTAGTCTTTTGGGTTT[A/C]TJGCATATATGTGTGTACAAAACACACACACACC CCTAATTCCTCAATGCTCTTGGCATAAGTTTATCTCTTACTGGTCTC
stSG3536	213	A G	---			AGTACAAACACAGATTTAAGAGCTCAGCAGTATTGACACGCTGGAAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTACCTACACAGCTGCTACAAAACCCAAATACAGAATGGCTTC TGTGATACTGGCCTTGTCTGAAACGCATCTCAGCTGCTATTCTATTGTTTATTTGTTAAATGAGCTTG TGCACCAATTAG[G/T]CTCTGCTGGGTGTTCTCAGTCTCTGCCATGAAGTATG
stSG3583	112	G A	---			GAAAAGCTTAACATACGATCCATGTGCAACCCCAACAGGATCTACGAACTCTGGCATGATCCA CATCGCTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[G/A]TAAACATACACAGTACTGT CTAGTTATCAACACCTAC
stSG3586	60	G C	---			CCTAGTAACATAGTGAGACCTCGTCTCTACTAAAAATTTAAAAATCAGGTGTGGTGTG[C/J]ACG CCTGTAGTCCCTACTTGGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGGCCATTGCACCTCCAGCTTGAGACTGTTTCAAAA
stSG3589	101	T C	---			ATATAGTGTGGTAGCATTATAAACTCCTTTAAAAAGCAATCTGGCCATATCAAAAGGCAAAAAAGT GTATATACCCCTGGCACAAAAACCCCAATGA[T/C]JCTATTTCGAAGATGTATCCAGATGAAA GTATCCAACAACAACAAAAAGCTATATACAC
stSG3590	70	A T	---			GAGAGATGAGCTATTTATCTTTTACTTAATGAAGATGTAAGAAATGATCTTCTTCTAAAAAAA AAA[A/T]TTTCTCTGATGCTCTTGACCCCTGTAGGAAACACATTCAGTTTCTACACT
stSG3619	78	A C	---			CAGTGAGACTTCTCATTTTATAGCAAATACATTTTTCAGCTTAAATTTTCTGAATTCATACGCT TCTGTCAATTT[A/C]AACAACTCCAGAGAAAACCTGGGCTCTATATATTTAAG
stSG3644	40	T C	---			ACATATGTAACCTGCCATTAGTAGCCATATTAGGATGAGAT[C/J]GGATTGAGAGGCATGAACCAAGG ATGCGTAATAATCATTATGAAATAATAAGTTATCTGGGGAACGGCCATTTGTCCAACATTTACTAA GTGCCTACTA
stSG3646	70	G A	---			CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGAACAATAATATGCTTACT GGT[G/A]ATATAACITTTGATACTTGGTTAAGATGGTGTCTGCTAAATTTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA

stSG3646 b	55	A G ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATA[A/G]TATGTCCTT ACTGGTGATATTAACTTTGATACTTTGGTTAAGATGGTGTCTGCTAAATTTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3646 a	43	A T ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATG[A/T]TGATAACAATAATATGTCCTT ACTGGTGATATTAACTTTGATACTTTGGTTAAGATGGTGTCTGCTAAATTTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3693 b	85	A C ---	---	ATTGTTTCCCTGAACATTCOCGTGGTCTCCCTCTGAAAGCCGATGACCATCCAACCCCTGGACTCACCT GAAATATCCTACGAGGC[A/C]TGGCCCTCCGAGACTGACGATTATTAAACCCACACGGAAGG
stSG3693 a	30	C T ---	---	ATTGTTTCCCTGAACATTCOCGTGGTCTCC[C/T]TCTGAAAGCCGATGACCATCCAACCCCTGGACTCA CCTGAAATATCCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAAACCCACACGGAAGG
stSG3698 b	145	G A ---	---	TCITGGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCCCAGGGTTGCTCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGGAGCTCCCAGGAATCCACAGTTCTTGGAAAGAGAGGGGCTCTAAGTCT TTATTGGG[G/A]AGAATACCCACCCACCTTCCCTCACTGCAGA
stSG3698 a	51	C G ---	---	TCITGGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCCCAGGGTTG[C/G]TCTCTGACTTCCA CCATTCACTGACTTTTATGCCAGAGGAGCTCCCAGGAATCCACAGTTCTTGAAGAGAGGGGCTCTA AGTCTTATTGGGGAGATACCCACCCACCTTCCCTCACTGCAGA
stSG3724	107	C T ---	---	ACCAGCCTCATGTGCAGAGGGTCTCCTGCTGGATCCCCAACTGGAGCCATCCCTGGGCCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGTCTCAGTGTGAAG[C/T]ACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGCT
stSG3725	104	G A ---	---	GCCAAACAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAATATATTATTACAGCAACAGCAACAGCC[C/G]A]AGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAATAACGGCACATTTA
stSG3751	128	G A ---	---	CGGAAGAAAGAAACACAAATCCACAGGAACAATCTATGGTTTATACCTTTTAGAAAGATGATTTTG AGGGCTTCAGTATTTAAAGGGGAAAGCAGGCTGGAGGGGAAAGAGAGAGGATATGGTCCC[G/A]TT GCTGACTCCATGTTGCAAGAG
stSG3787	49	T A ---	---	TTCTGTGCAAAAGAAATCCACATCATTGTTGGTAGCAGAGGATCTTTATTA]AAAGTTCCCTAAGA CACTAGGGGCATAAAACCAACAAATAAAATAAGGAGTGATAGGCTAAAGCAGTATCTTCCCT
stSG3880 b	115	G C ---	---	GACAAGAGGGGAAGAGATGGCCAGAGACCAGGGCTGGGGCAGCTGGGGTCCCTGAGTCCAGGCCG CACCACACGTCCTGTGGGTCAAGGCCCTCCTCTGGGGAGCAGGTCTA[G/C]GGCACGGAGGATGCAG GGCTGGAGGGGACCCACCTCGGGGACCCAAAGGAGTCCATTCTGCCCT

stSG3880 a	36 G C ---	---	GACAAGAGGGAAGAGATGGCCAGAGACCAGGGCTG[C]GCGAGCTGGGGTCCCTGAGTGCCAGG CGCCACCACACGTCCTGTGGGTCAAGGCCCTCCTCTGGGGAGCAGGTCTAGGGCACGGAGGATGCAG GGCTGGGAGGGGACCCACCTCGGGGACCCAAAGGAGTCCATTCTGCOCT
stSG3895	44 A G ---	---	AATCAGCCATTGTACACATTGCAGCTATGTATTGTTAGTGTG[C]GJTTTTTTTTCCATTAACTAA TACATGCCCTCATAGATATATCAATTAGTGTATCACCATTGGGAACAAGATGCTGATTCTCAACTG AAAAAT
stSG3902	104 T C ---	---	TCTGTTGAGACTGGAGAGACCAGGTACCAAGCACCAGACTCTGTGGGAACCTGGCTTCCTGATAACA TCATCTATTTACACCTAAATGTGAACCTGCTTTCTTTTC[C]TCAGCTCAATAGCTTAACATCTAATTC ATGTTGCTCCCTTTGCTGGACAAT
stSG3935	50 G A ---	---	GGGTGCTGACGGACAGGCACACCCAGGTTTCAACAAGCAATTTGTCC[C]G/C]CTAGTGTGCAGGC TCCTCCCCAGTTTCCACAGGCTGAGTACTATGGGGTCACAACCTTCTCTGGACGT
stSG40	25 A G ---	---	GAGGAAGAGGTTGAAGAAGTGTG[C]G/C]AAATATATTTAAGATTTCTTTGGGGAGAAATCTCGTGC CCAAACCTGGTGATGGATCCCTTACTATTAGAATAAGGAACAATAAACCCCTTGTGTATGTATCA CCCAA
stSG4009	32 A G ---	---	GTGTGGGCTGCTGATGATGAATGGCGCGCT[C]G/C]TACTCTTTACGGTCTTACACITTTATGCTCCT ATGAATTCCTGATGGGCTTTAAGGGCTGAACCATATCTGAAGTTTCCACACACTGCTTACA
stSG4033	123 T C ---	---	AGAAGCCTTGGGGACAATGGCAGTGCCCTTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAACCTACAGTGCAGTAACCAAGAACCTAATGTTTTCAAGCATAAAGGTACTTT[C]G]GTGAAC AGGTGGGCAACAC
stSG4038 a	29 G A ---	---	GCTGAGAGCACGTGTACAGCCACGCCTG[C]G/C]GAGGCCACCTCTGTGCAATAAACATGTTCTGOC CATGTTCTCAGTCAGGAGGTTCAAGGCTCCCGGAGAGCACCTGAGGGTTCCATCACT
stSG406	53 T C ---	---	ACTGTGGTTCAACAGTATTGCGTTGTCAGACTAGGAAAGCTAAACGAACAAA[C]G]GTTTTAGTT TTGCTGAAGACTGGCCTTATTAATGGACAGCTTTCCTAACAGAGATTATTAACTTTTATCAGGTGTT AACATCTGTTTCAGGAACATGGCA
stSG4095 b	55 G T ---	---	ATCTGGGCTGAATTAGTCAAGCAGGTCAGATACTATTGTCTGCTAGATGTATTAG[C]TATAAAAA GTTTGCTTCTGTAATACTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAATCAAG CCTTTGGACTAACCCAGGGCATGGCCCTTCATCCTGG
stSG4095 a	27 A C ---	---	ATCTGGGCTGAATTAGTCAAGCAGGTC[C]G]GATACTATTGTCTGCTAGATGTATTAGGATAAAAA GTTTGCTTCTGTAATACTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAATCAAG CCTTTGGACTAACCCAGGGCATTTGCCCTTCATCCTGG
stSG4120	65 G A ---	---	TGCATGTTTCCACATCTTTCAATAACAGCAAAATGTATAATAAATACGTACTTATGGATAATCAC[G/ A]CTTTTCCCTCAGAGAGCCCCACAGTTAAACACGTTCCAGCACACCATTAATCCACCGAGCT

stSG4128	54 A G ---	---	CTTGGCAGATAAGGGACTCGTTTGCAGATATGACTTTCCTTTGTGTACATTTCTTATATATTTT TACTTCTTCTGAAAATGCCACATAATTTGCAATAAATGATTCACCTCTTAGCTCCAAAAGCAAGTCC TTTATCAAAATGCAAAATGTTCCAGAGGG
stSG4209 b	128 G A ---	---	CACGAAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAAACATCCACATGGCACAAAGC AGGGCCGGCCACTCCAGGCAACGAAAGCCACCCCGAACCTTTCAGAGGCGCGACTCCCTC[G/A]GC AGGGGGACACGAGGCGACAGGTGCTTTGATGCTCCGAAAGAGCTGAGCTCCATTCCA
stSG4209 a	65 G A ---	---	CACGAAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAAACATCCACATGGCACAA[G /A]CAGGGCCGGCCACTCCAGGCAACGAAAGCCACCCCGAACCTTTCAGAGGCGCGACTCCCTCGGC AGGGGACACGAGGCGACAGGTGCTTTGATGCTCCGAAAGAGCTGAGCTCCATTCCA
stSG4254 b	31 G A ---	---	CATTACCCAGAACGCCATGGAGGACACAGAG[G/A]CCACGGCCGGGACTCCCGCGATGGCTGGGGGG GCTATGGCTCTGACAAAGAGGATGAGCGAGGGCCGGGGCTGCCTCCTCCCCCAGGGGCGACAGGTGAC TGGGGGACCATGGCCGAAGAGAGGATGACCGGTGATG
stSG4301	81 T G ---	---	TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGGGTAGTGGCTCCACACTTTCCAT TTAAGCAATAAATTT/GIAGCTTCTGAGTAGTTGTTCCAGTTTCAACCAACATTTTG
stSG4331 b	71 T G ---	---	CTCACAAGGCCAACACAGAAAAGATACAAATCATTCATCCAGCTAATATTTAGTTTATGACAC AGAGT/GTTCACAACAAGTTTAAAGTGCACCTGAAGAGCATGTTAAAGTTTAAAGTTATCACTT GGAGAGCAGATTTCTTGGCCTCGCCTTGATTTCTGTTTGAAGGGTGTGC
stSG4340	76 G A ---	---	TTTTCACAACATGGATGGACCTGGAGGCCATTAAGTGAAGTAATGATACAGAAAGTCAAAAACC ACATGTTCTC[G/A]TAAGTGGGAGATAAACAATGTGTACACCTGGACGTGGAGAGCAGAA
stSG4361 b	109 A C ---	---	TCCCAACCATTTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGGCAC AAGTTCITGGAAATTTCCATAAGGGATAACTGCATCTTTTGC[G/C]CCTTCACAACACTAGAAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
stSG4361 a	24 T C ---	---	TCCCAACCATTTGAGTGACAGAGCT/GCAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGG CACAAGTCTTGGAAATTTCCATAAGGGATAACTGCATCTTTTGCACCTTCACAACACTAGAAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
stSG4376	73 A G ---	---	TTTCACTGCTACTGGTTTCGGTGTCTGAGTCTCAAACTGCTTTGCAAGTGTCTCTCAAGGGGAG AACAG/GCTGGAACTGGGGCTCTGCAAGAGCCATTTCTTCCAAAGCCATTTCTTCTCAGCTGC
stSG4381	50 T C ---	---	GAAGGCCACAACACTCCATAGCCAGAGAAATGACAACATACGATTTCTTTT/C]TCAGTCTTGTAGT ATCCACAGTAGTGTCTGTCCATGTACAAGTGTGTCCAGAACACCCATTAAATTCATGCC
stSG4410	79 A/G ---	---	ACCAATGGTCTGCTATGTGCATCCGATATTTTGGCCGATCTGAAATCTGCAAGGGCTTAACCAT TCAAACACCGG[G/A]GTGACAACGAACCCAGTGGACTGTGAAACTCAGGCTGCAGGAGGTGGCTTGT CAGCTGGGT

s1SG443	65	CT	---			AGCAGATCAGTCAGCCACCTTGCTCTCTCTCTCTTTAGGGAGAGGCTAGGCAGTGAACACATCA/C/
s1SG4430	54	AG	---			TJGTATGCAATGAGAAATAACCAACTGGTAGGATGGGGAGGGGAGGCAGGGAATAGGCAC
a						AAATGGAAATCTATCTCTGGCTGTCTCTCAGGTC
s1SG4448	99	GA	---			ATGCACATTAATGAATGGCCTAACTACTTGGAACTTTAGTAGTTCTATAAGGTJAGJATTAAACATA
						GGTAGGATCCAGTTCTCTATGACAGGCTGCTGAAGGAACAGATATAGGCATCAAGAGGGCCATTTT
						CCCTCCCTCCCTCTCTCTCCCTCCAGTCTTTCCATCTGTTCCCTCCCTCCCTCCCTCCCTCCCTCCCT
						CGCCTAGCCCTGCCCTCTGGGGTCACTGCG/ATJGGGTTAGGCCCCCAAAAA
s1SG4449	92	TC	---			ATTAGCCATTCATCTTGAACAAATGCTTTACTGTAACTAAGAGTACTGTACTGATGATGTTACAAT
						TAACTTTGGACAACCTTAAACTTA/TJ/CTAGTGACATTTGCTGTCTAATAATCAAACTACTTCATCATA
						GGCTGAACATAATTATTAAGAGCAAAAGTTACCCCTCCC
						CAGACATGAGGGATGGCCCTGCTCTCTGGGACAGAGCCCTCA/CJAGATGATGTCCATGTTTGTGT
s1SG4467	42	CA	---			GAATGAAACTCAAACTCTCTCAGTTTATAGAGTCAATTTCTGTATCGAGCGACACACCGAGGAG
						CACACCTGCTTCCAAAGGCTGCTGCTCTGACACAGT
						ACATGTCAATTCCTGACCAGG/CJ/ATTAATAATAGTTTATTTAGAAGAAATGAGTTGAAGTGAGCGA
s1SG4475	21	AC	---			TTAAGAGACACAACTGGACTTTTGTTTCTTTTCTTACTGTAGCACCCAGGTTTCATG
						GTAACATCTGGGGTGGGGTGAGACAACA/CJ/ATGAACCAATAATTAATTAATTAATTAATTAATTAAT
						TCAAGGAGACTTTAATCTAGTTAATGTGAACGCGACCATCAATGGTTGTGAGGAAAGGGAGA
s1SG4477	32	AG	---			TGAAGTCTGCTCTGGGCAACGTTTGGCTCAATGAGTCAGACTTGGC
						TGAACCTAGAGCTGGTGGGAGCTGCAGGCGAGGGGCTGGGGGCGCAGATGAGCCGGCGGGGA
						CAGAGGGCTG/CJ/CGCCACGTCCTGGCGTTGGTAGAAGAGGACATAGGCTGCCTTGGACTCGATCT
s1SG4531	79	CT	---			GATTCTCATTTGACAGGGGAGACGCTGTTGTCATCA
s1SG4550	86	GA	---			TGCATTAAGGAATGATACGGCATAATTTGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
b						AAAAGAGACAGTGGGCAC/CJ/CAATTTGGAGGGGAAGCGGGCGAGGTTTATAGAGAAC
s1SG4550	85	CG	---			TGCATTAAGGAATGATACGGCATAATTTGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
a						AAAAGAGACAGTGGGCAC/CJ/CGCAATTTGGAGGGGAAGCGGGCGAGGTTTATAGAGAAC
						AATCAGGCACAAGCTCGGGAGAGAGCCCAACAAAAGCTCTTCTGCAC/CJ/ATGGGAGGGAGACAC
s1SG4590	47	AG	---			CATTGAAAAGGCATGCTCTCTCTCATGCAAGGAGGCTGGCTCCACAGGCATGGTCTCTTG
						AATCTGTATCACCCAGCGTGGT/CJ/CAATGTACTAGTAGCTTTCCACAGGGATTTTATACTATTC
						CTATAAGGTTTATCATGAATAAAAAGCTCACAACTCTTTTCAGGCCATTGCAGATTCACATTTATCT
s1SG4623	22	TC	---			TAATATTCCTGTTCAAGATGCTCTGGAG
						TAAAAAAAACAACCCCCCAAAAAACACCCAGAGTTTTTGTAGTTTTTATGTTTTTATGATTTTAAAG
						GTATTTCTTTCTTAGCTTCTAAATTTTGAGTCA/CJ/ATCAGAAAGTCTCCCTACTCCTCAAGGTGA
s1SG4843	102	AC	---			GAAAGGA

stSG6362	88 G C ---	---	TGTGAAATGTACACTCAGGTCTACAAATACCTATTATTCTCTGGTTAAGAAAGGTTTAGCAGGAGC CTCCAATGAGCACTGTATGTAG/CAG/AGAAAGGGAAGGAGCAGGAGGAGGAGACAGATCTGCACAGA AT
stSG8010	62 G T ---	---	CACATCTGTGTTCTGGAGCAAGGAAACACAGAAAGCCAGGAGTTTGGGTGTGCACTGG[G/T] GTCTTTCAACTGGGTGGAACCAAACTGAGTCCTTGAAGTCTCGCTCTGAGGCTGCAGAAGAATAGA TGCCTT
stSG8022	53 G A ---	---	AGCTCCTGACTCCCTGTTACGTGACGTGTCATGTTGGTAGCCTGAAATGGACCAC[G/A]GTGGGAGTTAT TTACACCATGGAACTGGAAACTGAAAACTCTACAAATCAATGCGTTATTCTTTATTTTCAGAGGGCAGGTT TATCAGCACACGCTGTATCTCC
stSG8032	67 G C ---	---	TGATTGTTAGGGATAAGTGGGCATTGTGTTACAAATTACTTCCAAAGAAATTCAGAAAAATTTGTGTGTT G/CJTGGAGGCGAGGTAGCAAGATAAAAGAGGGAGGACAGCTGGGGTTGGTAAAA
stSG8064	46 C A ---	---	AGCTGGCTCTTCTCTGTGCGTTCGGGAGGCTTACGTCCTCG[C/A]CCGTGGTCCCTGGGTGGCC TGCAGGACCAGGGGTGGGAAACAATGCCAGGGAGAAATTCCTGTACATCAACACAGGGAACA
stSG8064	23 G C ---	---	AGCTGGCTCTTCTCTGTGCGTTCGGGAGGCTTACGTCCTCGCCGCTGGTCCCTGGGTGGCC TGCAGGACCAGGGGTGGGAAACAATGCCAGGGAGAAATTCCTGTACATCAACACAGGGAACA
stSG8072	59 A G ---	---	CACCATCATCATCGAGTAGGCTGAGGAGCAGGAGGGGTGGGTCTTGTCTTAGGG[A/G]TGGC AGAGGAGAGGAAGTCCGAGTATTAGTGGCCGCATGCAAGCTTCAAGCCTGTCTGTTCAAAA
stSG8100	40 A G ---	---	ATACACCCACACACCCCACTCAACCTTGATCAAAATTC[A/G]AAGTGTAACTAAAGTATAAGAAT ATCATGACTAGTTAAAAGATAGCAATACCATAAGGTACAAGTTCAAGTATTAGTATAACCAAGTAT CTGAGTAACAAATGTCCTTGGAAATGGG
stSG8102	138 T C ---	---	AAGGCTCCTTTGAAAGCATGGTTTATTGTTCCATTTAACTTGTCTCAGCTATACCTGAAGTATGATT GACAAATAAACTTGCATATATTGAGATGTACAGTGTGATGATACATGTATGTATACAAATGTGAAA TGAT/CJTGTCAATAATCAATAATGGTATATTGGTTTAGGAAATGTAAGT
stSG8105	110 A G ---	---	CAGTGGTTCTCAAACTCCAGCGTACACGAGGATGGTCTTGTGCTTGTAAACACAGATGACTAGGCC CACCTGCGGAGTTCTGTGGAGTCTAGGCTGAGAAATTC[A/G]TTCTAACAAAGTCCCAGGTGA CCCTGAGGCTCTTGGACTGGGGAACATGCTTTGAG
stSG8130	96 T C ---	---	GTGTGTACATCATTTGGGAATGGAGGGAATAAAATGACTGGATGGTGGCTGCTTTTAAAGTTTCAAAAT GACATTCAGACAAGCGGTGCGCTGAGCCT/CJTGCCCTGTCTTCAGATCTTCACAGCACAGTTCC
stSG8130	36 C G ---	---	GTGTGTACATCATTTGGGAATGGAGGGAATAAAATGA[C/G]TGGATGGTGGCTGCTTTTAAAGTTTCA AATTGACATTCAGACAAGCGGTGCGCTGAGCCTGTGCTTCAGATCTTCACAGCACAGTTCC
stSG8145	124 T A ---	---	TTGTGGACTTCAAAATCTTCTTCAGATTTTAAATGACATTTATGATGTACATATTTTAAATTT AGACACATTTTAGAGAACACAAATGTGAACACAAATCTAAGAAATGAATGAGATGT[T/A]CTGAAA TCTGATTCAAACACTTATCTTAAACTGACTTCTGTCAATCTCTCTGCTGCTGTGAAAG

[illegible]

ESTD- AT3a	--	--	--	---	---	---	AGACCTCAGTTTCTCTGTAAAGGAAAGTTTGTCTTGGATCTCCATGGGCCAGCCAGCACTG GTGCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGACCAGGTGGAGGAATTTGAAAGGGCATTG GAATTCAGAGCAAAGACAGATATTAGAGCTGGGGAATGTGG
ESTD- B3AR	--	--	--	---	---	---	GGCTGCCAGGGTTCCGTGGAGCGGCCCTAGCCGGGCCCTGCTGGGCTGGGGTCTGCGCCACC GTGGAGGCAACCTGCTGGTCATCGTGCCATCGCCCGGACTCCGAGACTCCAGACCATGAACCAACGT GTTCTGACTTCGCTGGCCGAGCCGACCTGCTGATGGGACTCCTGCTGGTCCGCGCGGGGCCACCTT GGCGC
ESTD- BA511	--	--	--	---	---	---	GGGCAACATAGTGAAACCCCATCTCTACAAAAATACAAAAATTAGCCAGGTGTGGTAGCAAGTGC CTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGCTGCAG TGAGCCAAGATGGTGCCACTGCA
ESTD- BCL2	--	--	--	---	---	---	AGCTGGATTATACTCCTTCTTCTGGGGGCGTGGGTGGGAGCTGGGGCGAGAGGTGCCGTT GGCCCCGTTGCTTTCTCTGGGAGGATGGCGCACGCTGGGAGAACAGGTACGACAACCCGGGAG ATAGTATGAAGTACATCCATTATAAGCTGTGCGAGAGGGCTACGAGTGGGATCGGGGAGATGTGG GGCGCGCGCCCGGGGCGCGCCCGCACCGGGCATCTTCTCTCCCA
ESTD-BCR	--	--	--	---	---	---	CAGTGGCTAGTGGACGATGACATTCAGAAACCCATAGAGCCCCGGAGACTCATCTGCGCAAGA GACCAAGAGGTCAGCTTCTGTTGTCGGGAAAGGGAGGCGAGGTGACAAGCTAACTCTGCTTCAA ATCAACATCCGTGGACACTGTGTGGCTGCCATCTGCTCTGGCACA
ESTD- BRCA1a	--	--	--	---	---	---	AAGAAGAGAACTAGAAACAGTTAAGTGTCTAATAATGCTGAAGCCCCAAAGATCTCATGTTAA GTGGAGAAAGGGTTTGCAACTGAAAGATCTGTAGAGAGTAGAGTATTTCACTGGTACCTGGTAC TGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAAAGTTAGCACTCTAGGGAAGGCAAAAACAGAA CCAAATAAAT
ESTD- BRCA1b	--	--	--	---	---	---	ACTAAATGTAAGAAAAATCTGCTAGAGGAAAACTTTGAGGAACATTCAATGTCACCTGAAAGAGAA ATGGGAAATGAGAACATTCGAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAAATGTT TTTAAAGAACCCAGCTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTA TTAATGAAA
ESTD- BRCA1c	--	--	--	---	---	---	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTGTAGATGATGGTGAATAAAGGAAGATAC TAGTTTGTCTGAAAATGACATTAGGAAAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGAAAGGAGAG CTTAGCAGGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCAAGA AATTAGAGTCTCAGAAGAGAACTTATCTAGTAGGATGAAGAGCTTCCC
ESTD-C1R	--	--	--	---	---	---	ACACAGTGTGCACTGGGGCTGGGATCCCTCCTCCCTAATTTGCTCCGGGAAGCACATTCAATCA CCCAGTCAGTTTGGGGGACAGCCATGCACCTGAGCCTCTGCTAGCCCTTTCACCATGCATTCATCTAA GCTCTGCAAAAT
ESTD-C6	--	--	--	---	---	---	

ESTD-C7	--	--	--	--	---	---	---	---	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-CB22	--	--	--	--	---	---	---	---	GGCAAGTTTTTATTGATAGAGAGGAAATCAAATATATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAAC TGGGGATGGACAGACAATGGCAGTGCCAAACCCTAGGGCGGATACAAAAGAC AGGAAGGAAGGGTAGAACCATCAAAGAGGAATAGGCTGGTACCCCAAAGCAAGGAGGACCTAG TAACATAATTGCTTCATTATGGTCTTTCCCGGCTTCTCTCACACAC
ESTD-CB23	--	--	--	--	---	---	---	---	TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGGTCTTTCCCGGCTTCTCTCACACATACAGAGGCCCTACCCAGGACGACAGCT CTCAGAGCAACCCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAAAACGTTTCCCAACCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAA
ESTD-CB24	--	--	--	--	---	---	---	---	ACCAAGACAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAA AAAGTGTCCACCCGAGTCTGTTTGAAGCATCAGAAGCAGAGATCTCCACACCCAAAAG GCCACACTGGTATGCTGGCCACAGGCTTCTACCCGACACGTGGAGCTGAGCTGGTGGTGAATGG GAAGGAGTGCACAGTGGGTGACAGACAGACCCGAGCCCTCAAGGAG
ESTD-CB25	--	--	--	--	---	---	---	---	GTTTTCTTCAGACTGTGGCTTCACTCCGTAAGTGAGTCTCTCTTTCTCTCTATCTTTCGCCGTC TCTGCTCTCGAACAGGGCATGGAGAAATCCAGGACACAGGGCGTGAGGGAGCCAGAGCCACCTG TGACAGGTACCTACATGCTCTGTTCTTGTCACAGAGCTTACCAGCAAGGGTCTCTGCTGCCACC ATCCTCTATGAGATCTTGTAAGGAAGGCCACCTTGATGCCGTG
ESTD-CB27	--	--	--	--	---	---	---	---	TTTTCTGTTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTGTTGGGCTGGTTCATTTCAGGAGTCTGTGGAGTTCTGCTCATCTGCTGACCTATCTTCTGA TTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCAATGCTGCT TTCTCTGTTTCATCTGATGGAAGTCTCAACACCAATTTCCATACC
ESTD-COL2A1c	--	--	--	--	---	---	---	---	AGATGTATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTTATGCTCTCTTTCTGTCACCTTCAGGGTGTCAAGGTGGAAGAGGT GAACAGGGTCCCGTGGTCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACATACTGCGCTTG GTCAGCCTATTGAGCTGTAATCAACCATACCGTACCT
ESTD-COL2A1d	--	--	--	--	---	---	---	---	TGAGAGAACACCTAGTCTCCATCTTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTCTGGACCTGGAACACTGGACTCTTTCTACTGCAGCAGACAAGACTTACCC AAGAGAGATTAAATGGCAAAGATATACAATAAATTTTATTGACCAACACTATCATGGAACAGC ATT
ESTD-CPT2	--	--	--	--	---	---	---	---	GCCGAATGCCCGGAGTTCTCCAATGTGTGGAGAAGGCCCTAGAAGACATGTTTGATGCTTAGAA GGCAATCCCATCAAAAGTTAACTCTGGGCAGATGAAAAGCTACCATCCTTCCCTCATCATGAAAAC TGGGAGGCCGGGCATAGTGTCTATGCCTGTAATCCAGGATTTTGAGAGGCTGAGGCGGGTGGATCAC TTGAGGTGAGGAGTTTGAGACCAACCTTGGCCAACT

ESTD- CTLA-4	--	--	--	---	---	ATGGCTGGCCTTGGATTTCAGGGGACAAAGGCTAGCTGAACCTGGCTACCAGGACCTGGCCCTGCAC TCTCCTGTTTTTCTCTTCTATCCCTGCTTCTGCAAGCAATGCACGTGGCCCGCAGCTGCTGTGGT ACTGGCCAGCAGCCGAGGATCGCCAGCTTTGTGTGAGTATGCATCTCCAGGCAAGCCAC
ESTD- CYP2D6	--	--	--	---	---	CAGGCCAGCGTGGTCAGGTGCTACCATCCCGCAGAGAACAGGTGACGCCACCACTATGCACAGGT TCTCATCAITGAAGTCTCTCAGGGTTCCCTTGGCTGAGCAGGGCGGAGAGCATACTCGG
ESTD- D11S1873	--	--	--	---	---	AAAAAACATTTTAAACACCTTTTCAATCATATACACCATAAATTTCCATTTTTCACATAAGTCAGTT TGAGCTGAGTTTTTCCAAATACCTGCAATCTAAATGTCAATAGTAAATGCAAGTTTCAACAGACA ACTTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATACATATCTGGATTAAATATGCCCCATAT CTGCATGTC
ESTD- D17S33	--	--	--	---	---	CATCCCCAAGCCATCCTCTTAGCCACTGGCATTTTGGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCTTTGTAGTCCATGGGAAGGCTCCTCTGGGGCGGTG GGGTTGTGGCTATGTGGTCTTGTGTAGAGGGGGCTTTGGTTTCAAGTTGCACTATTGCGTTATT GCAGATTGCTTTGCTTCCACCTGAGCGAGCCTC
ESTD- D18S8	--	--	--	---	---	TTTGAGACCACCCCTGGCCAAACATGGCGAAATCACATCTCTACCAAAATTACAAAATTAGCTGGGTGT GGTGTACATGCTATCGTAATCCAGCTACATCGGAGGCTGAGGCAGGAGAAATGCTTGAACCCA GGAGGCAGAGCTTGCACTGAGCCCAAGATCACACCCTGCACTTACAGCCTGGGTGACACAGTGGAGA CTCTGTCTCAA
ESTD- D3S11	--	--	--	---	---	AACTGATTAGAACCTGAAATACATAATTTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAATCCAAATAAGTACACTGTAAATAAGAAATTTAACAGAAATATCATTTGT TTATTCAACTATTTATCACTTATTTTATTTGGTAAGCCATACTAAATTTCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	--	--	--	---	---	AGGTTCCACATTATTGCTGATGTTGCTGATGTTTCCAGGAGCCTTGATGTCATTTCTGTCCTCAG GTATCCACCTTGAGACGTACTTTTCAAAAACCTCTACAGCCGTTGTTGTTTAAATCAAGGTTGA ACATAAAGTA
ESTD- D3S2	--	--	--	---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCCCTGC TGAGTCTTATTCAAAACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGATTCCTCC AGAAGTGAACACTACTGCTCTAGAACCCAGAGTCATCTGGATGTTCTGTTCCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGCTCTTTATTGGAAGGATGCCGGTATGT
ESTD- D4S338	--	--	--	---	---	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGAAATGTAATT CTTAAACAATAAAGTGAAGTCCAAATTAATCTCTGATCCATGGACTGCAGAAATAAATGTTATTT TAGCTGTCAGAAAAACAATACTAATCTTGATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGTAATT GCCAATAAGCAGTAATAATTTGAGAGGAATCTTGTTTCAATGCAGTAG
ESTD- D4S95	--	--	--	---	---	CTTTCATGCACGATAGGCTTTCTCTACTAATCACAGAAATTTTGAGAAGAGCAAAACAACCTTCAAGG ATAATGGGCAATCACTTTCTTTCTCTTTAGAGTCTACCGG

ESTD- D7S399	--	---	---	---	---	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCCTACATCATCTTTTCAAAACATTTTCATCCATGGACTCCATAGTAG AATATTTGAAGAAACAACATGACAAACATTTTC
ESTD-DM	--	---	---	---	---	GTGGGACACCCGAGGGCTCCAGGCTGGGGCTTGACAGTGTGGCTCAAGCAGCTGCTCGGCCCTCCACT TCCATGGGTGTGGGCTGGGACCTCACTGCTCCTGGGAGAGGAGGAGTGGGAGGGAGACA GAATGCTGATTATCTGTGTGAGAACCAAGAACTTCTGGCTGTGGGTAGGGCAGCTGCTTCCAAAGACC TCTGATTTGAGGAAGGGAGCAGAGAGCGAAGAGAACAGAGT
ESTD- DRD1	--	---	---	---	---	TCCCAGCCCTATCGGTATATTGGACTATGACACTGACGTCTCTTGGAGAAGATCCAAOCCATCAC ACAAAACGGTCAGCACCCAACTGAACCTGCAGATGAATCCTGCCACACATGCTCATCCCCAAAAGCT AGAGGAGATTGCTCTGGGGCTCGCTATTAGAACTAAGGTAC
ESTD- DRD2	--	---	---	---	---	TCTGCCCTTTGTGCAGGAGGTGCCCGGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGGACCCGGTACAGCCCCATCCACCCAGCCACACAGCTGACTCTCCCCGACCCG TCCCACACGGTCTCCACAGCACTCCGACAGCCGACAGCCGACAGAGAAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	--	---	---	---	---	AAGACGATGGCCAGGATGAGCGCGCAGTAGGAGAGGGCATAGTAGGCATGTGGCGGGCTGGCTGG CACTGTGGAGTTCTGCCCCACAGGTGTAGTTCAAGTGGCCACTCAGCTGGCTCAGAGATGCCATA GCCAGAGGGAGGTGCGTGATGCCAAGGGCTTCTGTGAGGAGA
ESTD- ER882	--	---	---	---	---	TCTTTACAGATCCGCATCTGGGCTGTTGGGCATCGCTCCGCTAGGTGTACGGCTCCACACAGCTGG GGTGAGGGGTGGTGGTCACTGCCGGGGCCGGTGCAGACCCACCGGGGCTGGGAGGACTTCACCC CGCCTCACCTCCGTTTCTGCGAGCAGTCTCCGCATCGTGACT
ESTD- ETS2	--	---	---	---	---	ACTCACAGTGTCTTTAAGTGAATGGTCGAGAAAGAGGACCCAGGAAGCCGCTCCTGGCGCTGGCA GTCCGTGGGACGGGATGGTTCTGGCTGTTTGAGATTCTCAAAGGAGCGAGCATGTCTGTGGACACAC AGACTATTTTAGATTTCTTTTGCCTTTTGAACCCAGGAACAGAAATGCAAAACTCTTTTGAGAGG GTAGGAGGTGGGAAGGAACAACCATGTCTATTTTCAAGATTAGTTTG
ESTD-F2	--	---	---	---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCCAACTGTGCATGCACGCTTAACCTCT GCACCAATGGCCTCCAGGCCCGTAGGGAACTGGGGGATCTAGGGGATGGGTGAGGAATGGCCC AGCCAGTCCCGCGGTGCTGGTCCCAACAGAGGAGGCCGTGGAGGAGGAGACAGGAGATGGGC TGGATGAG
ESTD-F9	--	---	---	---	---	AGATCCTGATGATTTTTTCTAATTTTTTCTAATGTTTTTACAGTTTGAAGTTTTAGATTTATGCCCA TGCTCCATTTGAGTTAATTTTGTAAAGTATGATGTTTAACTCAAACTTCATTTTTTTTTTCCATA GGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAAC

ESTD- GCH	--	--	--	---	---	---	---	---	CGCAGACCGGTCAAGTGTGGGTGGGAGTGTGGAGGAAGGAGGAGGAACTGGGGGTTTAGGGACT TTCCGGGTGACTTTCCCGTTCTGTGCTTGCAGAGAAAGGGGGAGAACACAGAGCCAACTGGCTAA GTGTAAGGAGACCTCTGGTCGCACCGTGTGTTCTGCTGCCCTGTTACGCTGTCTGTCCGCGAGTCGA CTCTGTCCGGAAATCCGAGAGCT
ESTD-GCK	--	--	--	---	---	---	---	---	GTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGGTCACCATGAC AACACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGATCCCCACCCACACACTGGCTGG AGCAGGAAATGCCAGCGGCCCTGAGCCCCAGGGAAGGAGGCTAGGATGTGAGAGACACAGTCACC TGCAGCCTAATTACTCAAAAGCTGTCCGAGGTCACAG
ESTD- GNAT2	--	--	--	---	---	---	---	---	GACCCTGAGTAOCTOCTAGTGAGCAAGATGTCTCCGATCCAGGTCAAAOCCACAGGCATCATTG AAOCCAGTTTCCGTCAAAGACTTGAATTCAGGTAAGTGCATGGTTCCCTAGG
ESTD- GPPK2L	--	--	--	---	---	---	---	---	AGTCTTCATCTGCGGTGTCCAGGTAGATCCCTTTCACCCGCCGAGAACTGCTCGATATC
ESTD- HRAS	--	--	--	---	---	---	---	---	CTGGGCTGCCCGCAGCAGCTGCTGGCACCTGGACGGCGCCGAGGCTCACCTCTATAGTGGGGTGG TATTCGTCCACAAATGCATCTGGATCAGCT
ESTD- HSD3B1	--	--	--	---	---	---	---	---	TTGAAAGTTCTCCAGTTAACCCAGTCTATGTTGGCAATGTGGCTGGGCCACACTTCTGGCCTTG AGGCCCTGCAGACCCCAAGAGGCCCAAGCATCCGAGGACAGTTCTACTATATCTCAGATGACA CGCCTCACAAAGCTATGATAACCTTAATTACACCCTGAGCAAGAGTTCCGGCTCCGGCTTGATTCC AGATGGAGCTTCTTATCCCTGATGTATGGATTGGCTTCCCTGCTG
ESTD-HT2	--	--	--	---	---	---	---	---	GGGCTAAAATTTCCGAGCAACTTTGCATAGACTGTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGAGGAAGATGTTACAGTTTGTACAGAGAGATAAAAGGATAACCTGGGGTTTCTGTGC TTTGCTTCTCACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTCAAACAAGACACACCTT
ESTD-HT4	--	--	--	---	---	---	---	---	ACCAACGAGCCGCGATACAGACACTCTTAAGTTTGGCCCTAAGGCTCATCAAATCATTAGGCATTTT CTGATAAACTAGGTTCTTGGTGCTTCTATCGGCAAGAATGCGTACTTATTTGAATAGTAGAGGTAA ACCACACGCCCAAGAGTCACTGAGACTGGCAGCTTCTGCAGCAGGCGTGAACCCCGTAGCCTAAA TGACAGCCGAAGAGGCGCCGAAGACATGCAGATGTGC
ESTD-HT5	--	--	--	---	---	---	---	---	AACACACAAGCCCGCAGAGAAATGAACCTCGGACCCCTGGTTTACAAGACCAGTGTCTAACCCCT GAGCTATGGAGCCCTGCTGCTGTTGGTTTCTTCTCTTCTATGATTTATAGATTGATTTATGCTCCTA GCATTCGGGCTACCGAATAGGATGTAGCTTGAGTAAATTCAGGATATTCTCCTACAAAATGAAA ACATTTCTGGTCTCTGTAATCCCTCGAAAAGTTCT
ESTD- IGFBP1	--	--	--	---	---	---	---	---	ACCCAGTGGAGCCCGCTCATTTGACGGTCTTGGCAGGAGGTGCCCTGGGAGAAAGGAAGATGTTTC CAGGGCACACATAGCTTAGTGGAGACTC

ESTD- IGHV4-6	--	--	--	---	---	---	TTTACTATTTCAATGGATACAGAAATTGTGGGAGTCACTATATCTCTATGAACAAAAATTCAGATTT CAGTGTAAAGTAATGTTCCTACATGTGTGAGTGACGGGAGTGGTGGATCGGAGAGTGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATACTTCACAAAATACTAATAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	--	--	--	---	---	---	CAAAGTAAGCACCCCAATAATGTTAGCTATTACTATCATTAATTATTATTTATTTATTTT AGATGGAGTCTGGCTGTCAACCGGCTGGAGTGCAGTGGCACAATCTCGGCTCACTGCAAGCTCTG CCTCTGGGTTCATGCCATCTCTGCTCAGCTCAGCTCCGAGTAGCTGGAATACAGGCACCCGCCACT GTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTCACCGT
ESTD-IL1B	--	--	--	---	---	---	CCACTACAGATGGATAAATGGGTACAAATGAAGGGCCAATAGCCCTCCTGCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTGTTCTCTGCTCAGGAGCTCTCTGCAATTGCAGG
ESTD- KRT10	--	--	--	---	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAAATGCAATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTCTC TGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT18	--	--	--	---	---	---	ACCCTACCCCTCCCTAGCCGTGGGAGCAGGAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGAGGGCTGACATGAGACCTCAGACAGAACTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCGCTCAGGTTTACCACGTCAAGATTGACACA
ESTD- LF79	--	--	--	---	---	---	GGGTGATTTGAGGCTCAGTTAATATTCAAAAATGTAACCGTAGCAAAACTGCATTGGTATTTAGA AAATAAAAATTTCCAATATGTAGTGTGTTATACCTGCCTCTGCCATGCAGCATATAGCCTGT GGGAACAGGAGGGCTTCCCTTACCACCCAGA
ESTD- LMP2	--	--	--	---	---	---	TACACACTTCTTACCCATTCACTGAAAACGACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	--	--	--	---	---	---	TGTCAGTGTCCCTAGGGGCACTCAACACTCCAGCTCTTTCAGCTCTGGCCTGCTGCTGCTGCA AGGTTTTGCTTAATCTCAATCAATGTCTCTTCACTCTTTAGCAGCTGTGGGTTTTGTTGTTTC TTCGTTTTTGTAGTATCTGACTACTTTTTTAATTATAAAAGAGATGTATCTAAACAAAATAGAG ATTGTTATCAGAAAGTTCACAACATTTATTAATAATTTTTCACCTG
ESTD-MCC	--	--	--	---	---	---	TTGTGAGGAGTGTGCTGATGCTGCTGCCCTCCAGCTCTGTCCCTAGCCGAACCTCAGGACAACGTGCAG CATCCATGTAGGAGAGCCCTAGTCAAGTGAATGCTGAGGAAGCAGTAACACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGCTTCCAAAGGGTTTGGTCTAAGTGTGATTACCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATGTGTTCCCTGTTTAGCATGG
ESTD-NF1	--	--	--	---	---	---	ATTATCCAGATGAATTTACAAAACATAACAGATCCACAGACTGATATGGCTGGT

ESTD-NFKB1	--	--	--	---	---	---	---	---	---	AACATGGACTTGATATTTGTACAAAAAAGTTTATTTTCTAAAAAAGAAAAAGAA
ESTD-NPPA	--	--	--	---	---	---	---	---	---	AAATTTAAGGGTGACTTATATCCACACTGCACACTGCTAGCCCAAAACGCTTATTGTGGTAGG
ESTD-NRAMP	--	--	--	---	---	---	---	---	---	ATCAGCCCTCATTTTGTGCTTTGTGAACCTTTGTAGGGACGAGAAAGATCATTTGAAATTTCTGAG
ESTD-NRAS	--	--	--	---	---	---	---	---	---	AAAACCTCTTTAAACCTCACCTTTGTGGGTTTTTGGAGAAGGTTATCA
ESTD-OTC	--	--	--	---	---	---	---	---	---	TGTCCTAGGCCACGCCCTGCTTGTCTCCCTGGCTGTATCTTCTAGTACTGCAAGAGAACACAGAC
ESTD-PAI1	--	--	--	---	---	---	---	---	---	AT
ESTD-PAR	--	--	--	---	---	---	---	---	---	GGAGGAGGAGGTGGGAGGGGCTGTCTGCTCCAGGTCCACAGACCAGAGAGGCGCCTCAGTG
ESTD-PBDA	--	--	--	---	---	---	---	---	---	TATCCACACCCCAATGTGGCGCTGGGAGATGAAGAGGAGTTGATGCAGGT
ESTD-PS-1	--	--	--	---	---	---	---	---	---	GTGTTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTTCTGCAGGCATATAGAAATTTGGT
ESTD-PXIPI	--	--	--	---	---	---	---	---	---	GGGTTTTCTTTATGTAGGGTGATATGGATACITTTTGTGTTGATATATATAGCAATTTGAGGG
ESTD-Per/RDS	--	--	--	---	---	---	---	---	---	ACAAACCAGATAGGCAGAAATGGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTC
	--	--	--	---	---	---	---	---	---	ATCCCTGTGGTTTTATAAAAAAT
	--	--	--	---	---	---	---	---	---	GTGACCTTCTACITTTAAAAACITTTACGGGAGAAGAAATTAATATATGCTATGGCTATCAGCAGA
	--	--	--	---	---	---	---	---	---	TCTGAAATTTAGGATAAACAGAAAGGAGGTATGTAACA
	--	--	--	---	---	---	---	---	---	GCCACCACCCACCCACAGCACACCTCCAAACCTCAGCCAGACAGGTTGTTACACAAGAGAGCCC
	--	--	--	---	---	---	---	---	---	TCAGGGCACAGAGAGAGTCTGGACACGTGGGAGTCAGCGTGTATCATCGGAGGCGCGGGGCAC
	--	--	--	---	---	---	---	---	---	ATGGCAGGGATGAGGGAAGACCAAGAGTCTCTGTTGGGCCCAAGTCTTAGACAGACAAAAACCTAG
	--	--	--	---	---	---	---	---	---	ACAATCACGTGGCTGGCT
	--	--	--	---	---	---	---	---	---	CTCTTCAGGAACCCAGCTCTTACCACACGACTATTGCTGCCGAGAGGTACACCCCGTAGA
	--	--	--	---	---	---	---	---	---	ACTTCTTCTAACTGTAATTTAGTTAAAGGAATCGAACTGGCTCTGAAGACATGGAGATACTGCCT
	--	--	--	---	---	---	---	---	---	AATCGACTGGCTTTCATTAGCTCTGTGAGTGTCTTCTTCTTCTGTTCTAGAACGTTTCTAG
	--	--	--	---	---	---	---	---	---	GACTGGCAGTTTAAGCTTTCACCTTAGGCTTCTGTATACCCATGCCC
	--	--	--	---	---	---	---	---	---	CCTTCTCATGCCAGATGGAATTCAGTCCCTTCCAGATCTGCCTAACCTGTGACAGTCTAAAGAGT
	--	--	--	---	---	---	---	---	---	CTGAGCCGTGGCTGGGAGGGCAGGACTAATCCAAATCTTACCCGACGCTTGCTCGCATACAGACG
	--	--	--	---	---	---	---	---	---	GACAGTGTGGTGGCAACATTGAAAGCCTCGTACC
	--	--	--	---	---	---	---	---	---	GGGAGTAAACITTTGGATTGGGAGATTTTCATTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACA
	--	--	--	---	---	---	---	---	---	GCCAGTGGAGACTGGAACACACACCATAGCCTATTTCGTAGCCATATTAAATGGTTTGTGCCCTACATT
	--	--	--	---	---	---	---	---	---	ATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTCCAAATCTCCATCTCCATCACCTTTGGGCTTGT
	--	--	--	---	---	---	---	---	---	CTACTTTGCCACAGATTATCTGTA
	--	--	--	---	---	---	---	---	---	ATGAAACATGGTCTTTTAAATTTATGATATGTTTATAGCTATCTTAAAGGGCTCTTTTTTTTA
	--	--	--	---	---	---	---	---	---	ATGCAGAAAGAGGGGAAAAAGAGCGAGCTGTGGTGACAGGTTTCTTCTCAAGGCTCATACAGA
	--	--	--	---	---	---	---	---	---	TTCTGAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAGTCTTATGAAATTATATCTT
	--	--	--	---	---	---	---	---	---	ACCTACAGACGTGGCTGGATGGTGTGTCCAAACCCGAGGAATCTGAGAGGAGAGCAGGGCTGGCTG
	--	--	--	---	---	---	---	---	---	CTGGAGAAGAGCGTGGCGGAGACCTTGAAGGCGT

ESTD-RDS	--	--	--	--	---	---	CCCGAGGAATCTGAGCGAGCGAGGGCTGGCTGCTGGAGAAGAGCGTGCCGGAGACCTGGAAGG CCTTTCTGGAGAGTGTGAAGAGCTGGCAAGGGCAACAGGTGAAGCGAGGGCGAGACGCAGG CCAGGCCACAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCAC CCAAGAAAGTGGATCTCCCCCTCATCCAACTCCGAAAGTCTGAA
ESTD- RYR1	--	--	--	--	---	---	CTTCGTGACGGGAGGTACGCTCTCCGGCTCTTTATGGACATATGGATGAGTGTCTGACCATTTCCC CTGCTGACAGTGTATGACAGCGCAGACTTGTCTACTATGAGAGGGAGCTGTGTGCACTCATGCCCGC TCCCTCTGAGGCTGGAGCCACTGAGATCAGCTGGAGTGGAGGCCAAGCTGCGCTGGGGCCAGCCACT CCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCCGAGG
ESTD- SPTB	--	--	--	--	---	---	TGAACACCTGTGTCCGGAGCCAGGTGTGTCTCTCCGGAGCCTGAGGAGTTTGTGTGTGTG CAGTCCCCCGCCACCTGCTGGTTGAGCCTGGACATACACCTTCACCTCTTGGCCCGGAGAAGAC ATTTACCCACTGGCCATGTCCCTGGCTGTGTGACACACCTCTGTGAAGACCCCAACCCCTGCCCTCC CCACCCAAAGCCAGTTTCTAGCAAGGGCAGGAC
ESTD- SSA1	--	--	--	--	---	---	TTCACTTTGTGGATTGTTCTTTGCTGTGCAGCACCTTTCAACATGATGTATCCCATTTGTCCAAG TTTGCTTTGGCTGCTGTGTGGGATATTTGAAAGAGATCTTGGCAGTCCCATGTCTCTAGAGAG TTTTCCCAATGTTTCTGTAATAGTTTCATAGTTTGAGGCCCTAGATTTAAGTCTTTAATCCATTTTG ATTGATTCTGTA
ESTD-TAT	--	--	--	--	---	---	AAATGGTCAGGACCCTGATCCACAAGAGTGTACCATTTTCATCAGGGCCATCAGTTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCATTCATCTTAAATGACTTGTGGGACAGGATCA ATTCTCTCAGCTAGAACGTTTGTACAACCTTTCTTCCAGTATGGATGGGATTATGATGGGGGG GAGAAGCAAAATTTAAATAGGACCCATGAGACACATCA
ESTD- THRB	--	--	--	--	---	---	TGCGGCTTTCTCCGGCAGGTAGACTTCTTACTGGCTGTGATTTCCAAAGAGAAAGAGTCCCAAG CACACGAAACAGAGTTGCAGATCCCATGAGGCCAGTCTCAAAATCACACAGGATCACTTCATCCA CACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCCCTGTAGATGGG
ESTD- TNFA	--	--	--	--	---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCCAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGAGGACGGGTTTCCAGCTCCAGGTCCTACACACAAATCAGTCAGTG GCCAGAGACCCCCCTCAGATCGGAGCAGGGAGGATGGGGGTATCCCTTGATGCTT GTGTGTCCCCAACTTTCCAAATCCCCGCCCGCGATGG
ESTD-TYR	--	--	--	--	---	---	TAGTGAAGTTTTCATCTCTGTCAGCTTCTGGATTCTTGTCCACCCGCAACAAGAGTCTATGC CAAGGCAGAAAGCTGGTGTCTCATGGCAAAATCAATGTCTCTCCAGATTCAGATCCCCCAAGCA GTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGGTCATAAATATTGATGTCGTAAACAT GGGTGTTGATCCATTTTCATTTGGCCATAGGTCCTATGGGGATGACA

ESTD- TYRP1	--	--	--	---	---	AGTAGTGGATGAAGCTAACCCAGCCCTCCTCACTGATCATCAATGCTATGCTGAAGAATATGAA AAATCCAGAAATCCTAAATCAGTCTGTGCTTAACAAATGCCCTACTCTCTTATGCAATAGTATCACA AACCACTGGTTGAATATAATAGATTGAGTTAATTAAGTATTTCTTTCACTTTATTAACCTCTCTTCT AATACAAGCATATGTTAGAAATTAAGTTCTAGGCATACCT
ESTD- VB12	--	--	---	---	---	TTCCCAAGGCCTCAATACAAGCTTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGGTACAGAGACAGGAACACCCAGTG ACTTGAGATGTCACCAGACTGAGAACCCCGTTATATGTAAGTCTGGTATCGACAAGACCCCGGGGCATG GGCTGAGGCTGATCCATTACTCATAT
ESTD-VWF	--	--	---	---	---	AGGTAGGAAAGCAAGAGATTGATTAGTGAAGGAGAGAATGGACCTACCTCCACACTGTCCTTTGG TCCCTAGAGTCTG
ESTD-WT1	--	--	---	---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTGCTGCAGGATGCTG CGACGTGTGCTGGAGTAGCCCCGACTCTTGACGGTGGCATCTGAGACCAGTGAGAAACGCCCTT CATGTGTGCTTACCCAGGCTGCAA
ESTD- s14544	--	--	---	---	---	TTGGGAAGTTAGAGCCCTATATTAATACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCTCAGTTCGCTGTGTGGGTAGATGCAGGATTATATGATCCCGTTAACCC TCT
EST71770 6	--	--	---	---	---	AGCACCACTCTCAGCTCAAGCCTCAGCACCAGATGCTGTTCTATAGGATGACGTGCTGTTTACAA CATCTCCTCCATGAAGAGCACAGAGAGTTATTTATCCTGAAGTCCGGATCTATGACTCAGGACAT ATAATGTACTGTGATTGTGAACAACAAGAGAAACCACTGCAGAGTACCAAGTGTGGTGGAAAGG AGTGCCAGTCCAGGGTGACACTGGACAAAGAGGCCATCCAAAG
EST52418 6	--	--	---	---	---	CAAATTACAGGGTCAACTGCTATGATGTGTTTGGAGCCCACTACCCCTTTGGTGGCTACAAGATGTCG GGGAGTGGCCGGAGTTGGCGAGTACGGCTGCAGGCATACACTAAAGTGAAACTGTGAGTGTGG CCCCTCTATTTGCCAGCCCCCAGGGACAGAGCTGATCCTTGAACCTCTTAAGTTCACATGGCCAGGA CCAGTGAGCAGCAACAGGCCAGGGCTGGCTTATAGCCTCCAGCCCAAGACCTGGCTGCAGACAT AAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCTGCTGCTGCCCGG GTCACCTG
EST13586 3	--	--	---	---	---	AGGCAGAAACTGGCCCCCATGCGGGGACGTGGAAGGCCACTTGAGCTTCTGGAGAAGGACCTGA GGGACAAAGGTCAACTCCTTCTTCAACACCTTCAAGGAGAAAGAGAGCCAGGACAAGACTCTCTCCCT CCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGCAGCAGGAGGAGCAGGAGGATGCAGATGCTGGCC CCTTTGGAGAGCTGAGCTGCCCTGGTGC
EST51976 7	--	--	---	---	---	

EST11458 6						CCACITTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGCTCATCTTGTCTCGAGTTTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTTACCATTTTCCACAGTGGT CCCATTAAACACATTCTATGAGCCAGGAGAGATTACGTATTCCTGCAAGCCGGCTATGTGTCC CGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852 8						CGGCTTCTCTCCAGGTATTGTCAGAAAGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCCACTCTCTACGGTACAGAAAGGAGATGCATGAACAGCA GGAACACGTGGAAAAGGCCTGTTTCCAGTGTAAAGGCATGCAAAAGGCCCTCCACAGGCTGCTATAAT ACAGCCCT
EST62448 0						ACCTGGTGTGCTGGGTGAACCTGGTCTCTTGGCATTCGCGCCCTCCTGGGGCCCGCTGG TCTCTCTGGTGTGGGTAGTCTCGAGTCAACGGTCTCTCTAGTGAAGCTGGTCTGATGCAACC CTGGGAACGATGGTCCCCAGGTGCGATGGTCAACCCGACACAAGGGAGAGCGCGGTTACCTGG CAATAT
EST36027 2						AGTGACTTCCAAAGGAATGGCTACCCAACTTGCCTTCATCGCGCTGCTGGCCAACTATGCCCTCTCAGA ACATCACCTACCCTGCAAGAACAGCATTGCATACATGGATGAGGAGACTGGAAACCTGAAAAAGG CTGTCACTTACAGGGCTCTAATGATGTTGAACCTTGTGCTGAGGGCAACAGCAGGTTCACTTACACT GTTCTGTAGATGGCTGCTTAAAGACAAATGAATGGGAAAGACAA
EST12274 0						CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTCCAAATAGAGCCCTACCAAAGTGTAT TACATAAAGAAGTCAAGTGGTTTACTCCTCATGACCAATATCTTCCCTCTTAGGATGAGGTGA TAGTAAATGACCGATGGGGTGCAGAACTGTTCCCTGTCAACCATGGAGGATACTATAACTGTGAAGATAA ATTCAAGCCACAGAGCTTGCCAGATC
EST76807 7						ATGCTAAGGGGATCGGACATGAAAGGACCTGTGAGCCGATTGCTCTATCTCCAGGGCCCTGTCTATC CAGCTCACTCATCAATGGGCCAGTCAGGCCAGGCACTGGGCTCCGAGGACTCACCACTGCCCCCT GCTGCCATGTGGACTGGTCAAGTTGAGGACTTCTTG
EST44438 3						GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGACGTCCT GCTCCGACCTAAGCGGAGCAGCCTCAAGAGCCGAGCGAGGTGGG
EST12839 3						TGCAAAACACACAAAATCTTCCAGATGCCCTATGGCTGTGGAGAGCAGAAATATGGTCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAGATCAAGTCCAAAGG CCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGAAACTTGAATGTTATTCAACTGG ATTTCCAGTAGGTTTCACTTACTTATGAATATATGATACTTAGCTTAG
EST54419 8						CTTCTGCCTAATTGAATGATATTGTTGCTGTGGGACCTGAGCACCTTTATGGCACAATGATCATA TTTTCTTGACCCCTACTTACAATCCTGGGAGATGATTTGGGTTAGCGTGGTGTGTTGTTGTTACTA TAGTCCAAAGTGAA

EST10398 2	--	--	---	---	---	TGCTGGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGATGTTACATTTGGGCTTGACTTCCAACACGGAAG CATTGTTTCTTCGGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTG
EST36751 7	--	--	---	---	---	CCAAAGTCGTTCAATTTAGCTTTCAGGTTTAACTCGATTACTTTTCTATTCAAATCTCTGTAAAA TTGAATATGAACATTAGTTTCTGATCTATGTTTCAAGTTAAACAG
EST40562	--	--	---	---	---	CACGTGGAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGATCTGTCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTCACTGGATGCATTATAACAAATATTTTACCTTTGAAAAAATAATG AAGGATTGACCTGCTCGCTCTGGAAGAGATATCCGTACCTGACGTTTGAACAATACAGAT GCCTCCCTTGTAGCAGTTTTCAGCCTCCTCTACCCCTA
EST18288 3	--	--	---	---	---	GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATTTGCTGCTGAGAA GATTGACAGGTTATGCAGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGACGGAGCCAGTGTGG ACAGCACCTGGCTTCAACACCTACGTCCACTTCCAAGGTAAAGCAACCTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST70523 3	--	--	---	---	---	TTCCGGCAGCCCCCATCTTGGACCCCTGGTCCCCCTCAGGGGCCACCCCGGCACTCACCCGCTCT CGCTCTCGGTAAATCCGGCGGGCGCGTCTTGAGCACATAGCTGGACCGTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCCCGGGCTTGCAGGGGCCAGCCCTGCAGAGAGAGGGGTCCCTGTGGT TGAGCTGAACACAGCTGTGGAGTGTCTCCACGCTG
EST58707 7	--	--	---	---	---	CAGTGATCTGGAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGGTTACAGGAGCTTT AAGTTACGATCTTTGGCTCACATGAAGGCCAAATTCGAGAGACCTAGAAGATACACGAGACCGA ATGATCAATGGACATTCAGCAGGAACCTTCAACGATACCTGTCTCTGGTAGGCCAGGTTTATAGCA CACTTGTCACCTACATTTCTGATTGGTGGACTCTTGTGCTAAGAACCTT
EST74167 6	--	--	---	---	---	AGACCATGAAGGAGTTGAAGGCTACAAATCGGAACCTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGGGGCACGGCTGTCCAAGGAGCTGCAGGCGCGCAGCCCGGCTGGCGCGGACATGGAGGA CGTCGGCGCGCTGGTGAGTACCGCGGCGAGTGCAGGCCATGCTCGGCCAGACACCCGAGGAGG TGCGGGTGCGCCTCGCTCCACCTGGCAAGCTGGTAAAGCGGCTCCTC
EST43211 8	--	--	---	---	---	CGCCTGGTGCAGTACCGCGGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGAGCTGCGGGTGCG CCTCGCCTCCACCTCGCAAGCTGCGTAAGCGGCTCTCCGCGATGCCGATGACCTGCAGAAAGCGC TGGCAGTGTACAGCGCGGGCGCGAGGGCGCCAGCGGCTCAGCGCCATCCGCGAGCGCGCTG GGGCCCCGTGTGGAACAGGGCGCGGTGCGGGGCCGCCACTGTGGGCTC
EST36770 4	--	--	---	---	---	TGTAGCCAAAGTCACTGCATCATCTTTGGCTGTGGCAGGCTTGGCCAGTTTCCAGCTATAATCC ATCGAAATGATTTTTCATTGAGAACACCAATATTACAGTTTGTCTTCCATTATGAGTCCCAAAAT TCAACCTCCGATAGGCTGGGCTGACCAAAATATACTGGGTTCTGTTTCTCTTCTGATCAT TCTTACAAGTTATCTCTATTGGAAAGGCCCTAAAGAAGGCTTATG

EST26021 1	---	---	---	---	TAATGTAAGCTCATCCACCAAGAAGCCTGCACCATGTTTGGGTTGAGTGACATGTTGCAAAACCTGT CCATAAAGTAATTTTGTGAAAGAAGGAGCAAGAGAACATTCCTCTGACGACATTCACCTACCAATGA GCATTAGCTACTTTTCAGAAATTGAAGGAGAAATGCATTATGTGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTTCTTCTTTGCAACAAGACAAAGCAAGCC
EST51212 0	---	---	---	---	ATCCTGAGCTCGCCAATAAGCTTCTTGGTTCTACTTCTTCTTCCACAAGCCCCCAATTTACATTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCTTTGTGCTCCACTCAATACAAAAGGCCCTCTCT ACATCT
EST20118 2	---	---	---	---	GTTCGGAATCCTCCTCTGAAAGTGGCCGGTTTAACTCTGCTCATGACGCTGCGGCTGTGGTCCAGCT GAGGTGAGGGCTTGAAGCTGGGAGTGGGTTTAGGGACGCGGCTCTCTGCGTGATCCTTAAGCTCT GAGAGCAACCTCCCTTGAAGCTGGGAGTGGGTTTAGGGACGCGGCTCTCTGCGTGATCCTTAAGCT CTGAGA
EST53018 6	---	---	---	---	ACAATCCAGGTCACACATTCAGAAGAGGGGGTGGTGAGTGAGCCTGGGTAGGTCCAGTAATCCA AGGATTGAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC
EST68787 5	---	---	---	---	CTTCTATGGGATTTGACTTTATTTCTCCATTGCTTACCCTTTACAGGTGTTAATATAGTGAAGAAG GAAGCTTGAGCTCATGACAATTTGAAGCTGACAAATACACAAGAGGAAATAAATTCACAGTCAA AGAATCAAGCACTTTTCGAACATTTGAAGTTGTTTGAAGTTGCTGACCTTTAATACAACTAG CAGACGGAAGTGAAGTCAAGGTAAGAAAT
EST34088 2	---	---	---	---	GTGGGGCAACAGTGGGAGAGAGGGGCCAGGGGTATAAAGGGGCCACAGAGACCGGCTCAAGG ATCCCAAGGCCCACTCCCGAACCACCTCAGGGTCTGTGGACAGCTCACCTAGCTGCAATGGCTACA GGTAAG
EST37382 5	---	---	---	---	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCCACCCCCCTCTTCTCTCCCTTGGGA CTTTGAGTCAAAATGGCCTGGACTTGAGTCCCTGAACCAAGCAAGAGAAAAGAGGACCCCAAGAAAT CACAGGTGGGCACGTCGCGTCTACCGCCATCTCCCTTCTCACGGGAATTTTCAGGGTAAACT
EST74082	---	---	---	---	TCAGGGTGGCTGGACCCCAAGCCCAAGCTCTGACGAGGAGACGTGGCTGGGCTCGTGAAGCATG TGGGGTGAGCCCAAGGGGCCCAAGGCAAGGCACTGGCTTCAAGCTGCTCAGCCCTGCTGCTGAC CCAGATCACTGTCTTCTGCCATGGCCCTGTGGATGCGCTCTGCTGCGGCTGCTGGCCCTC TGGGGACCTGACCCAGCCGAGCCTTTGTGAACCAACACCTGTGCG
EST45311 0	---	---	---	---	GCCTCTCTCTTCCAAATCTGTCCCTATAGTTTCTCTATTAAGTGAACATGCAATCTTTTAGT GGATAGATGCACAAACACACAGCCATTATGGGAAGGATCCACGTGTGGCCATATTGTAAACA CATTTTCTGCAAAATCACCTCTTTCATTTAACAGCCCTTATCAATGGCCCTTTTCTTTTCAGTAGTA CATACACATCTGTGTCAATTTGTGAAT

EST65258 8	--	---	---	---	---	TGCCCCATCAGCGGGCGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACCAAGAAAT CCAGTTATTTCCACCCTCAAATGACAGCCATGGCCGGCGGGTCTTCTGGGGCTCGTCGGGGGG ACAGCTCCACTCTGACTGGCAGACTCTTTCATGGAGACTTGAGGAGGAGGGCTTGAGGTTGGTGAG GTTAGGTGCGTGTTCCTGTGCAAGTCAGGACATCAGTCTGATTAAA
EST38216 3	--	---	---	---	---	ATGCAGGATGAAGGTGGACAGGGAGGAGAGGGCCAACTGTATCCAGGGCCTGCAGATGTCGCTG GACTATGGGTTTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782	--	---	---	---	---	ATACTAGTACAAGTGGTAATTTTGATACATTACACTAAATTAATAGCAATTTGTTTAGCATTACCTAA TTTTTTCTGCTCCATGCAGACTGTAGCTTTACCTTAAATGCTTATTTAAATGACAGTGGAAAG TTTTTTTCTCGAAGTGCCAGTATCCAGAGTTTGGTTTTGAACTAGCAATGCCTGTGAAAAA GAACTGAATACCTAAGATTCTGTCTGGGGTTTTGGTGCATGCA
EST35879 9	--	---	---	---	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCCTCCAACTTTGTGCGTTCCACCGATG GAACTGCCGGCAAATCCTGACACGTGTGCCAGGGCTGTACCCAAATAGGTGAACATGGCTTCGAG AGAGTTGAACAGATTCTCGAAGACAGCAGCGGGATGGGGCAGGAGAGAGCTGCCTGGATGAA
EST68308 5	--	---	---	---	---	GGAAGAGATTTAAGAAGCTTGATTTGGACAATCTGGTCTTTGAGTGTGGAAGAGTTTCATGTCTCT GCTGAGTTACACAGAACTCTTTAGTACAGCAGTAATAGATATATTCGACACAGATGGGAATGGA GAAGTAGACTTTAAAGGTAAGAAAGTAGTTATTTTTTA
EST54045 6	--	---	---	---	---	GGAATATTAATAATTTTAAATACCTCCATTTTGCTTATCCTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTTATGATTGTGATGTGGCAATTTGTTCTTACAAAATCGGATGGGAAATCT GTTAAGTAAGTACTGTTTGCCTTGGAAATGGATTTTAAATGTTGACTTTATCAT
EST52908 0	--	---	---	---	---	ATCACAGGTCTCTGGTCTCTGCCATCATTTCTCTGGGAGAGATGGATGGTGGTCTGCAAGCCCTTTGG CAATGTGAGATTGATG
EST19590	--	---	---	---	---	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAGATGACATTGATGAGTGAAGATGTCGGCTCAGGAT GCCGGAAATGAC
EST76136	--	---	---	---	---	TGAAGCTTCTGCCAGCTTGCAATTTCTAGGAGAACCCGGCTCATACCTTTATCTATAGCCTTCCCC TAGGTCIT
EST58607 0	--	---	---	---	---	CTCTGGATGGGTTACAGGTGGCAGGCACAGCCAGTCCATCTGTAGTCATCATAGTTGTGGCTCC CAAGTTGCTCTCCTCACTGAGAACAAAGGACAGCCACATGGCGGGATGGCCGGGGAGTTCTGGT TGCGGCCACGGCTGTGCCCTCGTTGTGAACGGTAGCCTTTGCGGTTGCGATGCCTAAACCTTTGTTCT TGGCCAAGGAGGGCGGGTGCCATGCCCTGAGATGTAGATGCGGCC
Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer 6=SNP Reverse Primer 7=Sequence						

EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that
5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the
10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,
or a portion thereof which includes a polymorphic site,
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is
biallelic.
8. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is the reference base
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is an alternative form
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a
20 segment of a fragment shown in the Table, column 7 or
its complement.
11. The allele-specific oligonucleotide of claim 10 that is
a probe.

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12. The allele-specific oligonucleotide of claim 10,
wherein a central position of the probe aligns with the
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is
5 a primer.
14. The allele-specific oligonucleotide of claim 13,
wherein the 3' end of the primer aligns with the
polymorphic site of the fragment.
- 15 10 15. The allele-specific oligonucleotide of Claim 10, which
is selected from the group consisting of the nucleotide
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which
is selected from the group consisting of the nucleotide
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the
Table, column 7 or the complement thereof, wherein the
polymorphic site within the sequence or complement is
occupied by a base other than the reference base shown
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising
obtaining the nucleic acid from an individual; and
determining a base occupying any one of the polymorphic
sites shown in the Table.
- 25 19. The method of claim 18, wherein the determining
comprises determining a set of bases occupying a set of
the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method
5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.

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